

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION  
International Bureau

## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>C12N 15/12, C07K 14/47, 16/18, C12Q 1/68</b>		<b>A2</b>	(11) International Publication Number: <b>WO 99/33982</b>
			(43) International Publication Date: <b>8 July 1999 (08.07.99)</b>
(21) International Application Number: <b>PCT/US98/27610</b> (22) International Filing Date: <b>22 December 1998 (22.12.98)</b> (30) Priority Data: 60/068,755           23 December 1997 (23.12.97)   US 60/080,664           3 April 1998 (03.04.98)       US 60/105,234           21 October 1998 (21.10.98)   US 60/105,877           27 October 1998 (27.10.98)   US 09/217,471           21 December 1998 (21.12.98)   US (71) Applicants: <b>CHIRON CORPORATION [US/US]; 4560 Horton Street - R440, Emeryville, CA 94608 (US). HYSEQ INC. [US/US]; 675 Almanor Avenue, Sunnyvale, CA 94086 (US).</b> (72) Inventors: <b>WILLIAMS, Lewis, T.; 3 Miroflores, Tiburon, CA 94920 (US). ESCOBEDO, Jaime; 1470 Lavorna Road, Alamo, CA 94507 (US). INNIS, Michael, A.; 315 Constance Place, Moraga, CA 94556 (US). GARCIA, Pablo, Dominguez; 882 Chenery Street, San Francisco, CA 94131 (US). SUDDUTH-KLINGER, Julie; 280 Lexington Road, Kensington, CA 94707 (US). REINHARD, Christoph; 1633 Clinton Avenue, Alameda, CA 94501 (US). GIESE, Klaus; Chausseetrase 92, D-10115 Berlin (DE). RANDAZZO, Filippo; Apt. 403, 690 Chestnut Street, San Francisco, CA 94133 (US). KENNEDY, Giulia, C.; 360 Castenada Av-</b>		enue, San Francisco, CA 94116 (US). POT, David; 1565 5th Avenue #102, San Francisco, CA 94112 (US). KASSAM, Altaf; 2659 Harold Street, Oakland, CA 94602 (US). LAMSON, George; 232 Sandringham Drive, Moraga, CA 94556 (US). DRMANAC, Radoje; 850 East Greenwich Place, Palo Alto, CA 94303 (US). CRKVENJAKOV, Radomir; 762 Haverhill Drive, Sunnyvale, CA 94068 (US). DICKSON, Mark; 1411 Gabilan Drive #B, Hollister, CA 95025 (US). DRMANAC, Snezana; 850 East Greenwich Place, Palo Alto, CA 94303 (US). LABAT, Ivan; 140 Acalanes Drive, Sunnyvale, CA 94086 (US). LESHKOWITZ, Dena; 678 Durshire Way, Sunnyvale, CA 94087 (US). KITA, David; 899 Bounty Drive, Foster City, CA 94404 (US). GARCIA, Veronica; Apartment 412, 396 Ano Nuevo, Sunnyvale, CA 94086 (US). JONES, Lee, William; 396 Ano Nuevo #412, Sunnyvale, CA 94086 (US). STACHE-CRAIN, Birgit; 345 South Mary Avenue, Sunnyvale, CA 94086 (US). (74) Agent: <b>BLACKBURN, Robert, P.; Chiron Corporation, P.O. Box 8097, Emeryville, CA 94662-8097 (US).</b> (81) Designated States: <b>AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).</b>	
		<b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>	
(54) Title: <b>HUMAN GENES AND GENE EXPRESSION PRODUCTS I</b>			
(57) Abstract			
<p>This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, e.g., these genes and proteins, including probes, antisense constructs, and antibodies.</p>			

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

**NOVEL HUMAN GENES AND GENE EXPRESSION PRODUCTS I**Cross-References to Related Applications

This application is a continuation-in-part of U.S. provisional patent application serial  
5 no. 60/068,755, filed December 23, 1997, and of U.S. provisional patent application serial  
no. 60/080,664, filed April 3, 1998, and of U.S. provisional patent application serial no.  
60/105,234, filed October 21, 1998, each of which applications are incorporated herein by  
reference.

10 Field of the Invention

The present invention relates to novel polynucleotides, particularly to novel  
polynucleotides of human origin that are expressed in a selected cell type, are differentially  
expressed in one cell type relative to another cell type (*e.g.*, in cancerous cells, or in cells of a  
specific tissue origin) and/or share homology to polynucleotides encoding a gene product  
15 having an identified functional domain and/or activity.

Background of the Invention

Identification of novel polynucleotides, particularly those that encode an expressed  
gene product, is important in the advancement of drug discovery, diagnostic technologies,  
20 and the understanding of the progression and nature of complex diseases such as cancer.  
Identification of genes expressed in different cell types isolated from sources that differ in  
disease state or stage, developmental stage, exposure to various environmental factors, the  
tissue of origin, the species from which the tissue was isolated, and the like is key to  
identifying the genetic factors that are responsible for the phenotypes associated with these  
25 various differences

This invention provides novel human polynucleotides, the polypeptides encoded by  
these polynucleotides, and the genes and proteins corresponding to these novel  
polynucleotides.

30 Summary of the Invention

This invention relates to novel human polynucleotides and variants thereof, their  
encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides

and to proteins expressed by the genes. The invention also relates to diagnostic and therapeutic agents employing such novel human polynucleotides, their corresponding genes or gene products, *e.g.*, these genes and proteins, including probes, antisense constructs, and antibodies.

5                   Accordingly, in one embodiment, the present invention features a library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NOS:1-844. In related aspects, the invention features a library provided on a nucleic acid array, or in a computer-readable format.

                  In one embodiment, the library is comprises a differentially expressed polynucleotide  
10   comprising a sequence selected from the group consisting of SEQ ID NOS:9, 39, 42, 52, 62, 74, 119, 172, 317, and 379. In specific related embodiments, the library comprises: 1) a polynucleotide that is differentially expressed in a human breast cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214,  
15   219, 223, 258, 298, 317, 338, 379, 384, 386, and 388; 2) a polynucleotide differentially expressed in a human colon cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374; or 3) a polynucleotide differentially expressed in a human lung cancer cell, where the polynucleotide comprises a sequence selected from the group  
20   consisting of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

                  In another aspect, the invention features an isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOS:1-844 or a degenerate variant thereof. In related aspects, the  
25   invention features recombinant host cells and vectors comprising the polynucleotides of the invention, as well as isolated polypeptides encoded by the polynucleotides of the invention and antibodies that specifically bind such polypeptides.

                  In one embodiment, the invention features an isolated polynucleotide comprising a sequence encoding a polypeptide of a protein family selected from the group consisting of:  
30   4 transmembrane segments integral membrane proteins, 7 transmembrane receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases,



GATA family of transcription factors, G-protein alpha subunit, phorbol esters/diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, protein tyrosine phosphatase, trypsin, wnt family of developmental signaling proteins, and WW/rsp5/WWP domain containing proteins. In a specific related embodiment, the invention features a

5 polynucleotide comprising a sequence of one of SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, 341, 63, 116, 134, 136, 151, 384, 404, 308, 213, 367, 188, 251, 202, 315, 367, 397, 256, 382, 169, 23, 291, 324, 330, 341, 353, 188, 379, and 395.

In another embodiment, the invention features a polynucleotide comprising a sequence encoding a polypeptide having a functional domain selected from the group  
10 consisting of: Ank repeat, basic region plus leucine zipper transcription factors, bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease domain. In a specific related embodiment, the invention features a polynucleotide comprising a sequence of one of SEQ ID NOS: 116, 251, 374, 97, 136, 242, 379, 306, 386, 18, 335, 61, 306, 386, 322, 306, and  
15 395.

In another aspect, the invention features a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, where the method comprises the step of detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded  
20 by a gene corresponding to a sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, 388, 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, 374, 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400. Detection of the differentially expressed gene product is correlated with a  
25 cancerous state of the cell from which the test sample was derived. In one embodiment, the detecting is by hybridization of the test sample to a reference array, wherein the reference array comprises an identifying sequence of at least one of SEQ ID NOS: 1-844.

In one embodiment of the method of the invention, the cell is a breast tissue derived cell, and the differentially expressed gene product is encoded by a gene corresponding to a  
30 sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123,

144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

In another embodiment of the method of the invention, the cell is a colon tissue derived cell, and differentially expressed gene product is encoded by a gene corresponding to  
5 a sequence of at least one of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

In yet another embodiment of the method of the invention, the cell is a lung tissue derived cell, and differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260,  
10 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

Other aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

#### Detailed Description of the Invention

15 The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA and genes corresponding to these sequences, and to polypeptides and proteins encoded by these polynucleotides and genes.

Also included are polynucleotides that encode polypeptides and proteins encoded by the polynucleotides of the Sequence Listing. The various polynucleotides that can encode  
20 these polypeptides and proteins differ because of the degeneracy of the genetic code, in that most amino acids are encoded by more than one triplet codon. The identity of such codons is well-known in this art, and this information can be used for the construction of the polynucleotides within the scope of the invention.

Polynucleotides encoding polypeptides and proteins that are variants of the  
25 polypeptides and proteins encoded by the polynucleotides and related cDNA and genes are also within the scope of the invention. The variants differ from wild type protein in having one or more amino acid substitutions that either enhance, add, or diminish a biological activity of the wild type protein. Once the amino acid change is selected, a polynucleotide encoding that variant is constructed according to the invention.

30 The following detailed description describes the polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene product, expression of these polynucleotides and genes, identification of

structural motifs of the polynucleotides and genes, identification of the function of a gene product encoded by a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the  
5 polynucleotides and their encoded gene products for therapeutic and diagnostic purposes.

#### I. Polynucleotide Compositions

The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID  
10 NOS:1-844; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*,  
15 a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here.

20 The invention features polynucleotides that are expressed in cells of human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid compositions of the invention of particular interest comprise a sequence set forth in any one of SEQ ID NOS:1-844 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about  
25 100 nt in length, that uniquely identifies a polynucleotide sequence, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOS:1-844.

30 The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by

hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate).

- 5 Hybridization methods and conditions are well known in the art, see, *e.g.*, U.S. Patent No. 5,707,829. Nucleic acids that are substantially identical to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences (SEQ ID NOS:1-844) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate
- 10 homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice, canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

Preferably, hybridization is performed using at least 15 contiguous nucleotides of at least one of SEQ ID NOS: 1-844. That is, when at least 15 contiguous nucleotides of one of

15 the disclosed SEQ ID NOs. is used as a probe, the probe will preferentially hybridize with a gene or mRNA (of the biological material) comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids of the biological material that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. will hybridize with the same gene or mRNA if the cDNA from which they were derived

20 corresponds to one mRNA. Probes of more than 15 nucleotides can be used, but 15 nucleotides represents enough sequence for unique identification.

The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants, *etc.*). Variants of the polynucleotides of the invention are identified by hybridization of putative variants with

25 nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% base pair mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2%

30 base pair mismatches, as well as a single base-pair mismatch.

The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOS:1-844, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats, canines, felines, bovines, ovines, equines, yeast, nematodes, etc. Between mammalian species, *e.g.*, human and mouse, homologs have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as BLAST, described in Altschul *et al.*, *J. Mol. Biol.* (1990) 215:403-10.

In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject differentially expressed polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nucleotides selected from the polynucleotide sequences as shown in SEQ ID NOS:1-844. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of at least twelve nucleotides selected from the group consisting of the polynucleotides shown in SEQ ID NOS:1-844.

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOS:1-844. The probes are preferably at least about 12, 15, 16, 18, 20, 22, 24, or 25 nucleotide fragment of a corresponding contiguous sequence of SEQ ID NOS:1-844, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOS:1-844. More preferably,

probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence  
5 produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are  
10 typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule. They can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. They can be regulated by their  
15 own or by other regulatory sequences, as is known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques which are available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation,  
20 gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (*e.g.*, extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as  
25 triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the polynucleotide sequences as shown in SEQ ID NOS:1-844 or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA and Full-Length Human Gene and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOS:1-844, or a portion thereof comprising at least 12, 15, 18, or 20 nucleotides, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in U.S. Patent No.

5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent.

Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. Alternatively, many cDNA libraries are available commercially. (Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY). The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. Where the provided polynucleotides are isolated from cDNA libraries, the libraries are prepared from mRNA of human colon cells, more preferably, human colon cancer cells, even more preferably, from a highly metastatic colon cell, Km12L4-A.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from SEQ ID NOS:1-844. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments



are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by  
5 detection of released monoribonucleotides. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (*PCR Protocols: A Guide to Methods and Applications*, (1990) Academic Press, Inc.) is performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to  
10 the isolation of full-length cDNAs. Briefly, the provided polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large  
15 segments of a genome, such as P1 or YAC, as described in detail in Sambrook *et al.*, 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook *et al.*, such that adjacent and overlapping fragments of genomic  
20 DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed on a number of cell types to  
25 determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook *et al.*, *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

30 PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length

cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods. Gene trapping entails inserting a member of a cDNA library into a vector. The vector then is denatured to produce single stranded molecules. Next, a substrate-bound probe, such a biotinylated oligo, is used to trap cDNA inserts of interest.

- 5 Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence is based on the polynucleotide sequences of the invention. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber *et al.*, WO 95/04745 and
- 10 Gruber *et al.*, U.S. Pat. No. 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

- “Rapid amplification of cDNA ends,” or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs are ligated to an oligonucleotide linker, and amplified by PCR using two primers. One primer is based on sequence from the
- 15 instant polynucleotides, for which full length sequence is desired, and a second primer comprises sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this methods is reported in WO 97/19110. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) 15:890-893; Edwards *et al.*, *Nuc. Acids*
- 20 *Res.* (1991) 19:5227-5232). When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

- Another PCR-based method generates full-length cDNA library with anchored ends
- 25 without needing specific knowledge of the cDNA sequence. The method uses lock-docking primers (I-VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT). This method is described in WO 96/40998.

- 30 The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the “TATA” box, a sequence such as

TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is highly expressed or differentially  
5 expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook *et al.*, 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on  
10 optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 15 nucleotides (corresponding to at least 15 contiguous nucleotides of  
15 one of SEQ ID NOS: 1-844) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOS: 1-844; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an  
20 expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b); and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

The sequence of a nucleic acid comprising at least 15 contiguous nucleotides of at least any one of SEQ ID NOS: 1-844, preferably the entire sequence of at least any one of  
25 SEQ ID NOS: 1-844, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired. Where the entire sequence of any one of SEQ ID NOS: 1-844 is within the nucleic  
30 acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOS: 1-844.

## II. Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

The provided polynucleotide (*e.g.*, a polynucleotide having a sequence of one of SEQ ID NOS:1-844), the corresponding cDNA, or the full-length gene is used to express a partial  
5 or complete gene product.

Constructs of polynucleotides having sequences of SEQ ID NOS:1-844 can be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, *e.g.*, Stemmer *et al.*, *Gene (Amsterdam)* (1995) 164(1):49-53. In this method, assembly PCR (the synthesis of long  
10 DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process. For example, a 1.1-kb fragment containing the TEM-1 beta-lactamase-encoding gene (*bla*) can be assembled in a single  
15 reaction from a total of 56 oligos, each 40 nucleotides (nt) in length. The synthetic gene can be PCR amplified and cloned in a vector containing the tetracycline-resistance gene (Tc-R) as the sole selectable marker. Without relying on ampicillin (Ap) selection, 76% of the Tc-R colonies were Ap-R, making this approach a general method for the rapid and cost-effective synthesis of any gene.

Appropriate polynucleotide constructs are purified using standard recombinant DNA  
20 techniques as described in, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a  
25 polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Suitable vectors and host cells are described in U.S. Patent No. 5,654,173.

Bacteria. Expression systems in bacteria include those described in Chang *et al.*, *Nature* (1978) 275:615; Goeddel *et al.*, *Nature* (1979) 281:544; Goeddel *et al.*, *Nucleic Acids  
30 Res.* (1980) 8:4057; EP 0 036,776; U.S. Patent No. 4,551,433; DeBoer *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:21-25; and Siebenlist *et al.*, *Cell* (1980) 20:269.

Yeast. Expression systems in yeast include those described in Hinnen *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1978) 75:1929; Ito *et al.*, *J. Bacteriol.* (1983) 153:163; Kurtz *et al.*, *Mol. Cell. Biol.* (1986) 6:142; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Gleeson *et al.*, *J. Gen. Microbiol.* (1986) 132:3459; Roggenkamp *et al.*, *Mol. Gen. Genet.* (1986) 202:302; Das *et al.*, *J. Bacteriol.* (1984) 158:1165; De Louvencourt *et al.*, *J. Bacteriol.* (1983) 154:737; Van den Berg *et al.*, *Bio/Technology* (1990) 8:135; Kunze *et al.*, *J. Basic Microbiol.* (1985) 25:141; Cregg *et al.*, *Mol. Cell. Biol.* (1985) 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555; Beach and Nurse, *Nature* (1981) 300:706; Davidow *et al.*, *Curr. Genet.* (1985) 10:380; Gaillardin *et al.*, *Curr. Genet.* (1985) 10:49; Ballance *et al.*, *Biochem. Biophys. Res. Commun.* (1983) 112:284-289; Tilburn *et al.*, *Gene* (1983) 26:205-221; Yelton *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1984) 81:1470-1474; Kelly and Hynes, *EMBO J.* (1985) 4:475479; EP 0 244,234; and WO 91/00357.

Insect Cells. Expression of heterologous genes in insects is accomplished as described in U.S. Patent No. 4,745,051; Friesen *et al.*, "The Regulation of Baculovirus Gene Expression", in: *The Molecular Biology Of Baculoviruses* (1986) (W. Doerfler, ed.); EP 0 127,839; EP 0 155,476; and Vlak *et al.*, *J. Gen. Virol.* (1988) 69:765-776; Miller *et al.*, *Ann. Rev. Microbiol.* (1988) 42:177; Carbonell *et al.*, *Gene* (1988) 73:409; Maeda *et al.*, *Nature* (1985) 315:592-594; Lebacqz-Verheyden *et al.*, *Mol. Cell. Biol.* (1988) 8:3129; Smith *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1985) 82:8844; Miyajima *et al.*, *Gene* (1987) 58:273; and Martin *et al.*, *DNA* (1988) 7:99. Numerous baculoviral strains and variants and corresponding permissive insect host cells from hosts are described in Luckow *et al.*, *Bio/Technology* (1988) 6:47-55, Miller *et al.*, *Generic Engineering* (1986) 8:277-279, and Maeda *et al.*, *Nature* (1985) 315:592-594.

Mammalian Cells. Mammalian expression is accomplished as described in Dijkema *et al.*, *EMBO J.* (1985) 4:761, Gorman *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1982) 79:6777, Boshart *et al.*, *Cell* (1985) 41:521 and U.S. Patent No. 4,399,216. Other features of mammalian expression are facilitated as described in Ham and Wallace, *Meth. Enz.* (1979) 58:44, Barnes and Sato, *Anal. Biochem.* (1980) 102:255, U.S. Patent Nos. 4,767,704, 4,657,866, 4,927,762, 4,560,655, WO 90/103430, WO 87/00195, and U.S. RE 30,985.

Polynucleotide molecules comprising a polynucleotide sequence provided herein propagated by placing the molecule in a vector. Viral and non-viral vectors are used,

including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially. The partial or full-length polynucleotide is inserted into a vector typically by means of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence can be inserted by homologous recombination in vivo. Typically this is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence. Regions of homology are added by ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion of the desired nucleotide sequence, for example.

The polynucleotides set forth in SEQ ID NOS:1-844 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in U.S. Patent No. 5,641,670.

### III. Identification of Functional and Structural Motifs of Novel Genes

#### A. Screening Polynucleotide Sequences and Amino Acid Sequences Against Publicly Available Databases

5           Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. For example, sequences that show similarity with a chemokine sequence can exhibit chemokine activities. Also, sequences exhibiting similarity  
10 with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

          The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a  
15 tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides..

          Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient  
20 (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular Sequence Analysis" *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.  
25 Databases include Genbank, EMBL, and DNA Database of Japan (DDBJ).

          Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST, available over the world wide web at <http://www.ncbi.nlm.nih.gov/BLAST/>. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned  
30 subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, *supra*. Preferably, an alignment program that permits gaps in the sequence is

utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* (1997) 70: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a

5 MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases.

10 Results of individual and query sequence alignments can be divided into three categories, high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure. Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence

15 identity, and p value.

The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment, *e.g.*, contiguous region of the individual sequence that contains the greatest number of residues that are identical to the residues of the corresponding region of the aligned query sequence.

20 This number is divided by the total residue length of the query sequence to calculate a percentage. For example, a query sequence of 20 amino acid residues might be aligned with a 20 amino acid region of an individual sequence. The individual sequence might be identical to amino acid residues 5, 9-15, and 17-19 of the query sequence. The region of strongest alignment is thus the region stretching from residue 9-19, an 11 amino acid stretch.

25 The percentage of the alignment region length is: 11 (length of the region of strongest alignment) divided by (query sequence length) 20 or 55%.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequences found in the region of strongest

30 alignment. Thus, the percent identity in the example above would be 10 matches divided by 11 amino acids, or approximately, 90.9%



P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1990) 87:2264 and Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1993) 90. The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach  
5 described in Altschul *et al.*, *Nat. Genet.* (1994) 6:119. Alignment programs such as BLAST program can calculate the p value.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence  
10 also can indicate a similarity between the query and profile sequences. The boundaries of the region where the sequences align can be determined according to Doolittle, *supra*; BLAST or FAST programs; or by determining the area where sequence identity is highest.

High Similarity. In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length  
15 query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about  
20 78%; even more typically; at least about 80% sequence identity. Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p  
25 value is less than or equal to about  $10^{-2}$ ; more usually; less than or equal to about  $10^{-3}$ ; even more usually; less than or equal to about  $10^{-4}$ . More typically, the p value is no more than about  $10^{-5}$ ; more typically; no more than or equal to about  $10^{-10}$ ; even more typically; no more than or equal to about  $10^{-15}$  for the query sequence to be considered high similarity.

Weak Similarity. In general, where alignment results considered to be of weak  
30 similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of

alignment is, typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically, at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues.

- 5 Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically, at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

- 10 If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about  $10^{-2}$ ; more usually; less than or equal to about  $10^{-3}$ ; even more usually; less than or equal to about  $10^{-4}$ . More typically, the p value is no more than about  $10^{-5}$ ; more usually; no more than or equal to about  $10^{-10}$ ; even more usually; no more than or equal to about  $10^{-15}$  for the query sequence to be considered weak similarity.

- 15 Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even  
20 more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably,  
25 120 residues in length; even more preferably, 150 amino acid residues in length.

- Determining Activity from Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the  
30 polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the activity of the gene products (*e.g.*,

polypeptides) encoded by the provided polynucleotides or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney *et al.*, *Nucl. Acid Res.* (1996) 24(14): 2730-2739. MSAs of some protein families and motifs are publicly available. For example, <http://genome.wustl.edu/Pfam/> includes MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer *et al.*, *Proteins* (1997) 28: 405-420. Other sources over the world wide web include the site at <http://www.embl-heidelberg.de/argos/ali/ali.html>; alternatively, a message can be sent to [ALI@EMBL-HEIDELBERG.DE](mailto:ALI@EMBL-HEIDELBERG.DE) for the information. A brief description of these MSAs is reported in Pascarella *et al.*, *Prot. Eng.* (1996) 9(3):249-251. Techniques for building profiles from MSAs are described in Sonnhammer *et al.*, *supra*; Birney *et al.*, *supra*; and "Computer Methods for Macromolecular Sequence Analysis," *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile. The program is described in Birney *et al.*, *supra*. Other techniques to compare the sequence and profile are described in Sonnhammer *et al.*, *supra* and Doolittle, *supra*.

Next, methods described by Feng *et al.*, *J. Mol. Evol.* (1987) 25:351 and Higgins *et al.*, *CABIOS* (1989) 5:151 can be used to align the query sequence with the members of a family or motif, also known as a MSA. Computer programs, such as PILEUP, can be used. See Feng *et al.*, *infra*. In general, the following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak  
5 similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

10 Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. For example, most chemokines contain four conserved cysteines. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine,  
15 or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about  
20 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular  
25 positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

30 A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually,

at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically; at least about 55%.

5           B.     Screening Polynucleotide and Amino Acid Sequences Against Protein Profiles

          The identify and function of the gene that correlates to a polynucleotide described herein can be determined by screening the polynucleotides or their corresponding amino acid sequences against profiles of protein families. Such profiles focus on common structural  
10    motifs among proteins of each family. Publicly available profiles are described above in Section IVA. Additional or alternative profiles are described below.

          In comparing a novel polynucleotide with known sequences, several alignment tools are available. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) 25:351. Another method, GAP, uses the  
15    alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) 48:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith *et al.*, *Adv. Appl. Math.* (1981) 2:482. Exemplary protein profiles are provided below and in the examples.

20           Chemokines. Chemokines are a family of proteins that have been implicated in lymphocyte trafficking, inflammatory diseases, angiogenesis, hematopoiesis, and viral infection. See, for example, Rollins, *Blood* (1997) 90(3):909-928, and Wells *et al.*, *J. Leuk. Biol.* (1997) 61:545-550. U.S. Patent No. 5,605,817 discloses DNA encoding a chemokine expressed in fetal spleen. U.S. Patent No. 5,656,724 discloses chemokine-like proteins and  
25    methods of use. U.S. Patent No. 5,602,008 discloses DNA encoding a chemokine expressed by liver.

          Chemokine mutants are polypeptides having an amino acid sequence that possesses at least one amino acid substitution, addition, or deletion as compared to native chemokines. Fragments possess the same amino acid sequence of the native chemokines; mutants can  
30    lack the amino and/or carboxyl terminal sequences. Fusions are mutants, fragments, or native chemokines that also include amino and/or carboxyl terminal amino acid extensions.

The number or type of the amino acid changes is not critical, nor is the length or number of the amino acid deletions, or amino acid extensions that are incorporated in the chemokines as compared to the native chemokine amino acid sequences. A polynucleotide encoding one of these variant polypeptides will retain at least about 80% amino acid identity with at least one known chemokine. Preferably, these polypeptides will retain at least about 85% amino acid sequence identity, more preferably, at least about 90%; even more preferably, at least about 95%. In addition, the variants exhibit at least 80%; preferably about 90%; more preferably about 95% of at least one activity exhibited by a native chemokine, which includes immunological, biological, receptor binding, and signal transduction functions.

Assays for chemotaxis relating to neutrophils are described in Walz *et al.*, *Biochem. Biophys. Res. Commun.* (1987) 149:755, Yoshimura *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1987) 84:9233, and Schroder *et al.*, *J. Immunol.* (1987) 139:3474; to lymphocytes, Larsen *et al.*, *Science* (1989) 243:1464, Carr *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1994) 91:3652; to tumor-infiltrating lymphocytes, Liao *et al.*, *J. Exp. Med.* (1995) 182:1301; to hematopoietic progenitors, Aiuti *et al.*, *J. Exp. Med.* (1997) 185:111; to monocytes, Valente *et al.*, *Biochem.* (1988) 27:4162; and to natural killer cells, Loetscher *et al.*, *J. Immunol.* (1996) 156:322, and Allavena *et al.*, *Eur. J. Immunol.* (1994) 24:3233.

Assays for determining the biological activity of attracting eosinophils are described in Dahinden *et al.*, *J. Exp. Med.* (1994) 179:751, Weber *et al.*, *J. Immunol.* (1995) 154:4166, and Noso *et al.*, *Biochem. Biophys. Res. Commun.* (1994) 200:1470; for attracting dendritic cells, Sozzani *et al.*, *J. Immunol.* (1995) 155:3292; for attracting basophils, in Dahinden *et al.*, *J. Exp. Med.* (1994) 179:751, Alam *et al.*, *J. Immunol.* (1994) 152:1298, Alam *et al.*, *J. Exp. Med.* (1992) 176:781; and for activating neutrophils, Maghazaci *et al.*, *Eur. J. Immunol.* (1996) 26:315, and Taub *et al.*, *J. Immunol.* (1995) 155:3877. Native chemokines can act as mitogens for fibroblasts, assayed as described in Mullenbach *et al.*, *J. Biol. Chem.* (1986) 261:719.

Native chemokines exhibit binding activity with a number of receptors. Description of such receptors and assays to detect binding are described in, for example, Murphy *et al.*, *Science* (1991) 253:1280; Combadiere *et al.*, *J. Biol. Chem.* (1995) 270:29671; Daugherty *et al.*, *J. Exp. Med.* (1996) 183:2349; Samson *et al.*, *Biochem.* (1996) 35:3362; Raport *et al.*, *J.*

*Biol. Chem.* (1996) 271:17161; Combadiere *et al.*, *J. Leukoc. Biol.* (1996) 60:147; Baba *et al.*, *J. Biol. Chem.* (1997) 23:14893; Yosida *et al.*, *J. Biol. Chem.* (1997) 272:13803; Arvanitakis *et al.*, *Nature* (1997) 385:347, and other assays are known in the art.

Assays for kinase activation of chemokines are described by Yen *et al.*, *J. Leukoc. Biol.* (1997) 61:529; Dubois *et al.*, *J. Immunol.* (1996) 156:1356; Turner *et al.*, *J. Immunol.* (1995) 155:2437. Assays for inhibition of angiogenesis or cell proliferation are described in Maione *et al.*, *Science* (1990) 247:77. Glycosaminoglycan production can be induced by native chemokines, assayed as described in Castor *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1983) 80:765. Chemokine-mediated histamine release from basophils is assayed as described in Dahinden *et al.*, *J. Exp. Med.* (1989) 170:1787; and White *et al.*, *Immunol. Lett.* (1989) 22:151. Heparin binding is described in Luster *et al.*, *J. Exp. Med.* (1995) 182:219.

Chemokines can possess dimerization activity, which can be assayed according to Burrows *et al.*, *Biochem.* (1994) 33:12741; and Zhang *et al.*, *Mol. Cell. Biol.* (1995) 15:4851. Native chemokines can play a role in the inflammatory response of viruses. This activity can be assayed as described in Bleul *et al.*, *Nature* (1996) 382:829; and Oberlin *et al.*, *Nature* (1996) 382:833. Exocytosis of monocytes can be promoted by native chemokines. The assay for such activity is described in Ugucioni *et al.*, *Eur. J. Immunol.* (1995) 25:64. Native chemokines also can inhibit hematopoietic stem cell proliferation. The method for testing for such activity is reported in Graham *et al.*, *Nature* (1990) 344:442.

Death Domain Proteins. Several protein families contain death domain motifs (Feinstein and Kimchi, *TIBS Letters* (1995) 20:242). Some death domain containing proteins are implicated in cytotoxic intracellular signaling (Cleveland *et al.*, *Cell* (1995) 81:479, Pan *et al.*, *Science* (1997) 276:111; Duan *et al.*, *Nature* (1997) 385:86-89, and Chinnaiyan *et al.*, *Science* (1996) 274:990). U.S. Patent No. 5,563,039 describes a protein homologous to TRADD (Tumor Necrosis Factor Receptor-1 Associated Death Domain containing protein), and modifications of the active domain of TRADD that retain the functional characteristics of the protein, as well as apoptosis assays for testing the function of such death domain containing proteins. U.S. Patent No. 5,658,883 discloses biologically active TGF-B1 peptides. U.S. Patent No. 5,674,734 discloses RIP, which contains a C-terminal death domain and an N-terminal kinase domain.

Leukemia Inhibitory Factor (LIF). An LIF profile is constructed from sequences of leukemia inhibitor factor, CT-1 (cardiotrophin-1), CNTF (ciliary neurotrophic factor), OSM (oncostatin M), and IL-6 (interleukin-6). This profile encompasses a family of secreted cytokines that have pleiotropic effects on many cell types including hepatocytes, osteoclasts, neuronal cells and cardiac myocytes, and can be used to detect additional genes encoding such proteins. These molecules are all structurally related and share a common co-receptor gp130 which mediates intracellular signal transduction by cytoplasmic tyrosine kinases such as src.

Novel proteins related to this family are also likely to be secreted, to activate gp130 and to function in the development of a variety of cell types. Thus new members of this family would be candidates to be developed as growth or survival factors for the cell types that they stimulate. For more details on this family of cytokines, see Pennica *et al.*, *Cytokine and Growth Factor Reviews* (1996) 7:81-91. U.S. Patent No. 5,420,247 discloses LIF receptor and fusion proteins. U.S. Patent No. 5,443,825 discloses human LIF.

Angiopoietin. Angiopoietin-1 is a secreted ligand of the TIE-2 tyrosine kinase; it functions as an angiogenic factor critical for normal vascular development. Angiopoietin-2 is a natural antagonist of angiopoietin-1 and thus functions as an anti-angiogenic factor. These two proteins are structurally similar and activate the same receptor (Folkman *et al.*, *Cell* (1996) 87:1153, and Davis *et al.*, *Cell* (1996) 87:1161). The angiopoietin molecules are composed of two domains: a coiled-coil region and a region related to fibrinogen. The fibrinogen domain is found in many molecules including ficolin and tesascin, and is well defined structurally with many members.

Receptor Protein-Tyrosine Kinases. Receptor Protein-Tyrosine Kinases or RPTKs are described in Lindberg, *Annu. Rev. Cell Biol.* (1994) 10:251-337.

Growth Factors: (Epidermal Growth Factor) EGF and (Fibroblast Growth Factor) FGF. For a discussion of growth factor superfamilies, see *Growth Factors: A Practical Approach*, (Appendix A1) (1993) McKay and Leigh, Oxford University Press, NY, 237-243. U.S. Patent No. 4,444,760 discloses acidic brain fibroblast growth factor, which is active in the promotion of cell division and wound healing. U.S. Patent No. 5,439,818 discloses DNA encoding human recombinant basic fibroblast growth factor, which is active in wound healing. U.S. Patent No. 5,604,293 discloses recombinant human basic fibroblast growth



factor, which is useful for wound healing. U.S. Patent No. 5,410,832 discloses brain-derived and recombinant acidic fibroblast growth factor, which act as mitogens for mesoderm and neuroectoderm-derived cells in culture, and promote wound healing in soft tissue, cartilaginous tissue and musculo-skeletal tissue. U.S. Patent No. 5,387,673 discloses  
5 biologically active fragments of FGF.

Proteins of the TNF Family. A profile derived from the TNF family is created by aligning sequences of the following TNF family members: nerve growth factor (NGF), lymphotoxin, Fas ligand, tumor necrosis factor (TNF $\alpha$ ), CD40 ligand, TRAIL, ox40 ligand, 4-1BB ligand, CD27 ligand, and CD30 ligand. The profile is designed to identify sequences  
10 of proteins that constitute new members or homologues of this family of proteins. U.S. Patent No. 5,606,023 discloses mutant TNF proteins; U.S. Patent No. 5,597,899 and U.S. Patent No. 5,486,463 disclose TNF muteins; and U.S. Patent No. 5,652,353 discloses DNA encoding TNF $\alpha$  muteins.

Members of the TNF family of proteins have been show in vitro to multimerize, as  
15 described in Burrows *et al.*, *Biochem.* (1994) 33:12741 and Zhang *et al.*, *Mol. Cell. Biol.* (1995) 15:4851 and bind receptors as described in Browning *et al.*, *J. Immunol.* (1994) 147:1230, Androlewicz *et al.*, *J. Biol. Chem.*(1992) 267:2542, and Crowe *et al.*, *Science* (1994) 264:707.

In vivo, TNFs proteolytically cleave a target protein as described in Kriegel *et al.*,  
20 *Cell* (1988) 53:45 and Mohler *et al.*, *Nature* (1994) 370:218 and demonstrate cell proliferation and differentiation activity. T-cell or thymocyte proliferation is assayed as described in Armitage *et al.*, *Eur. J. Immunol.* (1992) 22:447; Current Protocols in Immunology, ed. J.E. Coligan *et al.*, 3.1-3.19; Takai *et al.*, *J. Immunol.* (1986) 137:3494-3500, Bertagnoli *et al.*, *J. Immunol.* (1990) 145:1706, Bertagnoli *et al.*, *J. Immunol.* (1991)  
25 133:327, Bertagnoli *et al.*, *J. Immunol.* (1992) 149:3778, and Bowman *et al.*, *J. Immunol.* (1994) 152:1756. B cell proliferation and Ig secretion are assayed as described in Maliszewski, *J. Immunol.* (1990) 144:3028, and Assays for B Cell Function: In Vitro Antibody Production, Mond and Brunswick, Current Protocols in Immunol., Coligan Ed vol 1 pp 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994, Kehrl *et al.*, *Science* (1987) 238:1144  
30 and Boussiotis *et al.*, *PNAS USA* (1994) 91:7007. Other in vivo activities include upregulation of cell surface antigens, upregulation of costimulatory molecules, and cellular

aggregation/adhesion as described in Barrett *et al.*, *J. Immunol.* (1991) 146:1722; Bjorck *et al.*, *Eur. J. Immunol.* (1993) 23:1771; Clark *et al.*, *Annu Rev. Immunol.* (1991) 9:97; Ranheim *et al.*, *J. Exp. Med.* (1994) 177:925; Yellin, *J. Immunol.* (1994) 153:666; and Gruss *et al.*, *Blood* (1994) 84:2305.

- 5 Proliferation and differentiation of hematopoietic and lymphopoietic cells has also been shown in vivo for TNFs, using assays for embryonic differentiation and hematopoiesis as described in Johansson *et al.*, *Cellular Biology* (1995) 15:141, Keller *et al.*, *Mol. Cell. Biol.* (1993) 13:473, McClanahan *et al.*, *Blood* (1993) 81:2903 and using assays to detect stem cell survival and differentiation as described in Culture of Hematopoietic Cells, Freshney *et al.* eds, pp 1-21, 23-29, 139-162, 163-179, and 265-268, Wiley-Liss, Inc., New York, NY, 1994, and Hirajama *et al.*, *PNAS USA* (1992) 89:5907.

- In vivo activities of TNFs also include lymphocyte survival and apoptosis, assayed as described in Darzynkewicz *et al.*, *Cytometry* (1992) 13:795; Gorczca *et al.*, *Leukemia* (1993) 7:659; Itoh *et al.*, *Cell* (1991) 66:233; Zacharduk, *J. Immunol.* (1990) 145:4037; Zamai *et al.*, *Cytometry* (1993) 14:891; and Gorczyca *et al.*, *Int'l J. Oncol.* (1992) 1:639. Some members of the TNF family are cleaved from the cell surface; others remain membrane bound. The three-dimensional structure of TNF is discussed in Sprang and Eck, Tumor Necrosis Factors; *supra*.

- TNF proteins include a transmembrane domain. The protein is cleaved into a shorter soluble version, as described in Kriegler *et al.*, *Cell* (1988) 53:45, Perez *et al.*, *Cell* (1990) 63:251, and Shaw *et al.*, *Cell* (1986) 46:659. The transmembrane domain is between amino acid 46 and 77 and the cytoplasmic domain is between position 1 and 45 on the human form of TNF $\alpha$ . The 3-dimensional motifs of TNF include a sandwich of two pleated  $\beta$  sheets. Each sheet is composed of anti-parallel  $\beta$  strands.  $\beta$  strands facing each other on opposite sites of the sandwich are connected by short polypeptide loops, as described in Van Ostade *et al.*, *Protein Engineering* (1994) 7(1):5, and Sprang *et al.*, Tumor Necrosis Factors; *supra*. Residues of the TNF family proteins that are involved in the  $\beta$  sheet secondary structure have been identified as described in Van Ostade *et al.*, *Protein Eng.* (1994) 7(1):5, and Sprang *et al.*, *supra*.

- 30 TNF receptors are disclosed in U.S. Patent No. 5,395,760. A profile derived from the TNF receptor family is created by aligning sequences of the TNF receptor family, including

Apo1/Fas, TNFR I and II, death receptor 3 (DR3), CD40, ox40, CD27, and CD30. Thus, the profile is designed to identify from the polynucleotides of the invention sequences of proteins that constitute new members or homologues of this family of proteins.

5 Tumor necrosis factor receptors exist in two forms in humans: p55 TNFR and p75 TNFR, both of which provide intracellular signals upon binding with a ligand. The extracellular domains of these receptor proteins are cysteine rich. The receptors can remain membrane bound, although some forms of the receptors are cleaved forming soluble receptors. The regulation, diagnostic, prognostic, and therapeutic value of soluble TNF receptors is discussed in Aderka, *Cytokine and Growth Factor Reviews*, (1996) 7(3):231.

10 PDGF Family. U.S. Patent No. 5,326,695 discloses platelet derived growth factor agonists; bioactive portions of PDGF-B are used as agonists. U.S. Patent No. 4,845,075 discloses biologically active B-chain homodimers, and also includes variants and derivatives of the PDGF-B chain. U.S. Patent No. 5,128,321 discloses PDGF analogs and methods of use. Proteins having the same bioactivity as PDGF are disclosed, including A and B chain  
15 proteins.

Kinase (Including MKK) Family. U.S. Patent No. 5,650,501 discloses serine/threonine kinase, associated with mitotic and meiotic cell division; the protein has a kinase domain in its N-terminal and 3 PEST regions in the C-terminus. U.S. Patent No. 5,605,825 discloses human PAK65, a serine protein kinase.

20 The foregoing discussion provides a few examples of the protein profiles that can be compared with the polynucleotides of the invention. One skilled in the art can use these and other protein profiles to identify the genes that correlate with the provided polynucleotides.

C. Identification of Secreted & Membrane-Bound Polypeptides

Both secreted and membrane-bound polypeptides of the present invention are of  
25 particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a  
30 fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) 78:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) 157: 105-132; and RAOAR algorithm, Degli Esposti *et al.*, *Eur. J. Biochem.* (1990) 190: 207-219.

Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and valine.

#### IV. Identification of the Function of an Expression Product of a Full-Length Gene Corresponding to a Polynucleotide

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine function of the expression product of a gene corresponding to a polynucleotide provided herein. These methods and compositions are particularly useful where the provided novel polynucleotide exhibits no significant or substantial homology to a sequence encoding a gene of known function. Antisense molecules and ribozymes can be constructed from synthetic polynucleotides. Typically, the phosphoramidite method of oligonucleotide synthesis is used. See Beaucage *et al.*, *Tet. Lett.* (1981) 22:1859 and U.S. Patent No. 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA,

phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City,  
5 California, USA. See Applied Biosystems User Bulletin 53 and Ogilvie *et al.*, *Pure & Applied Chem.* (1987) 59:325.

Phosphorothioate oligonucleotides can also be synthesized for antisense construction. A sulfurizing reagent, such as tetraethylthiuram disulfide (TETD) in acetonitrile can be used to convert the internucleotide cyanoethyl phosphite to the phosphorothioate triester within 15  
10 minutes at room temperature. TETD replaces the iodine reagent, while all other reagents used for standard phosphoramidite chemistry remain the same. Such a synthesis method can be automated using Models 392 and 394 by Applied Biosystems, for example.

Oligonucleotides of up to 200 nucleotides can be synthesized, more typically, 100 nucleotides, more typically 50 nucleotides; even more typically 30 to 40 nucleotides. These  
15 synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook *et al.*, *supra*.

#### A. Ribozymes

Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and  
20 the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an in vitro or in vivo context, by detecting the phenotypic effect.

25 One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme is disclosed in Usman *et al.*, *Current Opin. Struct. Biol.* (1996) 6:527. Usman also discusses the therapeutic uses of ribozymes. Ribozymes can also be prepared and used as described in Long *et al.*, *FASEB J.* (1993) 7:25; Symons, *Ann. Rev. Biochem.* (1992) 61:641; Perrotta *et al.*, *Biochem.* (1992) 31:16; Ojwang *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1992) 89:10802;  
30 and U.S. Patent No. 5,254,678. Ribozyme cleavage of HIV-I RNA is described in U.S.

Patent No. 5,144,019; methods of cleaving RNA using ribozymes is described in U.S. Patent No. 5,116,742; and methods for increasing the specificity of ribozymes are described in U.S. Patent No. 5,225,337 and Koizumi *et al.*, *Nucleic Acid Res.* (1989) 17:7059. Preparation and use of ribozyme fragments in a hammerhead structure are also described by Koizumi *et al.*, *Nucleic Acids Res.* (1989) 17:7059. Preparation and use of ribozyme fragments in a hairpin structure are described by Chowrira and Burke, *Nucleic Acids Res.* (1992) 20:2835. Ribozymes can also be made by rolling transcription as described in Daubendiek and Kool, *Nat. Biotechnol.* (1997) 15(3):273.

The hybridizing region of the ribozyme can be modified or can be prepared as a branched structure as described in Horn and Urdea, *Nucleic Acids Res.* (1989) 17:6959. The basic structure of the ribozymes can also be chemically altered in ways familiar to those skilled in the art, and chemically synthesized ribozymes can be administered as synthetic oligonucleotide derivatives modified by monomeric units. In a therapeutic context, liposome mediated delivery of ribozymes improves cellular uptake, as described in Birikh *et al.*, *Eur. J. Biochem.* (1997) 245:1.

Using the polynucleotide sequences of the invention and methods known in the art, ribozymes are designed to specifically bind and cut the corresponding mRNA species. Ribozymes thus provide a means to inhibit the expression of any of the proteins encoded by the disclosed polynucleotides or their full-length genes. The full-length gene need not be known in order to design and use specific inhibitory ribozymes. In the case of a polynucleotide or full-length cDNA of unknown function, ribozymes corresponding to that nucleotide sequence can be tested in vitro for efficacy in cleaving the target transcript. Those ribozymes that effect cleavage in vitro are further tested in vivo. The ribozyme can also be used to generate an animal model for a disease, as described in Birikh *et al.*, *supra*. An effective ribozyme is used to determine the function of the gene of interest by blocking its transcription and detecting a change in the cell. Where the gene is found to be a mediator in a disease, an effective ribozyme is designed and delivered in a gene therapy for blocking transcription and expression of the gene.

Therapeutic and functional genomic applications of ribozymes proceed beginning with knowledge of a portion of the coding sequence of the gene to be inhibited. Thus, for many genes, a partial polynucleotide sequence provides adequate sequence for constructing

an effective ribozyme. A target cleavage site is selected in the target sequence, and a ribozyme is constructed based on the 5' and 3' nucleotide sequences that flank the cleavage site. Retroviral vectors are engineered to express monomeric and multimeric hammerhead ribozymes targeting the mRNA of the target coding sequence. These monomeric and multimeric ribozymes are tested in vitro for an ability to cleave the target mRNA. A cell line is stably transduced with the retroviral vectors expressing the ribozymes, and the transduction is confirmed by Northern blot analysis and reverse-transcription polymerase chain reaction (RT-PCR). The cells are screened for inactivation of the target mRNA by such indicators as reduction of expression of disease markers or reduction of the gene product of the target mRNA.

B. Antisense

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

One rationale for using antisense methods to determine the function of the gene corresponding to a disclosed polynucleotide is the biological activity of antisense therapeutics. Antisense therapy for a variety of cancers is in clinical phase and has been discussed extensively in the literature. Reed reviewed antisense therapy directed at the Bcl-2 gene in tumors; gene transfer-mediated overexpression of Bcl-2 in tumor cell lines conferred resistance to many types of cancer drugs. (Reed, J.C., *N.C.I.* (1997) 89:988). The potential for clinical development of antisense inhibitors of *ras* is discussed by Cowser, L.M., *Anti-Cancer Drug Design* (1997) 12:359. Additional important antisense targets include

leukemia (Geurtz, A.M., *Anti-Cancer Drug Design* (1997) 12:341); human C-ref kinase (Monia, B.P., *Anti-Cancer Drug Design* (1997) 12:327); and protein kinase C (McGraw *et al.*, *Anti-Cancer Drug Design* (1997) 12:315).

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot", testing the polynucleotide as an antisense compound in the corresponding cancer cells clearly is warranted.

Ogunbiyi *et al.*, *Gastroenterology* (1997) 113(3):761 describe prognostic use of allelic loss in colon cancer; Barks *et al.*, *Genes, Chromosomes, and Cancer* (1997) 19(4):278 describe increased chromosome copy number detected by FISH in malignant melanoma; Nishizake *et al.*, *Genes, Chromosomes, and Cancer* (1997) 19(4):267 describe genetic alterations in primary breast cancer and their metastases and direct comparison using modified comparative genome hybridization; and Elo *et al.*, *Cancer Research* (1997) 57(16):3356 disclose that loss of heterozygosity at 16z24.1-q24.2 is significantly associated with metastatic and aggressive behavior of prostate cancer.

#### C. Dominant Negative Mutations

As an alternative method for identifying function of the gene corresponding to a polynucleotide disclosed herein, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced.

Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, *e.g.*, Herskowitz, *Nature* (1987) 329:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.



V. Construction of Polypeptides of the Invention and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides. These polypeptides can also be encoded by nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOS: 1-844 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof.

"Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by BLAST using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By homolog is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST algorithm, with the parameters described *supra*.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by

purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

5        Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or  
10       deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/hydrophilicity, and/or steric bulk of the amino acid substituted. For example, substitutions between the following groups are conservative: Gly/Ala, Val/Ile/Leu, Asp/Glu, Lys/Arg, Asn/Gln, Ser/Cys, Thr, and Phe/Trp/Tyr.

15       Variants can be designed so as to retain biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). In a non-limiting example, Osawa *et al.*, *Biochem. Mol. Int.* (1994) 34:1003, discusses the actin binding region of a protein from several different species. The actin binding regions of these species are considered  
20       homologous based on the fact that they have amino acids that fall within "homologous residue groups." Homologous residues are judged according to the following groups (using single letter amino acid designations): STAG; ILVMF; HRK; DEQN; and FYW. For example, and S, a T, an A or a G can be in a position and the function (in this case actin binding) is retained.

25       Additional guidance on amino acid substitution is available from studies of protein evolution. Go *et al.*, *Int. J. Peptide Protein Res.* (1980) 15:211, classified amino acid residue sites as interior or exterior depending on their accessibility. More frequent substitution on exterior sites was confirmed to be general in eight sets of homologous protein families regardless of their biological functions and the presence or absence of a prosthetic group.  
30       Virtually all types of amino acid residues had higher mutabilities on the exterior than in the interior. No correlation between mutability and polarity was observed of amino acid

residues in the interior and exterior, respectively. Amino acid residues were classified into one of three groups depending on their polarity: polar (Arg, Lys, His, Gln, Asn, Asp, and Glu); weak polar (Ala, Pro, Gly, Thr, and Ser), and nonpolar (Cys, Val, Met, Ile, Leu, Phe, Tyr, and Trp). Amino acid replacements during protein evolution were very conservative: 5 88% and 76% of them in the interior or exterior, respectively, were within the same group of the three. Inter-group replacements are such that weak polar residues are replaced more often by nonpolar residues in the interior and more often by polar residues on the exterior.

Additional guidance for production of polypeptide variants is provided in Querol *et al.*, *Prot. Eng.* (1996) 9:265, which provides general rules for amino acid substitutions to 10 enhance protein thermostability. New glycosylation sites can be introduced as discussed in Olsen and Thomsen, *J. Gen. Microbiol.* (1991) 137:579. An additional disulfide bridge can be introduced, as discussed by Perry and Wetzel, *Science* (1984) 226:555; Pantoliano *et al.*, *Biochemistry* (1987) 26:2077; Matsumura *et al.*, *Nature* (1989) 342:291; Nishikawa *et al.*, *Protein Eng.* (1990) 3:443; Takagi *et al.*, *J. Biol. Chem.* (1990) 265:6874; Clarke *et al.*, 15 *Biochemistry* (1993) 32:4322; and Wakarchuk *et al.*, *Protein Eng.* (1994) 7:1379. Metal binding sites can be introduced, according to Toma *et al.*, *Biochemistry* (1991) 30:97, and Haezebrouck *et al.*, *Protein Eng.* (1993) 6:643. Substitutions with prolines in loops can be made according to Masul *et al.*, *Appl. Env. Microbiol.* (1994) 60:3579; and Hardy *et al.*, *FEBS Lett.* 317:89.

20 Cysteine-depleted muteins are considered variants within the scope of the invention. These variants can be constructed according to methods disclosed in U.S. Patent No. 4,959,314, which discloses substitution of cysteines with other amino acids, and methods for assaying biological activity and effect of the substitution. Such methods are suitable for proteins according to this invention that have cysteine residues suitable for such 25 substitutions, for example to eliminate disulfide bond formation.

Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but 30 will usually not exceed about 1000 aa in length, where the fragment will have a stretch of

amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any SEQ ID NOS:1-844, or a homolog thereof.

The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to  
5 construct the corresponding variants.

## VI. Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide  
10 molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. In  
15 general, a disease marker is a representation of a gene product that is present in all affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either  
20 overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form includes an accessible computer data file (or, in biochemical  
25 form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous  
30 cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of

cells affected by various diseases or stages of disease will be readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater  
5 detail below.

The polynucleotide libraries of the subject invention include sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOS:1-844. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOS:1-844. The length and number of polynucleotides  
10 in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such  
15 a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of SEQ ID NOS:1-844, can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media  
20 include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture  
25 comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence  
30 information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of

computer-readable files (*e.g.*, searchable files, executable files, *etc.*, including, but not limited to, for example, search program software, *etc.*).

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the BLAST (Altschul *et al.*, *supra.*) and BLAZE (Brutlag *et al. Comp. Chem.* (1993) 17:203) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif with the stored sequence information. Search means are used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known algorithms are publicly known and commercially available, *e.g.* MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues.

A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, hairpin structures,

promoter sequences and other expression elements such as binding sites for transcription factors.

5 A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks fragments of the genome possessing varying degrees of homology to a target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences and identifies the degree of sequence similarity contained in the identified fragment.

10 A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the genome. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention.

As discussed above, the "library" of the invention also encompasses biochemical  
15 libraries of the polynucleotides of SEQ ID NOS:1-844, *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOS:1-844 is represented on the array. By array is  
20 meant a an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art, including those described in 5,242,974; 5,384,261; 5,405,783; 5,412,087;  
25 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,527,681; 5,529,756; 5,545,531; 5,554,501; 5,556,752; 5,561,071; 5,599,895; 5,624,711; 5,639,603; 5,658,734; WO 93/17126; WO 95/11995; WO 95/35505; EP 742287; and EP 799897. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary  
30 patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOS:1-844.

5 VII. Utilities

A. Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

Polynucleotide probes, generally comprising at least 12 contiguous nucleotides of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional  
10 disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Probes in Detection of Expression Levels. Nucleotide probes are used to detect  
15 expression of a gene corresponding to the provided polynucleotide. The references describe an example of a sandwich nucleotide hybridization assay. For example, in Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular  
20 condition. Probes are also used to detect products of amplification by polymerase chain reaction. The products of the reaction are hybridized to the probe and hybrids are detected. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as  
25 chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and U.S. Patent No. 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids (see, *e.g.*, Mullis *et al.*, *Meth. Enzymol.* (1987) 155:335; U.S. Patent No. 4,683,195; and U.S. Patent No. 4,683,202). Two primer  
30 polynucleotides nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these



polynucleotides, they need not hybridize to them or the complements. A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a large amount of target nucleic acids is generated by the polymerase, it is detected by methods such as Southern blots. When using the Southern blot method, the labeled probe will hybridize to a polynucleotide of the Sequence Listing or complement.

Furthermore, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989). mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe and then washed to remove any unhybridized probe. Next, the duplexes containing the labeled probe are detected. Typically, the probe is labeled with radioactivity.

Mapping. Polynucleotides of the present invention are used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in U.S. Patent No. 5,783,387.

For example, fluorescence in situ hybridization (FISH) on normal metaphase spreads facilitates comparative genomic hybridization to allow total genome assessment of changes in relative copy number of DNA sequences. See Schwartz and Samad, *Curr. Opin.*

*Biotechnol.* (1994) 8:70; Kallioniemi *et al.*, *Sem. Cancer Biol.* (1993) 4:41; Valdes *et al.*, *Methods in Molecular Biology* (1997) 68:1, Boultonwood, ed., Human Press, Totowa, NJ.

Preparations of human metaphase chromosomes are prepared using standard cytogenetic techniques from human primary tissues or cell lines. Nucleotide probes comprising at least 12 contiguous nucleotides selected from the nucleotide sequence shown in the Sequence

Listing are used to identify the corresponding chromosome. The nucleotide probes are labeled, for example, with a radioactive, fluorescent, biotinylated, or chemiluminescent label,

and detected by well known methods appropriate for the particular label selected. Protocols for hybridizing nucleotide probes to preparations of metaphase chromosomes are also well known in the art. A nucleotide probe will hybridize specifically to nucleotide sequences in the chromosome preparations that are complementary to the nucleotide sequence of the

5 probe.

Polynucleotides are mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels. See Leach *et al.*, *Advances in Genetics*, (1995) 33:63-99; Walter *et al.*, *Nature Genetics* (1994) 7:22; Walter and Goodfellow, *Trends in Genetics* (1992) 9:352. Panels for radiation hybrid mapping are available from Research  
10 Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are available via the world wide web at <http://F/shgc-www.stanford.edu>; and <http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl>. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web  
15 at <http://www.sph.umich.edu/group/statgen/software>.

In addition, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer. Polynucleotides based on the polynucleotides of the invention can be used to probe these regions. For example, if through profile searching a provided polynucleotide is identified as corresponding to a gene  
20 encoding a kinase, its ability to bind to a cancer-related chromosomal region will suggest its role as a kinase in one or more stages of tumor cell development/growth. Although some experimentation would be required to elucidate the role, the polynucleotide constitutes a new material for isolating a specific protein that has potential for developing a cancer diagnostic or therapeutic.

25 Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to  
30 polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

For example, a metastatic lesion is identified by its developmental organ or tissue source by identifying the expression of a particular marker of that organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified.

- 5 Expression of a particular polynucleotide is assayed by detection of either the corresponding mRNA or the protein product. Immunological methods, such as antibody staining, are used to detect a particular protein product. Hybridization methods can be used to detect particular mRNA species, including but not limited to in situ hybridization and Northern blotting.

- Use of Polymorphisms. A polynucleotide of the invention will be useful in forensics,  
10 genetic analysis, mapping, and diagnostic applications if the corresponding region of a gene is polymorphic in the human population. Particular polymorphic forms of the provided polynucleotides can be used to either identify a sample as deriving from a suspect or rule out the possibility that the sample derives from the suspect. Any means for detecting a polymorphism in a gene are used, including but not limited to electrophoresis of protein  
15 polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

#### B. Antibody Production

- Expression products of a polynucleotide of the invention, the corresponding mRNA or cDNA, or the corresponding complete gene are prepared and used for raising antibodies  
20 for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding  
25 native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

- Immunogens for raising antibodies are prepared by mixing the polypeptides encoded by the polynucleotides of the present invention with adjuvants. Alternatively, polypeptides are made as fusion proteins to larger immunogenic proteins. Polypeptides are also  
30 covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly.

Immunogens are administered to experimental animals such as rabbits, sheep, and mice, to generate antibodies. Optionally, the animal spleen cells are isolated and fused with myeloma cells to form hybridomas which secrete monoclonal antibodies. Such methods are well known in the art. According to another method known in the art, the selected polynucleotide is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for polypeptides encoded by a selected polynucleotide are made using standard methods known in the art.

The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, for example at least 15, 25, or 50 amino acids. A short sequence of a polynucleotide may then be unsuitable for use as an epitope to raise antibodies for identifying the corresponding novel protein, because of the potential for cross-reactivity with a known protein. However, the antibodies can be useful for other purposes, particularly if they identify common structural features of a known protein and a novel polypeptide encoded by a polynucleotide of the invention.

Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically polypeptides of the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

To test for the presence of serum antibodies to the polypeptide of the invention in a human population, human antibodies are purified by methods well known in the art. Preferably, the antibodies are affinity purified by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, genetically engineered antibody derivatives are made, such as single chain antibodies, according to methods well known in the art.

C. Use of Polynucleotides to Construct Arrays for Diagnostics

- 5 Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotide sequences in a sample. This technology can be used as a diagnostic and as a tool to test for differential expression to determine function of an encoded protein. Arrays can be created by spotting polynucleotide probes onto a substrate (*e.g.*, glass, nitrocellulose, *etc.*) in a two-dimensional matrix or array having bound probes.
- 10 The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (*e.g.*, using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the sample is washed
- 15 away. Techniques for constructing arrays and methods of using these arrays are described in EP No. 0 799 897; PCT No. WO 97/29212; PCT No. WO 97/27317; EP No. 0 785 280; PCT No. WO 97/02357; U.S. Pat. No. 5,593,839; U.S. Pat. No. 5,578,832; EP No. 0 728 520; U.S. Pat. No. 5,599,695; EP No. 0 721 016; U.S. Pat. No. 5,556,752; PCT No. WO 95/22058; and U.S. Pat. No. 5,631,734.
- 20 As discussed in some detail above, arrays can be used to examine differential expression of genes and can be used to determine gene function. For example, arrays of the instant polynucleotide sequences can be used to determine if any of the provided polynucleotides are differentially expressed between a test cell and control cell (*e.g.*, cancer cells and normal cells). For example, high expression of a particular message in a cancer
- 25 cell, which is not observed in a corresponding normal cell, can indicate a cancer specific protein. Exemplary uses of arrays are further described in, for example, Pappalarado *et al.*, *Sem. Radiation Oncol.* (1998) 8:217; and Ramsay *Nature Biotechnol.* (1998) 16:40.

D. Differential Expression

- The polynucleotides of the invention can also be used to detect differences in
- 30 expression levels between two cells, *e.g.*, as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families as described

above, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different  
5 tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (e.g., brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle,  
10 pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in  
15 diagnosis of cancer are described in U.S. Patent Nos. 5,688,641 and 5,677,125.

The polynucleotide-related genes in the two tissues are compared by any means known in the art. For example, the two genes can be sequenced, and the sequence of the gene in the tissue suspected of being diseased compared with the gene sequence in the normal tissue. The genes corresponding to a provided polynucleotide, or portions thereof, in  
20 the two tissues are amplified, for example using nucleotide primers based on the nucleotide sequence shown in the Sequence Listing, using the polymerase chain reaction. The amplified genes or portions of genes are hybridized to detectably labeled nucleotide probes selected from a nucleotide sequence shown in the Sequence Listing. A difference in the nucleotide sequence of the isolated gene in the tissue suspected of being diseased compared  
25 with the normal nucleotide sequence suggests a role of the gene product encoded by the subject polynucleotide in the disease, and provides guidance for preparing a therapeutic agent.

Alternatively, mRNA corresponding to a provided polynucleotide in the two tissues is compared. PolyA<sup>+</sup> RNA is isolated from the two tissues as is known in the art. For  
30 example, one of skill in the art can readily determine differences in the size or amount of mRNA transcripts between the two tissues using Northern blots and detectably labeled

nucleotide probes selected from the nucleotide sequence shown in the Sequence Listing.

Increased or decreased expression of a given mRNA in a tissue sample suspected of being diseased, compared with the expression of the same mRNA in a normal tissue, suggests that the expressed protein has a role in the disease, and also provides a lead for preparing a

5 therapeutic agent.

The comparison can also be accomplished by analyzing polypeptides between the matched samples. The sizes of the proteins in the two tissues are compared, for example, using antibodies of the present invention to detect polypeptides in Western blots of protein extracts from the two tissues. Other changes, such as expression levels and subcellular  
10 localization, can also be detected immunologically, using antibodies to the corresponding protein. A higher or lower level of expression of a given polypeptide in a tissue suspected of being diseased, compared with the same protein expression level in a normal tissue, is indicative that the expressed protein has a role in the disease, and provides guidance for preparing a therapeutic agent.

15 Similarly, comparison of polynucleotide sequences or of gene expression products, *e.g.*, mRNA and protein, between a human tissue that is suspected of being diseased and a normal tissue of a human, are used to follow disease progression or remission in the human. Such comparisons are made as described above. For example, increased or decreased expression of a gene corresponding to an inventive polynucleotide in the tissue suspected of  
20 being neoplastic can indicate the presence of neoplastic cells in the tissue. The degree of increased expression of a given gene in the neoplastic tissue relative to expression of the same gene in normal tissue, or differences in the amount of increased expression of a given gene in the neoplastic tissue over time, is used to assess the progression of the neoplasia in that tissue or to monitor the response of the neoplastic tissue to a therapeutic protocol over  
25 time.

The expression pattern of any two cell types can be compared, such as low and high metastatic tumor cell lines, malignant or non-malignant cells, or cells from tissue which have and have not been exposed to a therapeutic agent. A genetic predisposition to disease in a human is detected by comparing expression levels of an mRNA or protein corresponding to  
30 a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic

fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. The comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. Particular diagnostic and prognostic uses of the disclosed polynucleotides are described in more detail below.

10 E. Diagnostic, Prognostic, and Other Uses Based On Differential Expression

In general, diagnostic methods of the invention for involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (*e.g.*, breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (*e.g.*, cells substantially unaffected by cancer) and/or other control cells (*e.g.*, to differentiate a cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease.

The term “differentially expressed gene” is intended to encompass a polynucleotide that can, for example, include an open reading frame encoding a gene product (*e.g.*, a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, *i.e.*, a gene that is underexpressed or down-regulated in the test sample relative to a control sample. Furthermore, a difference in expression level associated with an increase in expression of at



least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1 ½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, *i.e.*, an overexpressed or up-regulated gene.

5 "Differentially expressed polynucleotide" as used herein means a nucleic acid molecule (RNA or DNA) having a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the  
10 presence of a differentially expressed gene in a sample. "Differentially expressed polynucleotides" is also meant to encompass fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

15 Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression  
20 product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number  
25 of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for  
30 determining the nucleic acid abundance in a sample are known to those of skill in the art, where particular methods of interest include those described in: Pietu *et al. Genome Res.*

(1996) 6:492; Zhao *et al.*, *Gene* (1995) 156:207; Soares, *Curr. Opin. Biotechnol.* (1977) 8:542; Raval, *J. Pharmacol Toxicol Methods* (1994) 32:125; Chalifour *et al.*, *Anal. Biochem* (1994) 216:299; Stolz *et al.*, *Mol. Biotechnol.* (1996) 6:225; Hong *et al.*, *Biosci. Reports* (1982) 2:907; and McGraw, *Anal. Biochem.* (1984) 143:298. Also of interest are the  
5 methods disclosed in WO 97/27317, the disclosure of which is herein incorporated by reference.

In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (*e.g.*, mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOS:1-844. The patient from whom the sample is obtained can be apparently  
10 healthy, susceptible to disease (*e.g.*, as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

In the assays of the invention, the diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least  
15 two or more, at least 3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOS:1-844, and can involve detection of expression of genes corresponding to all of SEQ ID NOS:1-844 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is designed to detect the presence or susceptibility of a patient to cancer, the assay preferably  
20 involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. For example, a higher level of expression of a polynucleotide corresponding to SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of a polynucleotide corresponding to SEQ ID  
25 NO:39 relative to a normal level is indicative of the presence of cancer in the patient. Further examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily  
30 skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes, (e.g. fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (e.g.  $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^3\text{H}$ , *etc.*), and the like. The detectable label can involve a two stage systems (e.g., biotin-avidin, hapten-anti-hapten antibody, *etc.*)

Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

Polypeptide detection in diagnosis. In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically bind a differentially expressed polypeptide of the invention are added to a sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (e.g., using radioisotopes, enzymes, fluorescers, chemiluminescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (e.g., biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, e.g. fluorescein, rhodamine, Texas red, *etc.*). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, *etc.* Any suitable alternative methods can of qualitative or quantitative

detection of levels or amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, etc.

In general, the detected level of differentially expressed polypeptide in the test sample is compared to a level of the differentially expressed gene product in a reference or control sample, *e.g.*, in a normal cell (negative control) or in a cell having a known disease state (positive control). For example, a higher level of expression of a polypeptide encoded by SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of the polypeptide encoded by SEQ ID NO:39 relative to a normal level is indicative of the presence of cancer in the patient.

mRNA detection. The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, *in situ* hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A<sup>+</sup> mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. For example, the level of mRNA of the invention in a tissue sample suspected of being cancerous or dysplastic is compared with the expression of the mRNA in a reference sample, *e.g.*, a positive or negative control sample (*e.g.*, normal tissue, cancerous tissue, *etc.*). In a specific non-limiting example, a higher level of mRNA corresponding to SEQ ID NO:52 relative to a level associated with a normal sample can indicate the presence of cancer in the patient from whom the sample is derived. In another example, detection of a lower level of mRNA corresponding to SEQ ID NO:39 relative to a normal level is indicative of the presence of cancer in the patient.

Any suitable method for detecting and comparing mRNA expression levels in a sample can be used in connection with the diagnostic methods of the invention (see, *e.g.*, U.S. 5,804,382). For example, mRNA expression levels in a sample can be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) *Science* 252:1651). Enumeration of the relative representation of ESTs within the library can be used

to approximate the relative representation of the gene transcript within the starting sample. The results of EST analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein.

Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (Velculescu et al., *Science* (1995) 270:484). In short, SAGE involves the isolation of short unique sequence tags from a specific location within each transcript (e.g., a sequence of any one of SEQ ID NOS:1-6). The sequence tags are concatenated, cloned, and sequenced. The frequency of particular transcripts within the starting sample is reflected by the number of times the associated sequence tag is encountered with the sequence population.

Gene expression in a test sample can also be analyzed using differential display (DD) methodology. In DD, fragments defined by specific sequence delimiters (e.g., restriction enzyme sites) are used as unique identifiers of genes, coupled with information about fragment length or fragment location within the expressed gene. The relative representation of an expressed gene with a sample can then be estimated based on the relative representation of the fragment associated with that gene within the pool of all possible fragments. Methods and compositions for carrying out DD are well known in the art, see, e.g., U.S. 5,776,683; and U.S. 5,807,680.

Alternatively, gene expression in a sample using hybridization analysis, which is based on the specificity of nucleotide interactions. Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized to a known capture sequence determined qualitatively or quantitatively, to provide information about the relative representation of a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (e.g., mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene. For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (*e.g.*, a polymorphism in an coding region or control region),  
5 that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, *etc.*

Changes in the promoter or enhancer sequence that affect expression levels of an differentially gene can be compared to expression levels of the normal allele by various  
10 methods known in the art. Methods for determining promoter or enhancer strength include quantitation of the expressed natural protein; insertion of the variant control element into a vector with a reporter gene such as  $\beta$ -galactosidase, luciferase, chloramphenicol acetyltransferase, *etc.* that provides for convenient quantitation; and the like.

A number of methods are available for analyzing nucleic acids for the presence of a  
15 specific sequence, *e.g.* a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by  
20 conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (*e.g.*, using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. The use of the polymerase chain reaction is described in Saiki, *et al.*, *Science* (1985) 239:487, and a review of techniques can be found in Sambrook, *et al.*, *Molecular Cloning: A Laboratory Manual*, (1989) pp. 14.2. Alternatively, various methods are known  
25 in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, for examples see Riley *et al.*, *Nucl. Acids Res.* (1990) 18:2887; and Delahunty *et al.*, *Am. J. Hum. Genet.* (1996) 58:1239.

The sample nucleic acid, *e.g.* amplified or cloned fragment, is analyzed by one of a  
30 number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods, and the sequence of bases compared to a selected sequence, *e.g.*, to a wild-type

sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (*e.g.*, by Southern blot, dot blot, *etc.*). The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in US 5,445,934, or in  
5 WO 95/35505, can also be used as a means of identifying polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a  
10 recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in an differentially expressed gene can be based on the  
15 functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded  
20 protein can be determined by comparison with the wild-type protein.

Pattern matching in diagnosis using arrays. In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP). The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the  
25 selected set of genes in a reference sample (*e.g.*, a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of SEQ ID NOS:1-844. Of particular interest is a selected set of genes that includes gene differentially expressed in the disease for which the test sample is to be screened.

30 "Reference sequences" or "reference polynucleotides" as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of

polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference sequences, preferably comprising positive and negative control sequences, can be included as reference sequences.

Additional suitable reference sequences are found in Genbank, Unigene, and other  
5 nucleotide sequence databases (including, *e.g.*, expressed sequence tag (EST), partial, and full-length sequences).

"Reference array" means an array having reference sequences for use in hybridization with a sample, where the reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include  
10 at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (*e.g.*, cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually  
15 be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more.

A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is  
20 associated with a selected cell type, *e.g.*, a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (*e.g.*, a cell of unknown or suspected disease state, from which mRNA is isolated).

"Diagnosis" as used herein generally includes determination of a subject's  
25 susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly  
30 encompasses diagnosis of subjects in the context of breast cancer (*e.g.*, carcinoma in situ (*e.g.*, ductal carcinoma in situ), estrogen receptor (ER)-positive breast cancer, ER-negative



breast cancer, or other forms and/or stages of breast cancer), lung cancer (*e.g.*, small cell carcinoma, non-small cell carcinoma, mesothelioma, and other forms and/or stages of lung cancer), and colon cancer (*e.g.*, adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

5       "Sample" or "biological sample" as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (*e.g.*, ductal adenocarcinoma), and the like. "Samples" is also meant to encompass derivatives and fractions of such samples (*e.g.*, cell lysates). Where the sample  
10 is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

      REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a  
15 format that allows for ready comparison of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, *e.g.*, by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The sequence information can then be stored in a  
20 format (*e.g.*, a computer-readable format) that allows for ready comparison of the REP with a TEP. The REP can be normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (*e.g.*, some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

25       TEPs can be generated in a manner similar to REPs, *e.g.*, by hybridizing a test sample to an array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously, or the TEP can  
30 be compared to previously generated and stored REPs.

In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described  
5 herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated using an array having the same or similar selected set of differentially expressed polynucleotides. Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples relative to the other.

10 Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. 5,134,854, and U.S. 5,445,934 using light-directed synthesis techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers.

15 Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published application no. WO 95/35505.

Methods for collection of data from hybridization of samples with a reference arrays are also well known in the art. For example, the polynucleotides of the reference and test  
20 samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the microarrays for the presence of the detectable label. Methods and devices for detecting fluorescently marked targets on devices are known in the art. Generally, such detection devices include a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the  
25 substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in U.S. Patent no. 5,631,734. A scanning laser microscope is described in Shalon et al., *Genome Res.* (1996) 6:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For  
30 any particular array element, the ratio of the fluorescent signal from one sample (e.g., a test

sample) is compared to the fluorescent signal from another sample (*e.g.*, a reference sample), and the relative signal intensity determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, *i.e.* data deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

10 In general, the test sample is classified as having a gene expression profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (*e.g.*, from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, *etc.*). The criteria for a match or a  
15 substantial match between a TEP and a REP include expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (*e.g.*, no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference  
20 sequence. In general, a pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (*e.g.*, arrays), design of  
25 oligonucleotides for use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. 5,800,992.

#### F. Use of the Polynucleotides of the Invention in Cancer

Oncogenesis involves the unbridled growth, dedifferentiation and abnormal  
30 migration of cells. Cancerous cells can have the ability to compress, invade, and destroy normal tissue. Cancerous cells may also metastasize to other parts of the body via the

bloodstream or the lymph system and colonize in these other areas. Different cancers are classified by the cell from which the cancerous cell is derived and from its cellular morphology and/or state of differentiation.

Somatic genetic abnormalities cause cancer initiation and progression. Cancer  
5 generally is clonally formed, *i.e.* gain of function of oncogenes and loss of function of tumor suppressor genes within a single cell transform the cell to be cancerous, and that single cell grows and divides to form a cancerous lesion. The genes known to be involved in cancer initiation and progression are involved in numerous cellular functions, including developmental differentiation, cell cycle regulation, cell signaling, immunological response,  
10 DNA replication, and DNA repair.

The identification and characterization of genetic or biochemical markers in blood or tissues that will detect the earliest changes along the carcinogenesis pathway and monitor the efficacy of various therapies and preventive interventions is a major goal of cancer research. Scientists have identified genetic changes in stool specimens that indicate the stages of colon  
15 cancer, and other biomarkers such as gene mutations, hormone receptors, proteins that inhibit metastasis, and enzymes that metabolize drugs are all being used to determine the severity and predict the course of breast, prostate, lung, and other cancers.

Recent advances in the pathogenesis of certain cancers has been helpful in determining patient treatment. The level of expression of certain polynucleotides can be  
20 indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients has defined certain prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting and gene therapy. Moreover, a promising level of one  
25 or more marker polynucleotides can provide impetus for not aggressively treating a particular patient, thus sparing the patient the deleterious side effects of aggressive therapy. Determining expression of certain polynucleotides and comparison of a patients profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of  
30 comfort level of the patient.

Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Different staging systems are used for different types of cancer, but each generally involves the following determinations: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. This system of staging is called the TNM system. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or another site, are called Stage IV, the most advanced stage.

Currently, the determination of staging is done using pathological techniques and is based more on the presence or absence of malignant tissue rather than the characteristics of the tumor type. Presence or absence of malignant tissue is based primarily on the gross morphology of the cells in the areas biopsied. The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggressivity of a cancer, *e.g.* the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. Based on the microscopic appearance of a tumor, pathologists will identify the grade of a tumor based on parameters such as cell morphology,

cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness. That is, undifferentiated or high-grade tumors grow more quickly than well differentiated or low-grade tumors. Information about tumor grade is useful in planning treatment and predicting prognosis.

5           The American Joint Commission on Cancer has recommended the following guidelines for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. Although grading is used by pathologists to describe most cancers, it plays a more important role in treatment planning for certain types than for others. An example is the Gleason

10          system that is specific for prostate cancer, which uses grade numbers to describe the degree of differentiation. Lower Gleason scores indicate well-differentiated cells. Intermediate scores denote tumors with moderately differentiated cells. Higher scores describe poorly differentiated cells. Grade is also important in some types of brain tumors and soft tissue sarcomas.

15          The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressivity of a tumor, such as metastatic potential.

Familial Cancer Genes. A number of cancer syndromes are linked to Mendelian

20          inheritance of a predisposition to develop particular cancers. The following table contains a list of cancer types that can be inherited, and for which the gene or genes responsible have been identified. Most of the cancer types listed can occur as part of several different genetic conditions, each caused by alterations in a different gene.

Cancer Type	Genetic Condition	Gene
Brain	Li-Fraumeni syndrome	TP53
	Neurofibromatosis 1	NF1
	Neurofibromatosis 2	NF2
	von Hippel-Lindau syndrome	VHL
	Tuberous sclerosis 2	TSC2
Breast	Hereditary breast/ovarian cancer 1	BRCA1
	Hereditary breast/ovarian cancer 2	BRCA2
	Li-Fraumeni syndrome	TP53
	Ataxia telangiectasia	ATM
Colon	Familial adenomatous polyposis (FAP)	APC
	Hereditary non-polyposis colon cancer (HNPCC) 1	HMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1

Cancer Type	Genetic Condition	Gene
		hPMS1 hPMS2
Endocrine (parathyroid, pituitary, GI endocrine)	Hereditary non-polyposis colon cancer (HNPCC) 3	MEN1
	Hereditary non-polyposis colon cancer (HNPCC) 4	
Endocrine (pheochromacytoma, medullary thyroid)	Multiple endocrine neoplasia 1 (MEN1)	RET
Endometrial	Multiple endocrine neoplasia 2 (MEN2)	hMSH2 hMLH1 hPMS1 hPMS2
	Hereditary non-polyposis colon cancer (HNPCC) 1	
	Hereditary non-polyposis colon cancer (HNPCC) 2	
	Hereditary non-polyposis colon cancer (HNPCC) 3	
Eye	Hereditary non-polyposis colon cancer (HNPCC) 4	RB1
	Hereditary retinoblastoma	
Hematologic (lymphomas and leukemia)	Li-Fraumeni syndrome	TP53
	Ataxia telangiectasia	ATM
Kidney	Hereditary Wilms' tumor	WT1
	von Hippel-Lindau syndrome	VHL
	Tuberous sclerosis 2	TSC2
Ovary	Hereditary breast/ovarian cancer 1	BRCA1
	Hereditary breast/ovarian cancer 2	BRCA2
Sarcoma	Hereditary retinoblastoma	RB1
	Li-Fraumeni syndrome	TP53
	Neurofibromatosis 1	NF1
Skin	Hereditary melanoma 1	CDKN2
	Hereditary melanoma 2	CDK4
	Basal cell naevus (Gorlin) syndrome	PTCH
Stomach	Hereditary non-polyposis colon cancer (HNPCC) 1	hMSH2
	Hereditary non-polyposis colon cancer (HNPCC) 2	hMLH1
	Hereditary non-polyposis colon cancer (HNPCC) 3	hPMS1
	Hereditary non-polyposis colon cancer (HNPCC) 4	hPMS2

The polynucleotides of the invention can be especially useful to monitor patients having any of the above syndromes to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. As can be seen from the table, a number of genes are involved in multiple forms of cancer. Thus, a polynucleotide of the invention identified as important for metastatic colon cancer can also have clinical implications for a patient diagnosed with stomach cancer or endometrial cancer.

Lung Cancer. Lung cancer is one of the most common cancers in the United States, accounting for about 15 percent of all cancer cases, or 170,000 new cases each year. At this time, over half of the lung cancer cases in the United States are in men, but the number found in women is increasing and will soon equal that in men. Today more women die of lung cancer than of breast cancer. Lung cancer is especially difficult to diagnose and treat because of the large size of the lungs, which allows cancer to develop for years undetected.

In fact, lung cancer can spread outside the lungs without causing any symptoms. Adding to the confusion, the most common symptom of lung cancer, a persistent cough, can often be mistaken for a cold or bronchitis.

Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma), which usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

Currently, CT scans, MRIs, X-rays, sputum cytology, and biopsies are used to diagnose nonsmall cell lung cancer. The form and cellular origin of the lung cancer is diagnosed primarily through biopsy from either a surgical biopsy or a needle aspiration of lung tissue, and usually the biopsy is prompted from an abnormality identified on an X-ray. In some cases, sputum cytology can reveal lung cancers in patients with normal X-rays or can determine the type of lung cancer, but because it cannot pinpoint the tumor's location, a positive sputum cytology test is usually followed by further tests. Since these tests are based in large part on gross morphology of the tissue, the diagnosis of a particular kind of tumor is largely subjective, and the diagnosis can vary significantly between clinicians.

The polynucleotides of the invention can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the



surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. The differential expression of a polynucleotide in hyperplasia can be used as a diagnostic marker for metastatic lung cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between high metastatic versus low metastatic lung cancer, *i.e.* SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 381, 395, and 400. Detection of malignant lung cancer with a higher metastatic potential can be determined using expression levels of any of these sequences alone or in combination with the levels of expression of other known genes.

Breast Cancer. The National Cancer Institute (NCI) estimates that about 1 in 8 women in the United States will develop breast cancer during her lifetime. Clinical breast examination and mammography are recommended as combined modalities for breast cancer screening, and the nature of the cancer will often depend upon the location of the tumor and the cell type from which the tumor is derived. The majority of breast cancers are adenocarcinomas subtypes, which can be summarized as follows:

Ductal carcinoma in situ (DCIS): Ductal carcinoma in situ is the most common type of noninvasive breast cancer. In DCIS, the malignant cells have not metastasized through the walls of the ducts into the fatty tissue of the breast. Comedocarcinoma is a type of DCIS that is more likely than other types of DCIS to come back in the same area after lumpectomy. It is more closely linked to eventual development of invasive ductal carcinoma than other forms of DCIS.

Infiltrating (or invasive) ductal carcinoma (IDC): this type of cancer has metastasized through the wall of the duct and invaded the fatty tissue of the breast. At this point, it has the potential to use the lymphatic system and bloodstream for metastasis to more distant parts of the body. Infiltrating ductal carcinoma accounts for about 80% of breast cancers.

Lobular carcinoma in situ (LCIS): While not a true cancer, LCIS (also called lobular neoplasia) is sometimes classified as a type of noninvasive breast cancer. It does not penetrate through the wall of the lobules. Although it does not itself usually become an

invasive cancer, women with this condition have a higher risk of developing an invasive breast cancer in the same breast, or in the opposite breast.

Infiltrating (or invasive) lobular carcinoma (ILC): ILC is similar to IDC, in that it has the potential metastasize elsewhere in the body. About 10% to 15% of invasive breast  
5 cancers are invasive lobular carcinomas. ILC can be more difficult to detect by mammogram than IDC.

Inflammatory breast cancer: This rare type of invasive breast cancer accounts for about 1% of all breast cancers and is extremely aggressive. Multiple skin symptoms associated with this cancer are caused by cancer cells blocking lymph vessels or channels in  
10 the skin over the breast.

Medullary carcinoma: This special type of infiltrating breast cancer has a relatively well defined, distinct boundary between tumor tissue and normal tissue. It accounts for about 5% of breast cancers. The prognosis for this kind of breast cancer is better than for other types of invasive breast cancer.

15 Mucinous carcinoma: This rare type of invasive breast cancer originates from mucus-producing cells. The prognosis for mucinous carcinoma is better than for the more common types of invasive breast cancer.

Paget's disease of the nipple: This type of breast cancer starts in the ducts and spreads to the skin of the nipple and the areola. It is a rare type of breast cancer, occurring in only  
20 1% of all cases. Paget's disease can be associated with in situ carcinoma, or with infiltrating breast carcinoma. If no lump can be felt in the breast tissue, and the biopsy shows DCIS but no invasive cancer, the prognosis is excellent.

Phyllodes tumor: This very rare type of breast tumor forms from the stroma of the breast, in contrast to carcinomas which develop in the ducts or lobules. Phyllodes (also  
25 spelled phylloides) tumors are usually benign, but are malignant on rare occasions. Nevertheless, malignant phyllodes tumors are very rare and less than 10 women per year in the US die of this disease. Benign phyllodes tumors are successfully treated by removing the mass and a narrow margin of normal breast tissue.

Tubular carcinoma: Accounting for about 2% of all breast cancers, tubular  
30 carcinomas are a special type of infiltrating breast carcinoma. They have a better prognosis than usual infiltrating ductal or lobular carcinomas.

High-quality mammography combined with clinical breast exam remains the only screening method clearly tied to reduction in breast cancer mortality. Lower dose x-rays, digitized computer rather than film images, and the use of computer programs to assist diagnosis, are almost ready for widespread dissemination. Other technologies also are being developed, including magnetic resonance imaging and ultrasound. In addition, a very low radiation exposure technique, positron emission tomography has the potential for detecting early breast cancer.

It is also possible to differentiate between non-cancerous breast tissue and malignant breast tissue by analyzing differential gene expression between tissues. In addition, there may be several possible alterations that lead to the various possible types of breast cancer. The different types of breast tumors (*e.g.*, invasive vs. non-invasive, ductal vs. axillary lymph node) can be differentiable from one another by the identification of the differences in genes expressed by different types of breast tumor tissues (Porter-Jordan *et al.*, *Hematol Oncol Clin North Am* (1994) 8:73). Breast cancer can thus be generally diagnosed by detection of expression of a gene or genes associated with breast tumors. Where enough information is available about the differential gene expression between various types of breast tumor tissues, the specific type of breast tumor can also be diagnosed.

For example, increased estrogen receptor (ER) expression in normal breast epithelium, while not itself indicative of malignant tissue, is a known risk marker for development of breast cancer. Khan SA *et al.*, *Cancer Res* (1994) 54:993. Malignant breast cancer is often divided into two groups, ER-positive and ER-negative, based on the estrogen receptor status of the tissue. The ER status represents different survival length and response to hormone therapy, and is thought to represent either: 1) an indicator of different stages of the disease, or 2) an indicator that allows differentiation between two similar but distinct diseases. K. Zhu *et al.*, *Med. Hypoth.* (1997) 49:69. A number of other genes are known to vary expression between either different stages of cancer or different types of similar breast cancer.

Similarly, the expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer. The differential expression of a polynucleotide in human breast tumor tissue can be used as a diagnostic marker for human breast cancer. The polynucleotides of the invention that would be especially useful for this purpose are

those that exhibit differential expression between breast cancer tissue with a high metastatic potential and a low metastatic potential, *i.e.* SEQ ID NOS: 9, 42, 52, 62, 65, 66, 68, 114, 123, 144, 172, 178, 214, 219, 223, 258, 317, and 379. Detection of breast cancer can be determined using expression levels of any of these sequences alone or in combination.

- 5 Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, *e.g.* ER expression. In addition, development of breast cancer can be detected by examining the ratio of SEQ ID NO: to the levels of steroid hormones (*e.g.*, testosterone or estrogen) or to other hormones
- 10 (*e.g.*, growth hormone, insulin). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

- Diagnosis of breast cancer can also involve comparing the expression of a
- 15 polynucleotide of the invention with the expression of other sequences in non-malignant breast tissue samples in comparison to one or more forms of the diseased tissue. A comparison of expression of one or more polynucleotides of the invention between the samples provides information on relative levels of these polynucleotides as well as the ratio of these polynucleotides to the expression of other sequences in the tissue of interest
- 20 compared to normal.

- This risk of breast cancer is elevated significantly by the presence of an inherited risk for breast cancer, such as a mutation in BRCA-1 or BRCA-2. New diagnostic tools are being developed to address the needs of higher risk patients to complement mammography and physical examinations for early detection of breast cancer, particularly among younger
- 25 women. The presence of antigen or expression markers in nipple aspirate fluid (NAF) samples collected from one or both breasts can be useful for useful for risk assessment or early cancer detection. Breast cytology and biomarkers obtained by random fine needle aspiration have been used to identify hyperplasia with atypia and overexpression of p53 and EGFR. The polynucleotides of the invention can be used in multivariate analysis with
- 30 expression studies with genes such as p53 and EGFR as risk predictors and as surrogate endpoint biomarkers for breast cancer.

As well as being used for diagnosis and risk assessment, the expression of certain genes can also correlated to prognosis of a disease state. The expression of particular gene have been used as prognostic indicators for breast cancer including increased expression of *c-erbB-2*, pS2, ER, progesterone receptor, epidermal growth factor receptor (EGFR), *neu*,  
5 *myc*, *bcl-2*, *int2*, cytosolic tyrosine kinase, cyclin E, *prad-1*, *hst*, uPA, PAI-1, PAI-2, cathepsin D, as well as the presence of a number of cancer-specific antigens, *e.g.* CEA, CA M26, CA M29 and CA 15.3. Davis, *Br. J. Biomed Sci.* (1996) 53:157. Poor prognosis has also been linked to a decrease in expression of certain genes, such as *p53*, *Rb*, *nm23*. The expression of the polynucleotides of the invention can be of prognostic value for determining  
10 the metastatic potential of a malignant breast cancer, as this molecules are differentially expressed between high and low metastatic potential tissues tumors. The levels of these polynucleotides in patients with malignant breast cancer can compared to normal tissue, malignant tissue with a known high potential metastatic level, and malignant tissue with a known lower level of metastatic potential to provide a prognosis for a particular patient.  
15 Such a prognosis is predictive of the extent and nature of the cancer. The determined prognosis is useful in determining the prognosis of a patient with breast cancer, both for initial treatment of the disease and for longer-term monitoring of the same patient. If samples are taken from the same individual over a period of time, differences in polynucleotide expression that are specific to that patient can be identified and closely  
20 watched.

Colon Cancer. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Indeed, colorectal cancer is the second most preventable cancer, after lung cancer. Colorectal cancer begins as polyps,  
25 which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. About 20 percent of all cases of colon cancer are thought to be related to heredity. Currently, multiple familial colorectal cancer disorders have been identified, which are summarized as follows:

30       Familial adenomatous polyposis (FAP): This condition results in a person having hundreds or even thousands of polyps in the colon and rectum that usually first appear during

the teenage years. Cancer nearly always develops in one or more of these polyps between the ages of 30 and 50.

Gardner's syndrome: Like FAP, Gardner's syndrome results in polyps and colorectal cancers that develop at a young age. It can also cause benign tumors of the skin, soft  
5 connective tissue and bones.

Hereditary nonpolyposis colon cancer (HNPCC): People with this condition tend to develop colorectal cancer at a young age, without first having many polyps. HNPCC has an autosomal dominant pattern of inheritance with variable but high penetrance estimated to be about 90%. HNPCC underlies 0.5%-10% of all cases of colorectal cancer. An understanding  
10 of the mechanisms behind the development of HNPCC is emerging, and genetic presymptomatic testing, now being conducted in research settings, soon will be available on a widespread basis for individuals identified at risk for this disease.

Familial colorectal cancer in Ashkenazi Jews: Recent research has found an inherited tendency to developing colorectal cancer among some Jews of Eastern European descent.

15 Like people with FAP, Gardner's syndrome, and HNPCC, their increased risk is due to an inherited mutation present in about 6% of American Jews.

Several tests are currently used to screen for colorectal cancer, including digital rectal examination, fecal occult blood test, sigmoidoscopy, colonoscopy, virtual colonoscopy and MRI. Each of these tests identifies potential colorectal cancer lesions, or a risk of  
20 development of these lesions, at a fairly gross morphological level.

The sequential alteration of a number of genes is associated with malignant adenocarcinoma, including the genes DCC, p53, ras, and FAP. For a review, see *e.g.* Fearon ER, *et al.*, *Cell* (1990) 61(5):759; Hamilton SR *et al.*, *Cancer* (1993) 72:957; Bodmer W, *et al.*, *Nat Genet.* (1994) 4(3):217; Fearon ER, *Ann N Y Acad Sci.* (1995) 768:101. Molecular  
25 genetic alterations are thus promising as potential diagnostic and prognostic indicators in colorectal carcinoma and molecular genetics of colorectal carcinoma since it is possible to differentiate between different types of colorectal neoplasias using molecular markers. Colorectal cancer can thus be generally diagnosed by detection of expression of a gene or genes associated with colorectal tumors.

30 Similarly, the expression of polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. The differential expression of a

polynucleotide in hyperplasia can be used as a diagnostic marker for colon cancer. The polynucleotides of the invention that would be especially useful for this purpose are those that exhibit differential expression between malignant metastatic colon cancer and normal patient tissue, *i.e.* SEQ ID NOS: 52, 119, 172, 288. Detection of malignant colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression.

Determination of the aggressive nature and/or the metastatic potential of a colon cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.* p53 expression. In addition, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

G. Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides.

A library of peptides can be synthesized following the methods disclosed in U.S. Pat. No. 5,010,175 ('175), and in WO 91/17823. As described below in brief, one prepares a mixture of peptides, which is then screened to identify the peptides exhibiting the desired signal transduction and receptor binding activity. In the '175 method, a suitable peptide synthesis support (*e.g.*, a resin) is coupled to a mixture of appropriately protected, activated amino acids. The concentration of each amino acid in the reaction mixture is balanced or adjusted in inverse proportion to its coupling reaction rate so that the product is an equimolar mixture of amino acids coupled to the starting resin. The bound amino acids are then deprotected, and reacted with another balanced amino acid mixture to form an equimolar mixture of all possible dipeptides. This process is repeated until a mixture of peptides of the desired length (*e.g.*, hexamers) is formed. Note that one need not include all amino acids in each step: one can include only one or two amino acids in some steps (*e.g.*, where it is

known that a particular amino acid is essential in a given position), thus reducing the complexity of the mixture. After the synthesis of the peptide library is completed, the mixture of peptides is screened for binding to the selected polypeptide. The peptides are then tested for their ability to inhibit or enhance activity. Peptides exhibiting the desired activity are then isolated and sequenced.

The method described in WO 91/17823 is similar. However, instead of reacting the synthesis resin with a mixture of activated amino acids, the resin is divided into twenty equal portions (or into a number of portions corresponding to the number of different amino acids to be added in that step), and each amino acid is coupled individually to its portion of resin.

The resin portions are then combined, mixed, and again divided into a number of equal portions for reaction with the second amino acid. In this manner, each reaction can be easily driven to completion. Additionally, one can maintain separate "subpools" by treating portions in parallel, rather than combining all resins at each step. This simplifies the process of determining which peptides are responsible for any observed receptor binding or signal transduction activity.

In such cases, the subpools containing, *e.g.*, 1-2,000 candidates each are exposed to one or more polypeptides of the invention. Each subpool that produces a positive result is then resynthesized as a group of smaller subpools (sub-subpools) containing, *e.g.*, 20-100 candidates, and reassayed. Positive sub-subpools can be resynthesized as individual compounds, and assayed finally to determine the peptides that exhibit a high binding constant. These peptides can be tested for their ability to inhibit or enhance the native activity. The methods described in WO 91/7823 and U.S. Patent No. 5,194,392 (herein incorporated by reference) enable the preparation of such pools and subpools by automated techniques in parallel, such that all synthesis and resynthesis can be performed in a matter of days.

Peptide agonists or antagonists are screened using any available method, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The methods described herein are presently preferred. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at



concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

5           The end results of such screening and experimentation will be at least one novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the  
10   receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

#### H.     Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions can comprise polypeptides, antibodies, or  
15   polynucleotides of the claimed invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a  
20   detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful  
25   to specify an exact effective amount in advance. However, the effective amount for a given situation is determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

30           A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a

therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents.

The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be

administered without undue toxicity. Suitable carriers can be large, slowly metabolized

5 macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of  
10 organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or  
15 emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

20 Delivery Methods. Once formulated, the compositions of the invention can be (1) administered directly to the subject (*e.g.*, as polynucleotide or polypeptides); (2) delivered *ex vivo*, to cells derived from the subject (*e.g.*, as in *ex vivo* gene therapy); or (3) delivered *in vitro* for expression of recombinant proteins (*e.g.*, polynucleotides). Direct delivery of the compositions will generally be accomplished by injection, either  
25 subcutaneously, intraperitoneally, intravenously or intramuscularly, or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

30 Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *e.g.*, International Publication No. WO

93/14778. Examples of cells useful in ex vivo applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both ex vivo and in vitro applications can be accomplished by, for example, dextran-mediated transfection, calcium phosphate

5 precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the  
10 disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide or corresponding polypeptide.

Preparation of antisense polynucleotides is discussed above. Neoplasias that are treated with the antisense composition include, but are not limited to, cervical cancers, melanomas, colorectal adenocarcinomas, Wilms' tumor, retinoblastoma, sarcomas,  
15 myosarcomas, lung carcinomas, leukemias, such as chronic myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and myeloid leukemia, and lymphomas, such as histiocytic lymphoma. Proliferative disorders that are treated with the therapeutic composition include disorders such as anhydric hereditary ectodermal dysplasia, congenital alveolar dysplasia, epithelial dysplasia of the cervix, fibrous dysplasia of bone, and  
20 mammary dysplasia. Hyperplasias, for example, endometrial, adrenal, breast, prostate, or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of the skin, are treated with antisense therapeutic compositions based upon a polynucleotide of the invention. Even in disorders in which mutations in the corresponding gene are not implicated, downregulation or inhibition of expression of a gene corresponding to a polynucleotide of the invention can  
25 have therapeutic application. For example, decreasing gene expression can help to suppress tumors in which enhanced expression of the gene is implicated.

Both the dose of the antisense composition and the means of administration are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors.

30 Administration of the therapeutic antisense agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized

administration, and topical administration. Preferably, the therapeutic antisense composition contains an expression construct comprising a promoter and a polynucleotide segment of at least 12, 22, 25, 30, or 35 contiguous nucleotides of the antisense strand of a polynucleotide disclosed herein. Within the expression construct, the polynucleotide segment is located downstream from the promoter, and transcription of the polynucleotide segment initiates at the promoter.

Various methods are used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues is also used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis *et al.*, *Trends Biotechnol.* (1993) 11:202; Chiou *et al.*, *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu *et al.*, *J. Biol. Chem.* (1988) 263:621; Wu *et al.*, *J. Biol. Chem.* (1994) 269:542; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) 87:3655; Wu *et al.*, *J. Biol. Chem.* (1991) 266:338. Preferably, receptor-mediated targeted delivery of therapeutic compositions containing antibodies of the invention is used to deliver the antibodies to specific tissue.

Therapeutic compositions containing antisense subgenomic polynucleotides are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 µg to about 2 mg, about 5 µg to about 500 µg, and about 20 µg to about 100 µg of DNA can also be used during a gene therapy protocol. Factors such as method of action and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is

desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine  
5 experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. A more complete description of gene therapy vectors, especially retroviral vectors, is contained in U.S. Serial No. 08/869,309, which is expressly incorporated herein, and in section G below.

For polynucleotide-related genes encoding polypeptides or proteins with anti-  
10 inflammatory activity, suitable use, doses, and administration are described in U.S. Patent No. 5,654,173. Therapeutic agents also include antibodies to proteins and polypeptides encoded by the polynucleotides of the invention and related genes, as described in U.S. Patent No. 5,654,173.

#### I. Gene Therapy

15 The therapeutic polynucleotides and polypeptides of the present invention can be utilized in gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) 1:51; Kimura, *Human Gene Therapy* (1994) 5:845; Connelly, *Human Gene Therapy* (1995) 1:185; and Kaplitt, *Nature Genetics* (1994) 6:148). Gene therapy vehicles for delivery of constructs including a coding  
20 sequence of a therapeutic of the invention can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches. Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

The present invention can employ recombinant retroviruses which are constructed to  
25 carry or express a selected nucleic acid molecule of interest. Retrovirus vectors that can be employed include those described in EP 0 415 731; WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; U.S. Patent No. 5, 219,740; WO 93/11230; WO 93/10218; Vile and Hart, *Cancer Res.* (1993) 53:3860; Vile *et al.*, *Cancer Res.* (1993) 53:962; Ram *et al.*, *Cancer Res.* (1993) 53:83; Takamiya *et al.*, *J. Neurosci. Res.* (1992) 33:493; Baba *et al.*, *J. Neurosurg.* (1993) 79:729; U.S. Patent No. 4,777,127; GB Patent No. 2,200,651; and EP 0  
30 345 242. Preferred recombinant retroviruses include those described in WO 91/02805.

Packaging cell lines suitable for use with the above-described retroviral vector constructs can be readily prepared (see, *e.g.*, WO 95/30763 and WO 92/05266), and used to create producer cell lines (also termed vector cell lines) for the production of recombinant vector particles. Within particularly preferred embodiments of the invention, packaging cell  
5 lines are made from human (such as HT1080 cells) or mink parent cell lines, thereby allowing production of recombinant retroviruses that can survive inactivation in human serum.

The present invention also employs alphavirus-based vectors that can function as gene delivery vehicles. Such vectors can be constructed from a wide variety of alphaviruses,  
10 including, for example, Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532). Representative examples of such vector systems include those described in U.S. Patent Nos. 5,091,309; 5,217,879; and 5,185,440; WO 92/10578; WO 94/21792; WO 95/27069; WO  
15 95/27044; and WO 95/07994. Gene delivery vehicles of the present invention can also employ parvovirus such as adeno-associated virus (AAV) vectors. Representative examples include the AAV vectors disclosed by Srivastava in WO 93/09239, Samulski *et al.*, *J. Virol.* (1989) 63:3822; Mendelson *et al.*, *Virol.* (1988) 166:154; and Flotte *et al.*, *PNAS* (1993) 90:10613.

Representative examples of adenoviral vectors include those described by Berkner, *Biotechniques* (1988) 6:616; Rosenfeld *et al.*, *Science* (1991) 252:431; WO 93/19191; Kolls  
20 *et al.*, *PNAS* (1994) 91:215; Kass-Eisler *et al.*, *PNAS* (1993) 90:11498; Guzman *et al.*, *Circulation* (1993) 88:2838; Guzman *et al.*, *Cir. Res.* (1993) 73:1202; Zabner *et al.*, *Cell* (1993) 75:207; Li *et al.*, *Hum. Gene Ther.* (1993) 4:403; Cailaud *et al.*, *Eur. J. Neurosci.* (1993) 5:1287; Vincent *et al.*, *Nat. Genet.* (1993) 5:130; Jaffe *et al.*, *Nat. Genet.* (1992) 1:372; and Levrero *et al.*, *Gene* (1991) 101:195. Exemplary adenoviral gene therapy vectors employable in this invention also include those described in WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655. Administration of DNA  
25 linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) 3:147 can be  
30 employed.

Other gene delivery vehicles and methods can be employed, including polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example Curiel, *Hum. Gene Ther.* (1992) 3:147; ligand linked DNA, for example see Wu, *J. Biol. Chem.* (1989) 264:16985; eukaryotic cell delivery vehicles cells, for example see U.S. Pat. No. 5,814,482; 5 WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338; deposition of photopolymerized hydrogel materials; hand-held gene transfer particle gun, as described in U.S. Patent No. 5,149,655; ionizing radiation as described in U.S. Patent No. 5,206,152 and in WO92/11033; nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) 14:2411, and in Woffendin, *Proc.* 10 *Natl. Acad. Sci.* (1994) 91:1581.

Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and U.S. Patent No. 5,580,859. Uptake efficiency can be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method can be improved 15 further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm. Liposomes that can act as gene delivery vehicles are described in U.S. Patent No. 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968.

Further non-viral delivery suitable for use includes mechanical delivery systems such 20 as the approach described in Woffendin *et al.*, *Proc. Natl. Acad. Sci. USA* (1994) 91(24):11581. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. Patent No. 25 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. Patent No. 5,206,152 and WO 92/11033.

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in 30 any way.

### EXAMPLES

The present invention is now illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, these embodiments are illustrative and are not meant to be construed as restricting the invention in any way.

5

Example 1: Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

Human colon cancer cell line Km12L4-A (Morika, W. A. K. et al., *Cancer Research* (1988) 48:6863) was used to construct a cDNA library from mRNA isolated from the cells.

- 10 As described in the above overview, a total of 4,693 sequences expressed by the Km12L4-A cell line were isolated and analyzed; most sequences were about 275-300 nucleotides in length. The KM12L4-A cell line is derived from the KM12C cell line. The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B<sub>2</sub> surgical specimen (Morikawa et al. *Cancer Res.* (1988) 48:6863). The KML4-A is
- 15 a highly metastatic subline derived from KM12C (Yeatman et al. *Nucl. Acids. Res.* (1995) 23:4007; Bao-Ling et al. *Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-A, etc.) are well-recognized in the art as a model cell line for the study of colon cancer (see, e.g., Moriakawa et al., *supra*; Radinsky et al. *Clin. Cancer Res.* (1995) 1:19; Yeatman et al., (1995) *supra*;
- 20 Yeatman et al. *Clin. Exp. Metastasis* (1996) 14:246).

- The sequences were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated
- 25 DNA Sequencing and Analysis Techniques" Adams et al., eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie et al. *Comput. Chem.* (1993) 17:191 ). Generally, masking does not influence the final search results, except to eliminate of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. Masking resulted in the
- 30 elimination of 43 sequences. The remaining sequences were then used in a BLASTN vs. Genbank search with search parameters of greater than 70% overlap, 99% identity, and a p value of less than  $1 \times 10^{-40}$ , which search resulted in the discarding of 1,432 sequences. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.



The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the Genbank search), (2) weak similarity (greater than 45% identity and p value of less than  $1 \times 10^{-5}$ ), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than  $1 \times 10^{-5}$ ). This search resulted in discard of 98 sequences as having greater than 70% overlap, greater than 99% identity, and p value of less than  $1 \times 10^{-40}$ .

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search resulted in discard of 1771 sequences (sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than  $1 \times 10^{-40}$ ; sequences with a p value of less than  $1 \times 10^{-65}$  when compared to a database sequence of human origin were also excluded). Second, a BLASTN vs. Patent GeneSeq database resulted in discard of 15 sequences (greater than 99% identity; p value less than  $1 \times 10^{-40}$ ; greater than 99% overlap).

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than  $1 \times 10^{-111}$  in relation to a database sequence of human origin were specifically excluded. The final result provided the 404 sequences listed in the accompanying Sequence Listing. The Sequence Listing is arranged beginning with sequences with no similarity to any sequence in a database searched, and ending with sequences with the greatest similarity. Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Polynucleotides that were determined to be novel were assigned a sequence identification number.

The novel polynucleotides and were assigned sequence identification numbers SEQ ID NOS: 1-404. The DNA sequences corresponding to the novel polynucleotides are provided in the Sequence Listing. The majority of the sequences are presented in the Sequence Listing in the 5' to 3' direction. A small number, 25, are listed in the Sequence Listing in the 5' to 3' direction but the sequence as written is actually 3' to 5'. These sequences are readily identified with the designation "AR" in the Sequence Name in Table 1 (inserted before the claims). The sequences correctly listed in the 5' to 3' direction in the Sequence Listing are designated "AF." The Sequence Listing filed herewith therefore contains 25 sequences listed in the reverse order, namely SEQ ID NOS:47, 97, 137, 171, 173, 179, 182, 194, 200, 202, 213, 227, 258, 264, 275, 302, 313, 324, 329, 330, 331, 338, 358, 379, and 404.

Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

5 In order to confirm the sequences of SEQ ID NOS:1-404, inserts of the clones corresponding to these polynucleotides were re-sequenced. These "validation" sequences are provided in SEQ ID NOS:405-800. These validation sequences were often longer than the original polynucleotide sequences. They validate, and thus often provide additional sequence information. Validation sequences can be correlated with the original sequences  
10 they validate by identifying those sequences of SEQ ID NOS:1-404 and the validation sequences of SEQ ID NOS:405-800 that share the same clone name in Table 1.

**Example 2: Results of Public Database Search to Identify Function of Gene Products**

SEQ ID NOS:1-404, as well as the validation sequences SEQ ID NOS:405-800, were  
15 translated in all three reading frames to determine the best alignment with the individual sequences. These amino acid sequences and nucleotide sequences are referred, generally, as query sequences, which are aligned with the individual sequences. Query and individual sequences were aligned using the BLAST programs, available over the world wide web at <http://www.ncbi.nlm.nih.gov/BLAST/>. Again the sequences were masked to various extents  
20 to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Table 2 (inserted before the claims) shows the results of the alignments. Table 2 refers to each sequence by its SEQ ID NO:, the accession numbers and descriptions of nearest neighbors from the Genbank and Non-Redundant Protein searches, and the p values  
25 of the search results. Table 1 identifies each SEQ ID NO: by SEQ name, clone ID, and cluster. As discussed above, a single cluster includes polynucleotides representing the same gene or gene family, and generally represents sequences encoding the same gene product.

For each of SEQ ID NOS:1-800, the best alignment to a protein or DNA sequence is included in Table 2. The activity of the polypeptide encoded by SEQ ID NOS:1-800 is the  
30 same or similar to the nearest neighbor reported in Table 2. The accession number of the nearest neighbor is reported, providing a reference to the activities exhibited by the nearest neighbor. The search program and database used for the alignment also are indicated as well as a calculation of the p value.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of SEQ ID NOS:1-800. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of SEQ ID NOS:1-800.

5 SEQ ID NOS:1-800 and the translations thereof may be human homologs of known genes of other species or novel allelic variants of known human genes. In such cases, these new human sequences are suitable as diagnostics or therapeutics. As diagnostics, the human sequences SEQ ID NOS:1-800 exhibit greater specificity in detecting and differentiating human cell lines and types than homologs of other species. The human polypeptides  
10 encoded by SEQ ID NOS:1-800 are likely to be less immunogenic when administered to humans than homologs from other species. Further, on administration to humans, the polypeptides encoded by SEQ ID NOS:1-800 can show greater specificity or can be better regulated by other human proteins than are homologs from other species.

15 **Example 3: Members of Protein Families**

After conducting a profile search as described in the specification above, several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 3). Thus the  
20 invention encompasses fragments, fusions, and variants of such polynucleotides that retain biological activity associated with the protein family and/or functional domain identified herein.

**Table 3** Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
24	4 transmembrane segments integral membrane proteins	1218	578	rev
41	4 transmembrane segments integral membrane proteins	1086	413	rev
101	4 transmembrane segments integral membrane proteins	1206	544	rev
157	4 transmembrane segments integral membrane proteins	721	33	rev
341	4 transmembrane segments integral membrane proteins	1253	613	rev
395	4 transmembrane segments integral membrane proteins	530	10	for
395	4 transmembrane segments integral membrane proteins	696	17	for
395	4 transmembrane segments integral membrane proteins	471	39	rev
24	7 transmembrane receptor (Secretin family)	1301	491	rev
41	7 transmembrane receptor (Secretin family)	1309	10	rev
101	7 transmembrane receptor (Secretin family)	1330	296	rev
157	7 transmembrane receptor (Secretin family)	1173	249	rev
291	7 transmembrane receptor (Secretin family)	1400	269	rev

**Table 3** Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
291	7 transmembrane receptor (Secretin family)	712	130	for
305	7 transmembrane receptor (Secretin family)	926	4	for
305	7 transmembrane receptor (Secretin family)	753	55	rev
315	7 transmembrane receptor (Secretin family)	1058	270	rev
341	7 transmembrane receptor (Secretin family)	1265	534	rev
116	Ank repeat	141	218	for
251	Ank repeat	290	207	for
251	Ank repeat	467	387	for
63	ATPases Associated with Various Cellular Activities	543	60	for
116	ATPases Associated with Various Cellular Activities	802	313	for
134	ATPases Associated with Various Cellular Activities	525	57	rev
136	ATPases Associated with Various Cellular Activities	712	163	for
151	ATPases Associated with Various Cellular Activities	719	73	for
151	ATPases Associated with Various Cellular Activities	386	13	for
384	ATPases Associated with Various Cellular Activities	664	140	for
404	ATPases Associated with Various Cellular Activities	704	52	for
374	Basic region plus leucine zipper transcription factors	298	146	for
97	Bromodomain (conserved sequence found in human, Drosophila and yeast proteins.)	230	63	for
136	EF-hand	121	207	for
242	EF-hand	238	155	for
379	EF-hand	212	126	for
308	Eukaryotic aspartyl proteases	1300	461	rev
213	GATA family of transcription factors	720	377	for
367	G-protein alpha subunit	971	467	rev
188	Phorbol esters/diacylglycerol binding	91	177	for
251	Phorbol esters/diacylglycerol binding	133	219	for
202	protein kinase	482	1	rev
202	protein kinase	970	1	rev
315	protein kinase	739	158	for
315	protein kinase	1023	197	for
367	protein kinase	1046	285	rev
397	protein kinase	511	6	for
256	Protein phosphatase 2C	13	90	for
256	Protein phosphatase 2C	163	86	for
382	Protein Tyrosine Phosphatase	261	2	for
306	SH3 Domain	141	296	for
386	SH3 Domain	359	209	for
169	Trypsin	764	164	rev
188	WD domain, G-beta repeats	480	382	for
188	WD domain, G-beta repeats	206	117	for
335	WD domain, G-beta repeats	3	92	for
23	wnt family of developmental signaling proteins	1151	335	rev
291	wnt family of developmental signaling proteins	779	89	rev
291	wnt family of developmental signaling proteins	1347	382	rev
324	wnt family of developmental signaling proteins	1180	499	rev
330	wnt family of developmental signaling proteins	1180	499	rev
341	wnt family of developmental signaling proteins	1399	560	rev

**Table 3** Polynucleotides encoding gene products of a protein family or having a known functional domain(s).

SEQ ID NO:	Biological Activity (Profile hit)	Start	Stop	Dir
353	wnt family of developmental signaling proteins	880	49	rev
188	WW/rsp5/WWP domain containing proteins	431	354	for
379	WW/rsp5/WWP domain containing proteins	12	89	for
395	WW/rsp5/WWP domain containing proteins	153	76	for
395	WW/rsp5/WWP domain containing proteins	156	64	for
61	Zinc finger, C2H2 type	254	192	for
306	Zinc finger, C2H2 type	428	367	for
386	Zinc finger, C2H2 type	191	253	for
322	Zinc finger, CCHC class	553	503	for
306	Zinc-binding metalloprotease domain	101	60	rev
395	Zinc-binding metalloprotease domain	28	69	rev

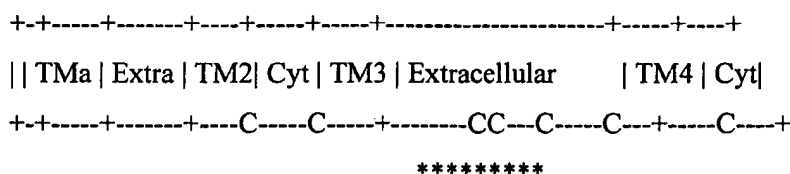
Start and stop indicate the position within the individual sequences that align with the query sequence having the indicated SEQ ID NO. The direction (Dir) indicates the orientation of the query sequence with respect to the individual sequence, where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence Listing.

Some polynucleotides exhibited multiple profile hits because, for example, the particular sequence contains overlapping profile regions, and/or the sequence contains two different functional domains. These profile hits are described in more detail below.

a) Four Transmembrane Integral Membrane Proteins. SEQ ID NOS: 24, 41, 101, 157, 341, and 395 correspond to a sequence encoding a polypeptide that is a member of the 4 transmembrane segments integral membrane protein family (transmembrane 4 family). The transmembrane 4 family of proteins includes a number of evolutionarily-related eukaryotic cell surface antigens (Levy *et al.*, *J. Biol. Chem.*, (1991) 266:14597; Tomlinson *et al.*, *Eur. J. Immunol.* (1993) 23:136; Barclay *et al.* The leucocyte antigen factbooks. (1993) Academic Press, London/San Diego). The proteins belonging to this family include: 1) Mammalian antigen CD9 (MIC3), which is involved in platelet activation and aggregation; 2) Mammalian leukocyte antigen CD37, expressed on B lymphocytes; 3) Mammalian leukocyte antigen CD53 (OX-44), which is implicated in growth regulation in hematopoietic cells; 4) Mammalian lysosomal membrane protein CD63 (melanoma-associated antigen ME491; antigen AD1); 5) Mammalian antigen CD81 (cell surface protein TAPA-1), which is implicated in regulation of lymphoma cell growth; 6) Mammalian antigen CD82 (protein

R2; antigen C33; Kangai 1 (KAI1)), which associates with CD4 or CD8 and delivers costimulatory signals for the TCR/CD3 pathway; 7) Mammalian antigen CD151 (SFA-1; platelet-endothelial tetraspan antigen 3 (PETA-3)); 8) Mammalian cell surface glycoprotein A15 (TALLA-1; MXS1); 9) Mammalian novel antigen 2 (NAG-2); 10) Human tumor-associated antigen CO-029; 11) *Schistosoma mansoni* and *japonicum* 23 Kd surface antigen (SM23 / SJ23).

The members of the 4 transmembrane family share several characteristics. First, they all are apparently type III membrane proteins, which are integral membrane proteins containing an N-terminal membrane-anchoring domain which is not cleaved during biosynthesis and which functions both as a translocation signal and as a membrane anchor. The family members also contain three additional transmembrane regions, at least seven conserved cysteines residues, and are of approximately the same size (218 to 284 residues). These proteins are collectively know as the "transmembrane 4 superfamily" (TM4) because they span plasma membrane four times. A schematic diagram of the domain structure of these proteins is as follows:



where Cyt is the cytoplasmic domain, TMa is the transmembrane anchor; TM2 to TM4 represents transmembrane regions 2 to 4, 'C' are conserved cysteines, and '\*' indicates the position of the consensus pattern. The consensus pattern spans a conserved region including two cysteines located in a short cytoplasmic loop between two transmembrane domains: Consensus pattern: G-x(3)-[LIVMF]-x(2)-[GSA]-[LIVMF](2)-G-C-x-[GA]-[STA]- x(2)-[EG]-x(2)-[CWN]-[LIVM](2).

b) Seven Transmembrane Integral Membrane Proteins. SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, and 341 correspond to a sequence encoding a polypeptide that is a member of the seven transmembrane receptor family. G-protein coupled receptors (Strosberg, *Eur. J. Biochem.* (1991) 196:1; Kerlavage, *Curr. Opin. Struct. Biol.* (1991) 1:394; and Probst *et al.*, *DNA Cell Biol.* (1992) 11:1; and Savarese *et al.*, *Biochem. J.* (1992) 293:1) (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. The tertiary structure of these receptors is thought to be highly similar. They have seven hydrophobic regions, each of which most probably spans

the membrane. The N-terminus is located on the extracellular side of the membrane and is often glycosylated, while the C-terminus is cytoplasmic and generally phosphorylated.

Three extracellular loops alternate with three intracellular loops to link the seven transmembrane regions. Most, but not all of these receptors, lack a signal peptide. The most conserved parts of these proteins are the transmembrane regions and the first two cytoplasmic loops. A conserved acidic-Arg-aromatic triplet is present in the N-terminal extremity of the second cytoplasmic loop (Attwood *et al.*, *Gene* (1991) 98:153) and could be implicated in the interaction with G proteins.

To detect this widespread family of proteins a pattern is used that contains the conserved triplet and that also spans the major part of the third transmembrane helix. Additional information about the seven transmembrane receptor family, and methods for their identification and use, is found in U.S. Patent No. 5,759,804. Due in part to their expression on the cell surface and other attractive characteristics, seven transmembrane protein family members are of particular interest as drug targets, as surface antigen markers, and as drug delivery targets (*e.g.*, using antibody-drug complexes and/or use of anti-seven transmembrane protein antibodies as therapeutics in their own right).

c) Ank Repeats. SEQ ID NOS: 116 and 251 represent polynucleotides encoding Ank repeat-containing proteins. The ankyrin motif is a 33 amino acid sequence named after the protein ankyrin which has 24 tandem 33-amino-acid motifs. Ank repeats were originally identified in the cell-cycle-control protein cdc10 (Breedon *et al.*, *Nature* (1987) 329:651). Proteins containing ankyrin repeats include ankyrin, myotropin, I-kappaB proteins, cell cycle protein cdc10, the Notch receptor (Matsuno *et al.*, *Development* (1997) 124(21):4265); G9a (or BAT8) of the class III region of the major histocompatibility complex (Biochem J. 290:811-818, 1993), FABP, GABP, 53BP2, Lin12, glp-1, SW14, and SW16. The functions of the ankyrin repeats are compatible with a role in protein-protein interactions (Bork, *Proteins* (1993) 17(4):363; Lambert and Bennet, *Eur. J. Biochem.* (1993) 211:1; Kerr *et al.*, *Current Op. Cell Biol.* (1992) 4:496; Bennet *et al.*, *J. Biol. Chem.* (1980) 255:6424).

The 90 kD N-terminal domain of ankyrin contains a series of 24 33-amino-acid ank repeats. (Lux *et al.*, *Nature* (1990) 344:36-42, Lambert *et al.*, *PNAS USA* (1990) 87:1730.)

The 24 ank repeats form four folded subdomains of 6 repeats each. These four repeat subdomains mediate interactions with at least 7 different families of membrane proteins. Ankyrin contains two separate binding sites for anion exchanger dimers. One site utilizes repeat subdomain two (repeats 7-12) and the other requires both repeat subdomains 3 and 4 (repeats 13-24). Since the anion exchangers exist in dimers, ankyrin binds 4 anion

exchangers at the same time. (Michaely and Bennett, *J. Biol. Chem.* (1995) 270(37):22050)

The repeat motifs are involved in ankyrin interaction with tubulin, spectrin, and other membrane proteins. (Lux *et al.*, *Nature* (1990) 344:36.)

The Rel/NF-kappaB/Dorsal family of transcription factors have activity that is controlled by sequestration in the cytoplasm in association with inhibitory proteins referred to as I-kappaB. (Gilmore, *Cell* (1990) 62:841; Nolan and Baltimore, *Curr Opin Genet Dev.* (1992) 2:211; Baeuerle, *Biochim Biophys Acta* (1991) 1072:63; Schmitz *et al.*, *Trends Cell Biol.* (1991) 1:130.) I-kappaB proteins contain 5 to 8 copies of 33 amino acid ankyrin repeats and certain NF-kappaB/rel proteins are also regulated by cis-acting ankyrin repeat containing domains including p105NF-kappaB which contains a series of ankyrin repeats (Diehl and Hannink, *J. Virol.* (1993) 67(12):7161). The I-kappaBs and Cactus (also containing ankyrin repeats) inhibit activators through differential interactions with the Rel-homology domain. The gene family includes proto-oncogenes, thus broadly implicating I-kappaB in the control of both normal gene expression and the aberrant gene expression that makes cells cancerous. (Nolan and Baltimore, *Curr Opin Genet Dev.* (1992) 2(2):211-220). In the case of rel/NF-kappaB and pp40/I-kappaB $\beta$ , both the ankyrin repeats and the carboxy-terminal domain are required for inhibiting DNA-binding activity and direct association of pp40/I-kappaB $\beta$  with rel/NF-kappaB protein. The ankyrin repeats and the carboxy-terminal of pp40/I-kappaB $\beta$  form a structure that associates with the rel homology domain to inhibit DNA binding activity (Inoue *et al.*, *PNAS USA* (1992) 89:4333).

The 4 ankyrin repeats in the amino terminus of the transcription factor subunit GABP $\beta$  are required for its interaction with the GABP $\alpha$  subunit to form a functional high affinity DNA-binding protein. These repeats can be crosslinked to DNA when GABP is bound to its target sequence. (Thompson *et al.*, *Science* (1991) 253:762; LaMarco *et al.*, *Science* (1991) 253:789).

Myotrophin, a 12.5 kDa protein having a key role in the initiation of cardiac hypertrophy, comprises ankyrin repeats. The ankyrin repeats are characteristic of a hairpin-like protruding tip followed by a helix-turn-helix motif. The V-shaped helix-turn-helix of the repeats stack sequentially in bundles and are stabilized by compact hydrophobic cores, whereas the protruding tips are less ordered.

d) ATPases Associated with Various Cellular Activities (AAA). SEQ ID NOS: 63, 116, 134, 136, 151, 384, and 404 polynucleotides encoding novel members of the "ATPases Associated with diverse cellular Activities" (AAA) protein family The AAA protein family



is composed of a large number of ATPases that share a conserved region of about 220 amino acids that contains an ATP-binding site (Froehlich *et al.*, *J. Cell Biol.* (1991) 114:443; Erdmann *et al.* *Cell* (1991) 64:499; Peters *et al.*, *EMBO J.* (1990) 9:1757; Kunau *et al.*, *Biochimie* (1993) 75:209-224; Confalonieri *et al.*, *BioEssays* (1995) 17:639;   
 5 <http://yeamob.pci.chemie.uni-tuebingen.de/AAA/Description.html>). The proteins that belong to this family either contain one or two AAA domains.

Proteins containing two AAA domains include: 1) Mammalian and drosophila NSF (N-ethylmaleimide-sensitive fusion protein) and the fungal homolog, SEC18, which are involved in intracellular transport between the endoplasmic reticulum and Golgi, as well as   
 10 between different Golgi cisternae; 2) Mammalian transitional endoplasmic reticulum ATPase (previously known as p97 or VCP), which is involved in the transfer of membranes from the endoplasmic reticulum to the golgi apparatus. This ATPase forms a ring-shaped homooligomer composed of six subunits. The yeast homolog, CDC48, plays a role in spindle pole proliferation; 3) Yeast protein PAS1 essential for peroxisome assembly and the   
 15 related protein PAS1 from *Pichia pastoris*; 4) Yeast protein AFG2; 5) *Sulfolobus acidocaldarius* protein SAV and *Halobacterium salinarium* cdcH, which may be part of a transduction pathway connecting light to cell division.

Proteins containing a single AAA domain include: 1) *Escherichia coli* and other bacteria ftsH (or hflB) protein. FtsH is an ATP-dependent zinc metalloprotease that   
 20 degrades the heat-shock sigma-32 factor, and is an integral membrane protein with a large cytoplasmic C-terminal domain that contain both the AAA and the protease domains; 2) Yeast protein YME1, a protein important for maintaining the integrity of the mitochondrial compartment. YME1 is also a zinc-dependent protease; 3) Yeast protein AFG3 (or YTA10). This protein also contains an AAA domain followed by a zinc-dependent protease domain;   
 25 4) Subunits from regulatory complex of the 26S proteasome (Hilt *et al.*, *Trends Biochem. Sci.* (1996) 21:96), which is involved in the ATP-dependent degradation of ubiquitinated proteins, which subunits include: a) Mammalian 4 and homologs in other higher eukaryotes, in yeast (gene YTA5) and fission yeast (gene mts2); b) Mammalian 6 (TBP7) and homologs in other higher eukaryotes and in yeast (gene YTA2); c) Mammalian subunit 7 (MSS1) and   
 30 homologs in other higher eukaryotes and in yeast (gene CIM5 or YTA3); d) Mammalian subunit 8 (P45) and homologs in other higher eukaryotes and in yeast (SUG1 or CIM3 or TBY1) and fission yeast (gene let1); e) Other probable subunits include human TBP1, which influences HIV gene expression by interacting with the virus tat transactivator protein, and yeast YTA1 and YTA6; 5) Yeast protein BCS1, a mitochondrial protein essential for the

expression of the Rieske iron-sulfur protein; 6) Yeast protein MSP1, a protein involved in intramitochondrial sorting of proteins; 7) Yeast protein PAS8, and the corresponding proteins PAS5 from *Pichia pastoris* and PAY4 from *Yarrowia lipolytica*; 8) Mouse protein SKD1 and its fission yeast homolog (SpAC2G11.06); 9) *Caenorhabditis elegans* meiotic spindle formation protein mei-1; 10) Yeast protein SAP1; 11) Yeast protein YTA7; and 12) *Mycobacterium leprae* hypothetical protein A2126A.

In general, the AAA domains in these proteins act as ATP-dependent protein clamps (Confalonieri *et al.* (1995) *BioEssays* 17:639). In addition to the ATP-binding 'A' and 'B' motifs, which are located in the N-terminal half of this domain, there is a highly conserved region located in the central part of the domain which was used in the development of the signature pattern. The consensus pattern is: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]-D-x-A-[LIFA]-x-R.

e) Basic Region Plus Leucine Zipper Transcription Factors. SEQ ID NO:374 correspond to a polynucleotide encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) 2:105; and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) 4:12) of eukaryotic DNA-binding transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. Members of the family include transcription factor AP-1, which binds selectively to enhancer elements in the cis control regions of SV40 and metallothionein IIA. AP-1, also known as c-jun, is the cellular homolog of the avian sarcoma virus 17 (ASV17) oncogene v-jun.

Other members of this protein family include jun-B and jun-D, probable transcription factors that are highly similar to jun/AP-1; the fos protein, a proto-oncogene that forms a non-covalent dimer with c-jun; the fos-related proteins fra-1, and fos B; and mammalian cAMP response element (CRE) binding proteins CREB, CREM, ATF-1, ATF-3, ATF-4, ATF-5, ATF-6 and LRF-1. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

f) Bromodomain. SEQ ID NO:97 corresponds to a polynucleotide encoding a polypeptide having a bromodomain region (Haynes *et al.*, 1992, *Nucleic Acids Res.* 20:2693-2603, Tamkun *et al.*, 1992, *Cell* 68:561-572, and Tamkun, 1995, *Curr. Opin. Genet. Dev.* 5:473-477), which is a conserved region of about 70 amino acids found in the following proteins: 1) Higher eukaryotes transcription initiation factor TFIID 250 Kd subunit (TBP-associated factor p250) (gene CCG1); P250 is associated with the TFIID TATA-box binding protein and seems essential for progression of the G1 phase of the cell

cycle. 2) Human RING3, a protein of unknown function encoded in the MHC class II locus;  
 3) Mammalian CREB-binding protein (CBP), which mediates cAMP-gene regulation by  
 binding specifically to phosphorylated CREB protein; 4) Mammalian homologs of brahma,  
 including three brahma-like human: SNF2a(hBRM), SNF2b, and BRG1; 5) Human BS69,  
 5 a protein that binds to adenovirus E1A and inhibits E1A transactivation; 6) Human peregrin  
 (or Br140).

The bromodomain is thought to be involved in protein-protein interactions and may  
 be important for the assembly or activity of multicomponent complexes involved in  
 transcriptional activation. The consensus pattern, which spans a major part of the  
 10 bromodomain, is: [STANVF]-x(2)-F-x(4)-[DNS]-x(5,7)-[DENQTF]-Y-[HFY]-x(2)-  
 [LIVMFY]-x(3)-[LIVM]-x(4)-[LIVM]-x(6,8)-Y-x(12,13)-[LIVM]-x(2)-N-[SACF]-x(2)-  
 [FY].

g) EF-Hand. SEQ ID NOS:136, 242, and 379 correspond to polynucleotides  
 encoding a novel protein in the family of EF-hand proteins. Many calcium-binding proteins  
 15 belong to the same evolutionary family and share a type of calcium-binding domain known  
 as the EF-hand (Kawasaki *et al.*, *Protein. Prof.* (1995) 2:305-490). This type of domain  
 consists of a twelve residue loop flanked on both sides by a twelve residue alpha-helical  
 domain. In an EF-hand loop the calcium ion is coordinated in a pentagonal bipyramidal  
 configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12;  
 20 these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position  
 12 provides two oxygens for liganding Ca (bidentate ligand).

Proteins known to contain EF-hand regions include: Calmodulin (Ca=4, except in  
 yeast where Ca=3) ("Ca=" indicates approximate number of EF-hand regions);  
 diacylglycerol kinase (EC 2.7.1.107) (DGK) (Ca=2); 2) FAD-dependent glycerol-3-  
 25 phosphate dehydrogenase (EC 1.1.99.5) from mammals (Ca=1); guanylate cyclase activating  
 protein (GCAP) (Ca=3); MIF related proteins 8 (MRP-8 or CFAG) and 14 (MRP-14)  
 (Ca=2); myosin regulatory light chains (Ca=1); oncomodulin (Ca=2); osteonectin (basement  
 membrane protein BM-40) (SPARC); and proteins that contain an "osteonectin" domain  
 (QR1, matrix glycoprotein SC1).

30 The consensus pattern includes the complete EF-hand loop as well as the first residue  
 which follows the loop and which seem to always be hydrophobic.

Consensus pattern: D-x-[DNS]-{ILVFYW}-[DENSTG]-[DNQGHRK]-{GP}-  
 [LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW]

h) Eukaryotic Aspartyl Proteases. SEQ ID NO:308 corresponds to a gene encoding a novel eukaryotic aspartyl protease. Aspartyl proteases, known as acid proteases, (EC 3.4.23.-) are a widely distributed family of proteolytic enzymes (Foltmann B., *Essays Biochem.* (1981) 17:52; Davies D.R., *Annu. Rev. Biophys. Chem.* (1990) 19:189; Rao J.K.M., *et al.*, *Biochemistry* (1991) 30:4663) known to exist in vertebrates, fungi, plants, retroviruses and some plant viruses. Aspartate proteases of eukaryotes are monomeric enzymes which consist of two domains. Each domain contains an active site centered on a catalytic aspartyl residue. The two domains most probably evolved from the duplication of an ancestral gene encoding a primordial domain. Currently known eukaryotic aspartyl proteases include: 1) Vertebrate gastric pepsins A and C (also known as gastricsin); 2) Vertebrate chymosin (rennin), involved in digestion and used for making cheese; 3) Vertebrate lysosomal cathepsins D (EC 3.4.23.5) and E (EC 3.4.23.34); 4) Mammalian renin (EC 3.4.23.15) whose function is to generate angiotensin I from angiotensinogen in the plasma; 5) Fungal proteases such as aspergillopepsin A (EC 3.4.23.18), candidapepsin (EC 3.4.23.24), mucoropepsin (EC 3.4.23.23) (mucor rennin), endothiapepsin (EC 3.4.23.22), polyporopepsin (EC 3.4.23.29), and rhizopuspepsin (EC 3.4.23.21); and 6) Yeast saccharopepsin (EC 3.4.23.25) (proteinase A) (gene PEP4). PEP4 is implicated in posttranslational regulation of vacuolar hydrolases; 7) Yeast barrierpepsin (EC 3.4.23.35) (gene BAR1); a protease that cleaves alpha-factor and thus acts as an antagonist of the mating pheromone; and 8) Fission yeast *ssa1* which is involved in degrading or processing the mating pheromones.

Most retroviruses and some plant viruses, such as badnaviruses, encode for an aspartyl protease which is an homodimer of a chain of about 95 to 125 amino acids. In most retroviruses, the protease is encoded as a segment of a polyprotein which is cleaved during the maturation process of the virus. It is generally part of the pol polyprotein and, more rarely, of the gag polyprotein. Because the sequence around the two aspartates of eukaryotic aspartyl proteases and around the single active site of the viral proteases is conserved, a single signature pattern can be used to identify members of both groups of proteases. The consensus pattern is: [LIVMFGAC]-[LIVMTADN]-[LIVFSA]-D-[ST]-G-[STAV]-[STAPDENQ]-x-[LIVMFSTNC]-x-[LIVMFGTA], where D is the active site residue.

i) GATA Family of Transcription Factors. SEQ ID NO:213 corresponds to a novel member of the GATA family of transcription factors. The GATA family of transcription factors are proteins that bind to DNA sites with the consensus sequence (A/T)GATA(A/G), found within the regulatory region of a number of genes. Proteins currently known to belong

to this family are: 1) GATA-1 (Trainor, C.D., *et al.*, *Nature* (1990) 343:92) (also known as Eryf1, GF-1 or NF-E1), which binds to the GATA region of globin genes and other genes expressed in erythroid cells. It is a transcriptional activator which probably serves as a general 'switch' factor for erythroid development; 2) GATA-2 (Lee, M.E., *et al.*, *J. Biol. Chem.* (1991) 266:16188), a transcriptional activator which regulates endothelin-1 gene expression in endothelial cells; 3) GATA-3 (Ho, I.-C., *et al.*, *EMBO J.* (1991) 10:1187), a transcriptional activator which binds to the enhancer of the T-cell receptor alpha and delta genes; 4) GATA-4 (Spieth, J., *et al.*, *Mol. Cell. Biol.* (1991) 11:4651), a transcriptional activator expressed in endodermally derived tissues and heart; 5) Drosophila protein pannier (or DGATAa) (gene pnr) which acts as a repressor of the achaete-scute complex (as-c); 6) Bombyx mori BCFI (Drevet, J.R., *et al.*, *J. Biol. Chem.* (1994) 269:10660), which regulates the expression of chorion genes; 7) Caenorhabditis elegans elt-1 and elt-2, transcriptional activators of genes containing the GATA region, including vitellogenin genes (Hawkins, M.G., *et al.*, *J. Biol. Chem.* (1995) 270:14666); 8) Ustilago maydis urbs1 (Voisard, C.P.O., *et al.*, *Mol. Cell. Biol.* (1993) 13:7091), a protein involved in the repression of the biosynthesis of siderophores; 9) Fission yeast protein GAF2.

All these transcription factors contain a pair of highly similar 'zinc finger' type domains with the consensus sequence C-x2-C-x17-C-x2-C. Some other proteins contain a single zinc finger motif highly related to those of the GATA transcription factors. These proteins are: 1) Drosophila box A-binding factor (ABF) (also known as protein serpent (gene srp)) which may function as a transcriptional activator protein and may play a key role in the organogenesis of the fat body; 2) Emericella nidulans are (Arst, H.N., Jr., *et al.*, *Trends Genet.* (1989) 5:291) a transcriptional activator which mediates nitrogen metabolite repression; 3) Neurospora crassa nit-2 (Fu, Y.-H., *et al.*, *Mol. Cell. Biol.* (1990) 10:1056), a transcriptional activator which turns on the expression of genes coding for enzymes required for the use of a variety of secondary nitrogen sources, during conditions of nitrogen limitation; 4) Neurospora crassa white collar proteins 1 and 2 (WC-1 and WC-2), which control expression of light-regulated genes; 5) Saccharomyces cerevisiae DAL81 (or UGA43), a negative nitrogen regulatory protein; 6) Saccharomyces cerevisiae GLN3, a positive nitrogen regulatory protein; 7) Saccharomyces cerevisiae GAT1; 8) Saccharomyces cerevisiae GZF3.

The consensus pattern for the GATA family is: C-x-[DN]-C-x(4,5)-[ST]-x(2)-W-[HR]-[RK]-x(3)-[GN]-x(3,4)-C-N-[AS]-C, where the four C's are zinc ligands.

j) G-Protein Alpha Subunit. SEQ ID NO:367 corresponds to a gene encoding a novel polypeptide of the G-protein alpha subunit family. Guanine nucleotide binding proteins (G-proteins) are a family of membrane-associated proteins that couple extracellularly-activated integral-membrane receptors to intracellular effectors, such as ion channels and enzymes that vary the concentration of second messenger molecules. G-proteins are composed of 3 subunits (alpha, beta and gamma) which, in the resting state, associate as a trimer at the inner face of the plasma membrane. The alpha subunit has a molecule of guanosine diphosphate (GDP) bound to it. Stimulation of the G-protein by an activated receptor leads to its exchange for GTP (guanosine triphosphate). This results in the separation of the alpha from the beta and gamma subunits, which always remain tightly associated as a dimer. Both the alpha and beta-gamma subunits are then able to interact with effectors, either individually or in a cooperative manner. The intrinsic GTPase activity of the alpha subunit hydrolyses the bound GTP to GDP. This returns the alpha subunit to its inactive conformation and allows it to reassociate with the beta-gamma subunit, thus restoring the system to its resting state.

G-protein alpha subunits are 350-400 amino acids in length and have molecular weights in the range 40-45 kDa. Seventeen distinct types of alpha subunit have been identified in mammals. These fall into 4 main groups on the basis of both sequence similarity and function: alpha-s, alpha-q, alpha-i and alpha-12 (Simon *et al.*, *Science* (1993) 252:802). Many alpha subunits are substrates for ADP-ribosylation by cholera or pertussis toxins. They are often N-terminally acylated, usually with myristate and/or palmitoylate, and these fatty acid modifications are probably important for membrane association and high-affinity interactions with other proteins. The atomic structure of the alpha subunit of the G-protein involved in mammalian vision, transducin, has been elucidated in both GTP- and GDB-bound forms, and shows considerable similarity in both primary and tertiary structure in the nucleotide-binding regions to other guanine nucleotide binding proteins, such as p21-ras and EF-Tu.

k) Phorbol Esters/Diacylglycerol Binding. SEQ ID NO:188 and 251 represent polynucleotides encoding a protein belonging to the family including phorbol esters/diacylglycerol binding proteins. Diacylglycerol (DAG) is an important second messenger. Phorbol esters (PE) are analogues of DAG and potent tumor promoters that cause a variety of physiological changes when administered to both cells and tissues. DAG activates a family of serine/threonine protein kinases, collectively known as protein kinase C (PKC) (Azzi *et al.*, *Eur. J. Biochem.* (1992) 208:547). Phorbol esters can directly stimulate PKC. The N-terminal region of PKC, known as C1, has been shown (Ono *et al.*, *Proc. Natl.*

*Acad. Sci. USA* (1989) 86:4868) to bind PE and DAG in a phospholipid and zinc-dependent fashion. The C1 region contains one or two copies (depending on the isozyme of PKC) of a cysteine-rich domain about 50 amino-acid residues long and essential for DAG/PE-binding. Such a domain has also been found in, for example, the following proteins.

5 (1) Diacylglycerol kinase (EC 2.7.1.107) (DGK) (Sakane *et al.*, *Nature* (1990) 344:345), the enzyme that converts DAG into phosphatidate. It contains two copies of the DAG/PE-binding domain in its N-terminal section. At least five different forms of DGK are known in mammals; and

(2) N-chimaerin, a brain specific protein which shows sequence similarities with the  
10 BCR protein at its C-terminal part and contains a single copy of the DAG/PE-binding domain at its N-terminal part. It has been shown (Ahmed *et al.*, *Biochem. J.* (1990) 272:767, and Ahmed *et al.*, *Biochem. J.* (1991) 280:233) to be able to bind phorbol esters.

The DAG/PE-binding domain binds two zinc ions; the ligands of these metal ions are probably the six cysteines and two histidines that are conserved in this domain. The  
15 signature pattern completely spans the DAG/PE domain. The consensus pattern is: H-x-[LIVMFYW]-x(8,11)-C-x(2)-C-x(3)-[LIVMFC]-x(5,10)-C-x(2)-C-x(4)-[HD]-x(2)-C-x(5,9)-C. All the C and H are probably involved in binding zinc.

1) Protein Kinase. SEQ ID NOS:202, 315, 367, and 397 represent polynucleotides encoding protein kinases. Protein kinases catalyze phosphorylation of proteins in a variety of  
20 pathways, and are implicated in cancer. Eukaryotic protein kinases (Hanks S.K., *et al.*, *FASEB J.* (1995) 9:576; Hunter T., *Meth. Enzymol.* (1991) 200:3; Hanks S.K., *et al.*, *Meth. Enzymol.* (1991) 200:38; Hanks S.K., *Curr. Opin. Struct. Biol.* (1991) 1:369; Hanks S.K., *et al.*, *Science* (1988) 241:42) are enzymes that belong to a very extensive family of proteins which share a conserved catalytic core common to both serine/threonine and tyrosine protein  
25 kinases. There are a number of conserved regions in the catalytic domain of protein kinases. Two of the conserved regions are the basis for the signature pattern in the protein kinase profile. The first region, which is located in the N-terminal extremity of the catalytic domain, is a glycine-rich stretch of residues in the vicinity of a lysine residue, which has been shown to be involved in ATP binding. The second region, which is located in the  
30 central part of the catalytic domain, contains a conserved aspartic acid residue which is important for the catalytic activity of the enzyme (Knighton D.R., *et al.*, *Science* (1991) 253:407). The protein kinase profile includes two signature patterns for this second region: one specific for serine/threonine kinases and the other for tyrosine kinases. A third profile is

based on the alignment in (Hanks S.K., *et al.*, *FASEB J.* (1995) 9:576) and covers the entire catalytic domain. The consensus patterns are as follows:

- 1) Consensus pattern: [LIV]-G-{P}-G-{P}-[FYWMGSTNH]-[SGA]-{PW}-  
[LIVCAT]-{PD}-x-[GSTACLIVMFY]-x(5,18)-[LIVMFYWCSTAR]-[AIVP]-  
5 [LIVMFAGCKR]-K, where K binds ATP. The majority of known protein kinases are detected by this pattern. Proteins kinases that are not detected by this consensus include viral kinases, which are quite divergent in this region and are completely missed by this pattern.
- 2) Consensus pattern: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-K-x(2)-N-  
10 [LIVMFYCT](3), where D is an active site residue. This consensus sequence identifies most serine/threonine-specific protein kinases with only 10 exceptions. Half of the exceptions are viral kinases, while the other exceptions include Epstein-Barr virus BGLF4 and Drosophila ninaC, which have Ser and Arg, respectively, instead of the conserved Lys. These latter two protein kinases are detected by the tyrosine kinase specific pattern described below.
- 15 3) Consensus pattern: [LIVMFYC]-x-[HY]-x-D-[LIVMFY]-[RSTAC]-x(2)-N-[LIVMFYC], where D is an active site residue. All tyrosine-specific protein kinases are detected by this consensus pattern, with the exception of human ERBB3 and mouse blk. This pattern also detects most bacterial aminoglycoside phosphotransferases (Benner S., *Nature* (1987) 329:21; Kirby R., *J. Mol. Evol.* (1992) 30:489) and herpesviruses ganciclovir  
20 kinases (Littler E., *et al.*, *Nature* (1992) 358:160), which are structurally and evolutionary related to protein kinases.

The protein kinase profile also detects receptor guanylate cyclases and 2-5A-dependent ribonucleases. Sequence similarities between these two families and the eukaryotic protein kinase family have been noticed previously. The profile also detects  
25 *Arabidopsis thaliana* kinase-like protein TMKL1 which seems to have lost its catalytic activity.

If a protein analyzed includes the two of the above protein kinase signatures, the probability of it being a protein kinase is close to 100%. Eukaryotic-type protein kinases have also been found in prokaryotes such as *Myxococcus xanthus* (Munoz-Dorado J., *et al.*,  
30 *Cell* (1991) 67:995) and *Yersinia pseudotuberculosis*. The patterns shown above has been updated since their publication in (Bairoch A., *et al.*, *Nature* (1988) 331:22).

m) Protein Phosphatase 2C. SEQ ID NO:256 corresponds to a polynucleotide encoding a novel protein phosphatase 2C (PP2C), which is one of the four major classes of mammalian serine/threonine specific protein phosphatases. PP2C (Wenk *et al.*, *FEBS Lett.*



(1992) 297:135) is a monomeric enzyme of about 42 Kd which shows broad substrate specificity and is dependent on divalent cations (mainly manganese and magnesium) for its activity. Three isozymes are currently known in mammals: PP2C-alpha, -beta and -gamma.

n) Protein Tyrosine Phosphatase. SEQ ID NO:382 represents a polynucleotide  
5 encoding a protein tyrosine kinase. Tyrosine specific protein phosphatases (EC 3.1.3.48) (PTPase) (Fischer *et al.*, *Science* (1991) 253:401; Charbonneau *et al.*, *Annu. Rev. Cell Biol.* (1992) 8:463; Trowbridge, *J. Biol. Chem.* (1991) 266:23517; Tonks *et al.*, *Trends Biochem. Sci.* (1989) 14:497; and Hunter, *Cell* (1989) 58:1013) catalyze the removal of a phosphate group attached to a tyrosine residue. These enzymes are very important in the control of cell  
10 growth, proliferation, differentiation and transformation. Multiple forms of PTPase have been characterized and can be classified into two categories: soluble PTPases and transmembrane receptor proteins that contain PTPase domain(s).

Soluble PTPases include PTPN3 (H1) and PTPN4 (MEG), enzymes that contain an N-terminal band 4.1-like domain and could act at junctions between the membrane and  
15 cytoskeleton; PTPN6 (PTP-1C; HCP; SHP) and PTPN11 (PTP-2C; SH-PTP3; Syp), enzymes that contain two copies of the SH2 domain at its N-terminal extremity.

Dual specificity PTPases include DUSP1 (PTPN10; MAP kinase phosphatase-1; MKP-1) which dephosphorylates MAP kinase on both Thr-183 and Tyr-185; and DUSP2 (PAC-1), a nuclear enzyme that dephosphorylates MAP kinases ERK1 and ERK2 on both  
20 Thr and Tyr residues.

Structurally, all known receptor PTPases are made up of a variable length extracellular domain, followed by a transmembrane region and a C-terminal catalytic cytoplasmic domain. Some of the receptor PTPases contain fibronectin type III (FN-III) repeats, immunoglobulin-like domains, MAM domains or carbonic anhydrase-like domains  
25 in their extracellular region. The cytoplasmic region generally contains two copies of the PTPase domain. The first seems to have enzymatic activity, while the second is inactive but seems to affect substrate specificity of the first. In these domains, the catalytic cysteine is generally conserved but some other, presumably important, residues are not.

PTPase domains consist of about 300 amino acids. There are two conserved  
30 cysteines and the second one has been shown to be absolutely required for activity. Furthermore, a number of conserved residues in its immediate vicinity have also been shown to be important. The consensus pattern for PTPases is: [LIVMF]-H-C-x(2)-G-x(3)-[STC]-[STAGP]-x-[LIVMFY]; C is the active site residue.

o) SH3 Domain. SEQ ID NO:306 and 386 represent polynucleotides encoding SH3 domain proteins. The Src homology 3 (SH3) domain is a small protein domain of about 60 amino acid residues first identified as a conserved sequence in the non-catalytic part of several cytoplasmic protein tyrosine kinases (e.g. Src, Abl, Lck) (Mayer *et al.*, *Nature* (1988) 332:272). The domain has also been found in a variety of intracellular or membrane-associated proteins (Musacchio *et al.*, *FEBS Lett.* (1992) 307:55; Pawson *et al.*, *Curr. Biol.* (1993) 3:434; Mayer *et al.*, *Trends Cell Biol.* (1993) 3:8; and Pawson *et al.*, *Nature* (1995) 373:573).

The SH3 domain has a characteristic fold that consists of five or six beta-strands arranged as two tightly packed anti-parallel beta sheets. The linker regions may contain short helices (Kuriyan *et al.*, *Curr. Opin. Struct. Biol.* (1993) 3:828). It is believed that SH3 domain-containing proteins mediate assembly of specific protein complexes via binding to proline-rich peptides (Morton *et al.*, *Curr. Biol.* (1994) 4:615). In general, SH3 domains are found as single copies in a given protein, but there is a significant number of proteins with two SH3 domains and a few with 3 or 4 copies.

SH3 domains have been identified in, for example, protein tyrosine kinases, such as the Src, Abl, Bkt, Csk and ZAP70 families of kinases; mammalian phosphatidylinositol-specific phospholipase C-gamma-1 and -2; mammalian phosphatidyl inositol 3-kinase regulatory p85 subunit; mammalian Ras GTPase-activating protein (GAP); mammalian Vav oncoprotein, a guanine nucleotide exchange factor of the CDC24 family; *Drosophila* lethal(1)discs large-1 tumor suppressor protein (gene Dlg1); mammalian tight junction protein ZO-1; vertebrate erythrocyte membrane protein p55; *Caenorhabditis elegans* protein lin-2; rat protein CASK; and mammalian synaptic proteins SAP90/PSD-95, CHAPSYN-110/PSD-93, SAP97/DLG1 and SAP102. Novel SH3-domain containing polypeptides will facilitate elucidation of the role of such proteins in important biological pathways, such as ras activation.

p) Trypsin. SEQ ID NO:169 corresponds to a novel serine protease of the trypsin family. The catalytic activity of the serine proteases from the trypsin family is provided by a charge relay system involving an aspartic acid residue hydrogen-bonded to a histidine, which itself is hydrogen-bonded to a serine. The sequences in the vicinity of the active site serine and histidine residues are well conserved in this family of proteases (Brenner S., *Nature* (1988) 334:528). Proteases known to belong to the trypsin family include: 1) Acrosin; 2) Blood coagulation factors VII, IX, X, XI and XII, thrombin, plasminogen, and protein C; 3) Cathepsin G; 4) Chymotrypsins; 5) Complement components C1r, C1s, C2, and complement

factors B, D and I; 6) Complement-activating component of RA-reactive factor; 7) Cytotoxic cell proteases (granzymes A to H); 8) Duodenase I; 9) Elastases 1, 2, 3A, 3B (protease E), leukocyte (medullasin); 10) Enterokinase (EC 3.4.21.9) (enteropeptidase); 11) Hepatocyte growth factor activator; 12) Hepsin; 13) Glandular (tissue) kallikreins (including EGF-binding protein types A, B, and C, NGF-gamma chain, gamma-renin, prostate specific antigen (PSA) and tonin); 14) Plasma kallikrein; 15) Mast cell proteases (MCP) 1 (chymase) to 8; 16) Myeloblastin (proteinase 3) (Wegener's autoantigen); 17) Plasminogen activators (urokinase-type, and tissue-type); 18) Trypsins I, II, III, and IV; 19) Trypsases; 20) Snake venom proteases such as ancrod, batroxobin, cerastobin, flavoxobin, and protein C activator; 21) Collagenase from common cattle grub and collagenolytic protease from Atlantic sand fiddler crab; 22) Apolipoprotein(a); 23) Blood fluke cercarial protease; 24) Drosophila trypsin like proteases: alpha, easter, snake-locus; 25) Drosophila protease stubble (gene sb); and 26) Major mite fecal allergen Der p III. All the above proteins belong to family S1 in the classification of peptidases (Rawlings N.D., *et al.*, *Meth. Enzymol.* (1994) 244:19; <http://www.expasy.ch/cgi-bin/lists?peptidas.txt>) and originate from eukaryotic species. It should be noted that bacterial proteases that belong to family S2A are similar enough in the regions of the active site residues that they can be picked up by the same patterns.

The consensus patterns for this trypsin protein family are: 1) [LIVM]-[ST]-A-[STAG]-H-C, where H is the active site residue. All sequences known to belong to this class detected by the pattern, except for complement components C1r and C1s, pig plasminogen, bovine protein C, rodent urokinase, ancrod, gyroxin and two insect trypsins; 2) [DNSTAGC]-[GSTAPIMVQH]-x(2)-G-[DE]-S-G-[GS]-[SAPHV]-[LIVMFYWH]-[LIVMFYSTANQH], where S is the active site residue. All sequences known to belong to this family are detected by the above consensus sequences, except for 18 different proteases which have lost the first conserved glycine. If a protein includes both the serine and the histidine active site signatures, the probability of it being a trypsin family serine protease is 100%.

q) WD Domain, G-Beta Repeats. SEQ ID NOS:188 and 335 represent novel members of the WD domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) 56:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but

they seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition.

In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem  
 5 repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). Such a repetitive segment has been shown to exist in a number of other proteins including: human LIS1, a neuronal protein involved in type-1 lissencephaly; and mammalian coatomer beta' subunit (beta'-COP), a component of a cytosolic protein complex that reversibly associates with Golgi membranes to form vesicles  
 10 that mediate biosynthetic protein transport.

The consensus pattern for the WD domain/G-Beta repeat family is: [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

r) wnt Family of Developmental Signaling Proteins. SEQ ID NO: 23, 291, 324, 330,  
 15 341, and 353 correspond to novel members of the wnt family of developmental signaling proteins. Wnt-1 (previously known as int-1), the seminal member of this family, (Nusse R., *Trends Genet.* (1988) 4:291) is a proto-oncogene induced by the integration of the mouse mammary tumor virus. It is thought to play a role in intercellular communication and seems to be a signalling molecule important in the development of the central nervous system  
 20 (CNS). The sequence of wnt-1 is highly conserved in mammals, fish, and amphibians. Wnt-1 was found to be a member of a large family of related proteins (Nusse R., *et al.*, *Cell* (1992) 69:1073; McMahon A.P., *Trends Genet.* (1992) 8:1; Moon R.T., *BioEssays* (1993) 15:91) that are all thought to be developmental regulators. These proteins are known as wnt-2 (also known as irp), wnt-3, -3A, -4, -5A, -5B, -6, -7A, -7B, -8, -8B, -9 and -10. At least  
 25 four members of this family are present in *Drosophila*; one of them, wingless (wg), is implicated in segmentation polarity. All these proteins share the following features characteristics of secretory proteins: a signal peptide, several potential N-glycosylation sites and 22 conserved cysteines that are probably involved in disulfide bonds. The Wnt proteins seem to adhere to the plasma membrane of the secreting cells and are therefore likely to  
 30 signal over only few cell diameters. The consensus pattern, which is based upon a highly conserved region including three cysteines, is as follows: C-K-C-H-G-[LIVMT]-S-G-x-C. All sequences known to belong to this family are detected by the provided consensus pattern.

s) Ww/rsp5/WWP Domain-Containing Proteins. SEQ ID NOS:188, 379, and 395 represent polynucleotides encoding a polypeptide in the family of WW/rsp5/WWP domain-

containing proteins. The WW domain (Bork *et al.*, *Trends Biochem. Sci.* (1994) 19:531; Andre *et al.*, *Biochem. Biophys. Res. Commun.* (1994) 205:1201; Hofmann *et al.*, *FEBS Lett.* (1995) 358:153; and Sudol *et al.*, *FEBS Lett.* (1995) 369:67), also known as rsp5 or WWP), was originally discovered as a short conserved region in a number of unrelated proteins, among them dystrophin, the gene responsible for Duchenne muscular dystrophy. The domain, which spans about 35 residues, is repeated up to 4 times in some proteins. It has been shown (Chen *et al.*, *Proc. Natl. Acad. Sci. USA* (1995) 92:7819) to bind proteins with particular proline-motifs, [AP]-P-P-[AP]-Y, and thus resembles somewhat SH3 domains. It appears to contain beta-strands grouped around four conserved aromatic positions, generally Trp. The name WW or WWP derives from the presence of these Trp as well as that of a conserved Pro. It is frequently associated with other domains typical for proteins in signal transduction processes.

Proteins containing the WW domain include:

1. Dystrophin, a multidomain cytoskeletal protein. Its longest alternatively spliced form consists of an N-terminal actin-binding domain, followed by 24 spectrin-like repeats, a cysteine-rich calcium-binding domain and a C-terminal globular domain. Dystrophins form tetramers and is thought to have multiple functions including involvement in membrane stability, transduction of contractile forces to the extracellular environment and organization of membrane specialization. Mutations in the dystrophin gene lead to muscular dystrophy of Duchenne or Becker type. Dystrophin contains one WW domain C-terminal of the spectrin-repeats.
2. Vertebrate YAP protein, which is a substrate of an unknown serine kinase. It binds to the SH3 domain of the Yes oncoprotein via a proline-rich region. This protein appears in alternatively spliced isoforms, containing either one or two WW domains.
3. IQGAP, which is a human GTPase activating protein acting on ras. It contains an N-terminal domain similar to fly muscle mp20 protein and a C-terminal ras GTPase activator domain.

For the sensitive detection of WW domains, the profile spans the whole homology region as well as a pattern. The consensus for this family is: W-x(9,11)-[VFY]-[FYW]-x(6,7)-[GSTNE]-[GSTQCR]-[FYW]-x(2)-P.

t) Zinc Finger, C2H2 Type. SEQ ID NO:61, 306, and 386 correspond to polynucleotides encoding novel members of the of the C2H2 type zinc finger protein family. Zinc finger domains (Klug *et al.*, *Trends Biochem. Sci.* (1987) 12:464; Evans *et al.*, *Cell* (1988) 52:1; Payre *et al.*, *FEBS Lett.* (1988) 234:245; Miller *et al.*, *EMBO J.* (1985) 4:1609;

and Berg, *Proc. Natl. Acad. Sci. USA* (1988) 85:99) are nucleic acid-binding protein structures first identified in the *Xenopus* transcription factor TFIIA. These domains have since been found in numerous nucleic acid-binding proteins. A zinc finger domain is composed of 25 to 30 amino acid residues. Two cysteine or histidine residues are positioned at both extremities of the domain, which are involved in the tetrahedral coordination of a zinc atom. It has been proposed that such a domain interacts with about five nucleotides.

Many classes of zinc fingers are characterized according to the number and positions of the histidine and cysteine residues involved in the zinc atom coordination. In the first class to be characterized, called C2H2, the first pair of zinc coordinating residues are cysteines, while the second pair are histidines. A number of experimental reports have demonstrated the zinc-dependent DNA or RNA binding property of some members of this class.

Mammalian proteins having a C2H2 zipper include (number in parenthesis indicates number of zinc finger regions in the protein): basoonuclin (6), BCL-6/LAZ-3 (6), erythroid krueppel-like transcription factor (3), transcription factors Sp1 (3), Sp2 (3), Sp3 (3) and Sp4 (3), transcriptional repressor YY1 (4), Wilms' tumor protein (4), EGR1/Krox24 (3), EGR2/Krox20 (3), EGR3/Pilot (3), EGR4/AT133 (4), Evi-1 (10), GLI1 (5), GLI2 (4+), GLI3 (3+), HIV-EP1/ZNF40 (4), HIV-EP2 (2), KR1 (9+), KR2 (9), KR3 (15+), KR4 (14+), KR5 (11+), HF.12 (6+), REX-1 (4), Zfx (13), Zfy (13), Zfp-35 (18), ZNF7 (15), ZNF8 (7), ZNF35 (10), ZNF42/MZF-1 (13), ZNF43 (22), ZNF46/Kup (2), ZNF76 (7), ZNF91 (36), ZNF133 (3).

In addition to the conserved zinc ligand residues, it has been shown that a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld *et al.*, *J. Biomol. Struct. Dyn.* (1993) 11:557) The best conserved position is found four residues after the second cysteine; it is generally an aromatic or aliphatic residue.

The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc ligands.

u) Zinc Finger, CCHC Class. SEQ ID NO:322 corresponds to a polynucleotide encoding a novel member of the zinc finger CCHC family. The CCHC zinc finger protein family to date has been mostly composed of retroviral gag proteins (nucleocapsid). The prototype structure of this family is from HIV. The family also contains members involved in eukaryotic gene regulation, such as *C. elegans* GLH-1. The consensus sequence of this family is based upon the common structure of an 18-residue zinc finger.

v) Zinc-Binding Metalloprotease Domain. SEQ ID NO:306 and 395 represent polynucleotides encoding novel members of the zinc-binding metalloprotease domain protein family. The majority of zinc-dependent metalloproteases (with the notable exception of the carboxypeptidases) share a common pattern of primary structure (Jongeneel *et al.*, *FEBS Lett.* (1989) 242:211; Murphy *et al.*, *FEBS Lett.* (1991) 289:4; and Bode *et al.*, *Zoology* (1996) 99:237) in the part of their sequence involved in the binding of zinc, and can be grouped together as a superfamily, known as the metzincins, on the basis of this sequence similarity. Examples of these proteins include: 1) Angiotensin-converting enzyme (EC 3.4.15.1) (dipeptidyl carboxypeptidase I) (ACE), the enzyme responsible for hydrolyzing angiotensin I to angiotensin II. 2) Mammalian extracellular matrix metalloproteinases (known as matrixins) (Woessner, *FASEB J.* (1991) 5:2145): MMP-1 (EC 3.4.24.7) (interstitial collagenase), MMP-2 (EC 3.4.24.24) (72 Kd gelatinase), MMP-9 (EC 3.4.24.35) (92 Kd gelatinase), MMP-7 (EC 3.4.24.23) (matrilysin), MMP-8 (EC 3.4.24.34) (neutrophil collagenase), MMP-3 (EC 3.4.24.17) (stromelysin-1), MMP-10 (EC 3.4.24.22) (stromelysin-2), and MMP-11 (stromelysin-3), MMP-12 (EC 3.4.24.65) (macrophage metalloelastase). 3) Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1), which processes the precursor of endothelin to release the active peptide.

A signature pattern which includes the two histidine and the glutamic acid residues is sufficient to detect this superfamily of proteins, having the consensus pattern: [GSTALIVN]-x(2)-H-E-[LIVMFYW]-{DEHRKP}-H-x-[LIVMFYWGSPQ]. The two H's are zinc ligands, and E is the active site residue.

Example 4: Differential Expression of Polynucleotides of the Invention : Description of Libraries and Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 4 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepared the cDNA library, the "nickname" of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

**Table 4 Description of cDNA Libraries**

<b>Library (lib #)</b>	<b>Description</b>	<b>Number of Clones in this Clustering</b>
1	Km12 L4 Human Colon Cell Line, High Metastatic Potential (derived from Km12C) "High Colon"	307133
2	Km12C Human Colon Cell Line, Low Metastatic Potential "Low Colon"	284755
3	MDA-MB-231 Human Breast Cancer Cell Line, High Metastatic Potential; micro-metastases in lung "High Breast"	326937
4	MCF7 Human Breast Cancer Cell, Non Metastatic "Low Breast"	318979
8	MV-522 Human Lung Cancer Cell Line, High Metastatic Potential "High Lung"	223620
9	UCP-3 Human Lung Cancer Cell Line, Low Metastatic Potential "Low Lung"	312503
12	Human microvascular endothelial cells (HMEC) – Untreated PCR (OligodT) cDNA library	41938
13	Human microvascular endothelial cells (HMEC) – bFGF treated PCR (OligodT) cDNA library	42100
14	Human microvascular endothelial cells (HMEC) – VEGF treated PCR (OligodT) cDNA library	42825
15	Normal Colon – UC#2 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	34285
16	Colon Tumor – UC#2 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	35625
17	Liver Metastasis from Colon Tumor of UC#2 Patient PCR (OligodT) cDNA library "High Colon Metastasis Tissue"	36984
18	Normal Colon – UC#3 Patient PCR (OligodT) cDNA library "Normal Colon Tumor Tissue"	36216
19	Colon Tumor – UC#3 Patient PCR (OligodT) cDNA library "High Colon Tumor Tissue"	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient PCR (OligodT) cDNA library "High Colon Metastasis Tissue"	30956



The KM12L4 and KM12C cell lines are described in Example 1 above. The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line  
5 was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran *et al.*,  
10 *Cancer Res.* (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar *et al.*, *J Med Chem* (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson *et al.*, *Br J Cancer* (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang *et al.*, *Nucleic Acids Res* (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki *et al.*, *Int J Cancer* (1987) 40:46 (UCP-3); Varki *et al.*, *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki *et al.*, *Anticancer Res.* (1990) 10:637; (MV-522);  
15 Kelner *et al.*, *Anticancer Res* (1995) 15:867 (MV-522); and Zhang *et al.*, *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3).

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate  
20 the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each  
25 oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together  
30 computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the

highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

5 Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1<sup>st</sup>), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2<sup>nd</sup>). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between  
10 the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a  
15 second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total  
20 number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is  
25 determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974).

Tables 5 to 7 (inserted before the claims) show the number of clones in each of the above libraries that were analyzed for differential expression. Examples of differentially expressed polynucleotides of particular interest are described in more detail below.

30

Example 5: Polynucleotides Differentially Expressed in High Metastatic Potential Breast Cancer Cells Versus Low Metastatic Breast Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential breast cancer tissue and low

metastatic breast cancer cells. Expression of these sequences in breast cancer can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A  
5 patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

10 The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential  
15 expression between high metastatic potential breast cancer cells and low metastatic potential breast cancer cells.

**Table 8.** Differentially expressed polynucleotides: High metastatic potential breast cancer vs. low metastatic breast cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	Ratio
9	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
42	High Breast > Low Breast (Lib3 > Lib4)	307	196	75	2.549721
52	High Breast > Low Breast (Lib3 > Lib4)	19	1364	525	2.534854
62	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
65	High Breast > Low Breast (Lib3 > Lib4)	5749	9	0	8.780930
66	High Breast > Low Breast (Lib3 > Lib4)	6455	6	0	5.853953
68	High Breast > Low Breast (Lib3 > Lib4)	6455	6	0	5.853953
114	High Breast > Low Breast (Lib3 > Lib4)	2030	32	4	7.805271
123	High Breast > Low Breast (Lib3 > Lib4)	3389	13	2	6.341782
144	High Breast > Low Breast (Lib3 > Lib4)	4623	12	2	5.853953
172	High Breast > Low Breast (Lib3 > Lib4)	102	278	116	2.338217
178	High Breast > Low Breast (Lib3 > Lib4)	3681	10	1	9.756589
214	High Breast > Low Breast (Lib3 > Lib4)	3900	8	1	7.805271
219	High Breast > Low Breast (Lib3 > Lib4)	3389	13	2	6.341782
223	High Breast > Low Breast (Lib3 > Lib4)	1399	19	7	2.648217
258	High Breast > Low Breast (Lib3 > Lib4)	4837	10	0	9.756589
317	High Breast > Low Breast (Lib3 > Lib4)	1577	25	3	8.130490
379	High Breast > Low Breast (Lib3 > Lib4)	260	27	2	13.17139
4	Low Breast > High Breast (Lib4 > Lib3)	3706	22	4	5.637215
39	Low Breast > High Breast (Lib4 > Lib3)	4016	6	0	6.149690
74	Low Breast > High Breast (Lib4 > Lib3)	6268	18	3	6.149690
81	Low Breast > High Breast (Lib4 > Lib3)	40392	8	1	8.199586
130	Low Breast > High Breast (Lib4 > Lib3)	13183	7	0	7.174638
157	Low Breast > High Breast (Lib4 > Lib3)	5417	9	0	9.224535
162	Low Breast > High Breast (Lib4 > Lib3)	9685	7	0	7.174638
183	Low Breast > High Breast (Lib4 > Lib3)	7337	16	3	5.466391
202	Low Breast > High Breast (Lib4 > Lib3)	6124	9	1	9.224535
298	Low Breast > High Breast (Lib4 > Lib3)	1037	22	4	5.637215
338	Low Breast > High Breast (Lib4 > Lib3)	689	36	17	2.170478
384	Low Breast > High Breast (Lib4 > Lib3)	697	72	30	2.459876
386	Low Breast > High Breast (Lib4 > Lib3)	4568	9	0	9.224535
388	Low Breast > High Breast (Lib4 > Lib3)	5622	13	2	6.662164

5 **Example 6:** Polynucleotides Differentially Expressed in High Metastatic Potential Lung Cancer Cells Versus Low Metastatic Lung Cancer Cells

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential lung cancer tissue and low metastatic lung cancer cells. Expression of these sequences in lung cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells are associated can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these

polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential lung cancer cells and low metastatic potential lung cancer cells:

**Table 9** Differentially expressed polynucleotides: High metastatic potential lung cancer vs. low metastatic lung cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	Ratio
400	High Lung > Low Lung (Lib8 > Lib 9)	14929	23	16	2.008868
9	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
34	High Lung > Low Lung (Lib8 > Lib9)	5832	5	0	6.987366
42	High Lung > Low Lung (Lib8 > Lib9)	307	79	27	4.088903
62	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
74	High Lung > Low Lung (Lib8 > Lib9)	6268	5	0	6.987366
106	High Lung > Low Lung (Lib8 > Lib9)	10717	8	0	11.17978
119	High Lung > Low Lung (Lib8 > Lib9)	8	1355	122	15.52111
361	High Lung > Low Lung (Lib8 > Lib9)	1120	5	0	6.987366
369	High Lung > Low Lung (Lib8 > Lib9)	2790	6	0	8.384840
371	High Lung > Low Lung (Lib8 > Lib9)	8847	6	1	8.384840
379	High Lung > Low Lung (Lib8 > Lib9)	260	15	0	20.96210
395	High Lung > Low Lung (Lib8 > Lib9)	13538	9	1	12.57726
135	Low Lung > High Lung (Lib9 > Lib8)	36313	30	1	21.46731
154	Low Lung > High Lung (Lib9 > Lib8)	5345	27	6	3.220097
160	Low Lung > High Lung (Lib9 > Lib8)	4386	21	3	5.009039
260	Low Lung > High Lung (Lib9 > Lib8)	4141	27	4	4.830145
308	Low Lung > High Lung (Lib9 > Lib8)	15855	213	12	12.70149
323	Low Lung > High Lung (Lib9 > Lib8)	5257	25	5	3.577885
349	Low Lung > High Lung (Lib9 > Lib8)	2797	14	1	10.01807
381	Low Lung > High Lung (Lib9 > Lib8)	2428	19	2	6.797982

**Example 7: Polynucleotides Differentially Expressed in High Metastatic Potential Colon Cancer Cells Versus Low Metastatic Colon Cancer Cells**

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and low

metastatic colon cancer cells. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

**Table 11:** Differentially expressed polynucleotides: High metastatic potential colon cancer vs. low metastatic colon cancer cells

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	Ratio
1	High Colon > Low Colon (Lib1 > Lib2)	6660	7	0	6.489973
176	High Colon > Low Colon (Lib1 > Lib2)	3765	19	6	2.935940
241	High Colon > Low Colon (Lib1 > Lib2)	4275	11	2	5.099264
362	High Colon > Low Colon (Lib1 > Lib2)	6420	8	0	7.417112
374	High Colon > Low Colon (Lib1 > Lib2)	6420	8	0	7.417112
39	Low Colon > High Colon (Lib2 > Lib1)	4016	14	5	3.020043
97	Low Colon > High Colon (Lib2 > Lib1)	945	21	9	2.516702
134	Low Colon > High Colon (Lib2 > Lib1)	2464	19	5	4.098630
317	Low Colon > High Colon (Lib2 > Lib1)	1577	40	12	3.595289
357	Low Colon > High Colon (Lib2 > Lib1)	4309	13	4	3.505407

**Example 8: Polynucleotides Differentially Expressed at Higher Levels in High Metastatic Potential Colon Cancer Patient Tissue Versus Normal Patient Tissue**

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells are associated can be

indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

- 5        The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

- 10       The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and normal colon cells:

**Table 11:** Differentially expressed polynucleotides: High metastatic potential colon tissue vs. normal colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	Ratio
52	High Colon Metastasis Tissue > Normal Colon Tissue of UC#3 (Lib20 > Lib18)	19	10	0	11.69918
52	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	19	13	2	6.025646
172	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	102	65	22	2.738930

- 15    Example 9: Polynucleotides Differentially Expressed at Higher Levels in High Colon Tumor Potential Patient Tissue Versus Metastasized Colon Cancer Patient Tissue

- 20       A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells. Expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the transformation of precancerous tissue to malignant tissue. This information can be useful in the prevention of achieving the advanced malignant state in these tissues, and can be important in risk assessment for a patient.

- 25       The following table summarizes identified polynucleotides with differential expression between high tumor potential colon cancer tissue and cells derived from high metastatic potential colon cancer cells:

**Table 12:** Differentially expressed polynucleotides: High tumor potential colon tissue vs. metastatic colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	Ratio
52	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	19	69	10	5.160829
119	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	8	14	1	10.47124
172	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	102	43	10	3.216168

5 **Example 10:** Polynucleotides Differentially Expressed at Higher Levels in High Tumor Potential Colon Cancer Patient Tissue Versus Normal Patient Tissue

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can be valuable in determining  
 10 diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. For example, sequences that are highly expressed in the potential colon cancer cells are associated with or can be indicative of increased expression of genes or regulatory sequences involved in early tumor progression. A patient sample displaying an increased  
 15 level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and normal colon cells:

20 **Table 13:** Differentially expressed polynucleotides: High tumor potential colon tissue vs. normal colon tissue

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	Ratio
52	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	19	13	2	6.255508
288	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	1267	7	0	6.125253
52	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	19	69	0	60.37750
119	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	8	14	1	12.25050
172	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	102	43	7	5.375222



**Example 11: Polynucleotides Differentially Expressed Across Multiple Libraries**

A number of polynucleotide sequences have been identified that are differentially expressed between cancerous cells and normal cells across all three tissue types tested (*i.e.*, breast, colon, and lung). Expression of these sequences in a tissue or any origin can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. These polynucleotides can also serve as non-tissue specific markers of, for example, risk of metastasis of a tumor. The following table summarizes identified polynucleotides that were differentially expressed but without tissue type-specificity in the breast, colon, and lung libraries tested.

**Table 14: Polynucleotides Differentially Expressed Across Multiple Library Comparisons**

SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	Ratio
9	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
39	Low Breast > High Breast (Lib4 > Lib3)	4016	6	0	6.149690
	Low Colon > High Colon (Lib2 > Lib1)	4016	14	5	3.020043
42	High Breast > Low Breast (Lib3 > Lib4)	307	196	75	2.549721
	High Lung > Low Lung (Lib8 > Lib9)	307	79	27	4.088903
52	High Breast > Low Breast (Lib3 > Lib4)	19	1364	525	2.534854
	High Colon Metastasis Tissue > Normal Colon Tissue of UC#3 (Lib20 > Lib18)	19	10	0	11.69918
	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	19	13	2	6.025646
	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	19	69	10	5.160829
	High Colon Tumor Tissue > Normal Tissue of UC#2 (Lib16 > Lib15)	19	13	2	6.255508
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	19	69	0	60.37750
62	High Breast > Low Breast (Lib3 > Lib4)	2623	31	4	7.561356
	High Lung > Low Lung (Lib8 > Lib9)	2623	6	1	8.384840
74	High Lung > Low Lung (Lib8 > Lib9)	6268	5	0	6.987366
	Low Breast > High Breast (Lib4 > Lib3)	6268	18	3	6.149690
119	High Colon Tumor Tissue > Metastasis Tissue of UC#3 (Lib19 > Lib20)	8	14	1	10.47124
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	8	14	1	12.25050
	High Lung > Low Lung (Lib8 > Lib9)	8	1355	122	15.52111
172	High Breast > Low Breast (Lib3 > Lib4)	102	278	116	2.338217
	High Colon Metastasis Tissue > Normal Tissue in UC#2 (Lib17 > Lib15)	102	65	22	2.738930
	High Colon Tumor Tissue > Metastasis	102	43	10	3.216168

WO 99/33982		PCT/US98/27610			
SEQ ID NO.	Differential Expression	Cluster ID	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	Ratio
	Tissue of UC#3 (Lib19 > Lib20)				
	High Colon Tumor Tissue > Normal Tissue of UC#3 (Lib19 > Lib18)	102	43	7	5.375222
317	High Breast > Low Breast (Lib3 > Lib4)	1577	25	3	8.130490
	Low Colon > High Colon (Lib2 > Lib1)	1577	40	12	3.595289
379	High Breast > Low Breast (Lib3 > Lib4)	260	27	2	13.17139
	High Lung > Low Lung (Lib8 > Lib9)	260	15	0	20.96210

**Example 12: Polynucleotides Exhibiting Colon-Specific Expression**

The cDNA libraries described herein were also analyzed to identify those polynucleotides that were specifically expressed in colon cells or tissue, *i.e.*, the polynucleotides were identified in libraries prepared from colon cell lines or tissue, but not in libraries of breast or lung origin. The polynucleotides that were expressed in a colon cell line and/or in colon tissue, but were present in the breast or lung cDNA libraries described herein, are shown in Table 15.

**Table 15** Polynucleotides specifically expressed in colon cells.

SEQ ID NO.	Cluster	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	SEQ ID NO.	Cluster	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library
5	36535	2	0	229	39648	2	0
13	27250	2	0	231	85064	1	0
19	16283	3	0	234	39391	2	0
24	16918	4	0	236	39498	2	0
26	40108	2	0	242	22113	3	0
32	32663	1	1	247	19255	2	0
43	39833	2	0	252	22814	3	0
47	18957	3	0	253	39563	2	0
48	39508	2	0	254	39420	2	0
56	7005	8	2	257	39412	2	0
58	18957	3	0	261	38085	2	0
59	18957	3	0	265	40054	1	0
60	16283	3	0	266	39423	2	0
64	13238	4	1	267	39453	2	0
70	39442	2	0	270	78091	1	0
71	17036	4	0	276	39168	2	0
73	7005	8	2	277	39458	2	0
83	11476	6	0	278	14391	3	1
86	39425	2	0	279	39195	2	0
94	21847	2	1	282	12977	5	0
100	16731	3	1	284	14391	3	1
101	12439	4	0	290	16347	4	0
113	17055	4	0	293	39478	2	0
120	67907	1	0	294	39392	2	0
121	12081	4	0	297	39180	2	0
124	39174	2	0	299	6867	7	3

WO 99/33982				PCT/US98/27610			
SEQ ID NO.	Cluster	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library	SEQ ID NO.	Cluster	Clones in 1 <sup>st</sup> Library	Clones in 2 <sup>nd</sup> Library
126	8210	2	6	301	41633	1	1
128	40455	2	0	302	23218	3	0
139	22195	3	0	303	39380	2	0
143	86859	1	0	309	84328	1	0
150	8672	4	4	314	14367	3	0
153	16977	4	0	320	39886	2	0
156	17036	4	0	324	9061	5	2
159	40044	2	0	327	16653	3	1
161	40044	2	0	328	16985	4	0
163	22155	3	0	329	12977	5	0
166	15066	4	0	330	9061	5	2
170	11465	5	0	333	16392	3	0
176	3765	19	6	342	39486	2	0
181	86110	1	0	344	6874	6	3
182	39648	2	0	345	6874	6	3
185	17076	4	0	353	11494	4	0
186	22794	2	0	354	17062	3	0
187	39171	2	0	355	16245	4	0
194	40455	2	0	356	83103	1	0
199	16317	3	0	358	13072	4	1
210	39186	2	0	366	14364	1	0
211	40122	2	0	368	84182	1	0
218	26295	2	0	372	56020	1	0
222	4665	5	9	389	7514	5	3
226	82498	1	0	391	7570	5	3
227	35702	2	0	393	23210	3	0

In addition to the above, SEQ ID NOS:159 and 161 were each present in one clone in each of Lib16 (Normal Colon Tumor Tissue), and SEQ ID NOS:344 and 345 were each present in one clone in Lib17 (High Colon Metastasis Tissue). No clones corresponding to the colon-specific polynucleotides in the table above were present in any of Libraries 3, 4, 8, or 9. The polynucleotide provided above can be used as markers of cells of colon origin, and find particular use in reference arrays, as described above.

#### Example 13: Identification of Contiguous Sequences Having a Polynucleotide of the Invention

The novel polynucleotides were used to screen publicly available and proprietary databases to determine if any of the polynucleotides of SEQ ID NOS:1-404 would facilitate identification of a contiguous sequence, *e.g.*, the polynucleotides would provide sequence that would result in 5' extension of another DNA sequence, resulting in production of a longer contiguous sequence composed of the provided polynucleotide and the other DNA sequence(s). Contigging was performed using the AssemblyLign program with the following

parameters: 1) Overlap: Minimum Overlap Length: 30; % Stringency: 50; Minimum Repeat Length: 30; Alignment: gap creation penalty: 1.00, gap extension penalty: 1.00; 2) Consensus: % Base designation threshold: 80.

Using these parameters, 44 polynucleotides provided contiged sequences. These  
5 contiged sequences are provided as SEQ ID NOS:801-844. The contiged sequences can be correlated with the sequences of SEQ ID NOS:1-404 upon which the contiged sequences are based by identifying those sequences of SEQ ID NOS:1-404 and the contiged sequences of SEQ ID NOS:801-844 that share the same clone name in Table 1. It should be noted that of these 44 sequences that provided a contiged sequence, the following members of that group  
10 of 44 did not contig using the overlap settings indicated in parentheses (Stringency/Overlap): SEQ ID NO:804 (30%/10); SEQ ID NO:810 (20%/20); SEQ ID NO:812 (30%/10); SEQ ID NO:814 (40%/20); SEQ ID NO:816 (30%/10); SEQ ID NO:832 (30%/10); SEQ ID NO:840 (20%/20); SEQ ID NO:841 (40%/20). To generalize, the indicated polynucleotides did not contig using a minimum 20% stringency, 10 overlap. There was a corresponding increase in  
15 the number of degenerate codons in these sequences.

The contiged sequences (SEQ ID NO:801-844) thus represent longer sequences that encompass a polynucleotide sequence of the invention. The contiged sequences were then translated in all three reading frames to determine the best alignment with individual sequences using the BLAST programs as described above for SEQ ID NOS:1-404 and the  
20 validation sequences SEQ ID NOS:405-800. Again the sequences were masked using the XBLAST program for masking low complexity as described above in Example 1 (Table 2). Several of the contiged sequences were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein families (and thus represent new members of these protein families) and/or comprising a known functional domain (Table 16). Thus the  
25 invention encompasses fragments, fusions, and variants of such polynucleotides that retain biological activity associated with the protein family and/or functional domain identified herein.

**Table 16. Profile hits using contiged sequences**

SEQ ID NO.	Sequence Name	Profile	Start (Stop)	Score
809	Contig_RTA00000177AF.n.18.3. Seq_THC123051	ATPases	778 (1612)	6040
824	Contig_RTA00000187AF.g.24.1. Seq_THC168636	homeobox	531 (707)	12080
824	Contig_RTA00000187AF.g.24.1. Seq_THC168636	MAP kinase kinase	769 (1494)	5784
833	Contig_RTA00000190AF.j.4.1. Seq_THC228776	protein kinase	170 (1010)	5027
833	Contig_RTA00000190AF.j.4.1. Seq_THC228776	protein kinase	170 (1010)	5027

All stop/start sequences are provided in the forward direction.

5       The profiles for the ATPases (AAA) and protein kinase families are described above in Example 2. The homeobox and MAP kinase kinase protein families are described further below.

Homeobox domain. The 'homeobox' is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp1-10, Oxford University Press, Oxford, (1994); Buerklin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring *Trends Biochem. Sci.* (1992) 17:277-280; Gehring *et al Annu. Rev. Genet.* (1986) 20:147-173; Schofield *Trends Neurosci.* (1987) 10:3-6; <http://copan.bioz.unibas.ch/homeo.html>) first identified in number of Drosophila homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below. The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

[illegible]

The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain. The consensus pattern is as follows: [LIVMFYVG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

5        MAP kinase kinase (MAPKK). MAP kinases (MAPK) are involved in signal transduction, and are important in cell cycle and cell growth controls. The MAP kinase kinases (MAPKK) are dual-specificity protein kinases which phosphorylate and activate MAP kinases. MAPKK homologues have been found in yeast, invertebrates, amphibians, and mammals. Moreover, the MAPKK/MAPK phosphorylation switch constitutes a basic  
10    module activated in distinct pathways in yeast and in vertebrates. MAPKK regulation studies have led to the discovery of at least four MAPKK convergent pathways in higher organisms. One of these is similar to the yeast pheromone response pathway which includes the *ste11* protein kinase. Two other pathways require the activation of either one or both of the serine/threonine kinase-encoded oncogenes *c-Raf-1* and *c-Mos*. Additionally, several  
15    studies suggest a possible effect of the cell cycle control regulator cyclin-dependent kinase 1 (*cdc2*) on MAPKK activity. Finally, MAPKKs are apparently essential transducers through which signals must pass before reaching the nucleus. For review, see, *e.g.*, *Biologique Cell* (1993) 79:193-207; Nishida *et al.*, *Trends Biochem Sci* (1993) 18:128-31; Ruderman *Curr Opin Cell Biol* (1993) 5:207-13; Dhanasekaran *et al.*, *Oncogene* (1998) 17:1447-55;  
20    Kiefer *et al.*, *Biochem Soc Trans* (1997) 25:491-8; and Hill, *Cell Signal* (1996) 8:533-44.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

25        All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of  
30    prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the  
5 appended claims.

Deposit Information:

The following materials were deposited with the American Type Culture Collection:  
CMCC = (Chiron Master Culture Collection)

10

Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

cDNA Library ES1 - ATCC#  
 Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001395A:C03	4016	79.A1.sp6:130016.Seq
M00001395A:C03	4016	RTA00000118A.c.4.1
M00001449A:D12	3681	RTA00000131A.g.15.2
M00001449A:D12	3681	79.E1.sp6:130064.Seq
M00001452A:D08	1120	79.C2.sp6:130041.Seq
M00001452A:D08	1120	RTA00000118A.p.15.3
M00001513A:B06	4568	79.D4.sp6:130055.Seq
M00001513A:B06	4568	RTA00000122A.d.15.3
M00001517A:B07	4313	79.F4.sp6:130079.Seq
M00001517A:B07	4313	RTA00000122A.n.3.1
M00001533A:C11	2428	RTA00000123A.l.21.1
M00001533A:C11	2428	79.A5.sp6:130020.Seq
M00001533A:C11	2428	RTA00000123A.l.21.1.Seq_THC205063
M00001542A:A09	22113	79.F5.sp6:130080.Seq
M00001542A:A09	22113	RTA00000125A.c.7.1

cDNA Library ES2 - ATCC#  
 Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001343C:F10	2790	80.E1.sp6:130256.Seq
M00001343C:F10	2790	RTA00000177AF.e.2.1.Seq_THC229461
M00001343C:F10	2790	RTA00000177AF.e.2.1
M00001343D:H07	23255	100.C1.sp6:131446.Seq
M00001343D:H07	23255	RTA00000177AF.e.14.3.Seq_THC228776
M00001343D:H07	23255	80.F1.sp6:130268.Seq
M00001343D:H07	23255	RTA00000177AF.e.14.3
M00001345A:E01	6420	172.E1.sp6:133925.Seq
M00001345A:E01	6420	RTA00000177AF.f.10.3
M00001345A:E01	6420	RTA00000177AF.f.10.3.Seq_THC226443
M00001345A:E01	6420	80.G1.sp6:130280.Seq
M00001347A:B10	13576	80.D2.sp6:130245.Seq
M00001347A:B10	13576	100.E1.sp6:131470.Seq
M00001347A:B10	13576	RTA00000177AF.g.16.1
M00001353A:G12	8078	80.E3.sp6:130258.Seq
M00001353A:G12	8078	RTA00000177AR.l.13.1
M00001353A:G12	8078	172.C3.sp6:133903.Seq
M00001353D:D10	14929	RTA00000177AF.m.1.2
M00001353D:D10	14929	80.F3.sp6:130270.Seq
M00001353D:D10	14929	172.D3.sp6:133915.Seq
M00001361A:A05	4141	80.B4.sp6:130223.Seq
M00001361A:A05	4141	RTA00000177AF.p.20.3
M00001362B:D10	5622	80.D4.sp6:130247.Seq
M00001362B:D10	5622	RTA00000178AF.a.11.1



## cDNA Library ES3 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001362C:H11	945	RTA00000178AR.a.20.1
M00001362C:H11	945	100.E4.sp6:131473.Seq
M00001362C:H11	945	80.E4.sp6:130259.Seq
M00001362C:H11	945	180.C2.sp6:135940.Seq
M00001376B:G06	17732	RTA00000178AR.i.2.2
M00001376B:G06	17732	80.B5.sp6:130224.Seq
M00001387A:C05	2464	80.D6.sp6:130249.Seq
M00001387A:C05	2464	RTA00000178AF.n.18.1
M00001412B:B10	8551	RTA00000179AF.p.21.1
M00001412B:B10	8551	80.G7.sp6:130286.Seq
M00001415A:H06	13538	80.B8.sp6:130227.Seq
M00001415A:H06	13538	RTA00000180AF.a.24.1
M00001416B:H11	8847	80.C8.sp6:130239.Seq
M00001416B:H11	8847	RTA00000180AF.b.16.1
M00001429D:D07	40392	RTA00000180AF.j.8.1
M00001429D:D07	40392	80.H9.sp6:130300.Seq
M00001448D:H01	36313	80.A11.sp6:130218.Seq
M00001448D:H01	36313	RTA00000181AF.e.23.1

## cDNA Library ES4 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001463C:B11	19	RTA00000182AF.b.7.1
M00001463C:B11	19	89.D1.sp6:130703.Seq
M00001470A:B10	1037	89.F2.sp6:130728.Seq
M00001470A:B10	1037	RTA00000121A.f.8.1
M00001497A:G02	2623	89.F3.sp6:130729.Seq
M00001497A:G02	2623	RTA00000183AF.a.6.1
M00001500A:E11	2623	RTA00000183AF.b.14.1
M00001500A:E11	2623	89.A4.sp6:130670.Seq
M00001501D:C02	9685	RTA00000183AF.c.11.1.Seq_THC109544
M00001501D:C02	9685	RTA00000183AF.c.11.1
M00001501D:C02	9685	89.C4.sp6:130694.Seq
M00001504C:H06	6974	89.F4.sp6:130730.Seq
M00001504C:H06	6974	RTA00000183AF.d.9.1
M00001504C:H06	6974	RTA00000183AF.d.9.1.Seq_THC223129
M00001504D:G06	6420	173.F5.SP6:134133.Seq
M00001504D:G06	6420	89.G4.sp6:130742.Seq
M00001504D:G06	6420	RTA00000183AF.d.11.1.Seq_THC226443
M00001504D:G06	6420	RTA00000183AF.d.11.1
M00001528A:C04	35555	89.B6.sp6:130684.Seq
M00001528A:C04	7337	RTA00000123A.b.17.1
M00001528A:C04	35555	184.A5.sp6:135530.Seq

## cDNA Library ES5 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001537B:G07	3389	RTA00000183AF.m.19.1
M00001537B:G07	3389	89.A8.sp6:130674.Seq
M00001541A:D02	3765	89.C8.sp6:130698.Seq
M00001541A:D02	3765	RTA00000135A.d.1.1
M00001544B:B07	6974	89.A9.sp6:130675.Seq
M00001544B:B07	6974	RTA00000184AF.a.15.1
M00001546A:G11	1267	89.D9.sp6:130711.Seq
M00001546A:G11	1267	RTA00000125A.o.5.1
M00001549B:F06	4193	89.G9.sp6:130747.Seq
M00001549B:F06	4193	RTA00000184AF.e.13.1
M00001556A:F11	1577	173.C9.SP6:134101.Seq
M00001556A:F11	1577	89.F11.sp6:130737.Seq
M00001556A:F11	1577	RTA00000184AF.i.23.1
M00001556B:C08	4386	RTA00000184AF.j.4.1
M00001556B:C08	4386	89.H11.sp6:130761.Seq

## cDNA Library ES6 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001563B:F06	102	RTA00000184AF.o.5.1
M00001563B:F06	102	90.B1.sp6:130871.Seq
M00001571C:H06	5749	90.E1.sp6:130907.Seq
M00001571C:H06	5749	RTA00000185AF.a.19.1
M00001594B:H04	260	90.D2.sp6:130896.Seq
M00001594B:H04	260	RTA00000185AR.i.12.2
M00001597C:H02	4837	90.E2.sp6:130908.Seq
M00001597C:H02	4837	RTA00000185AR.k.3.2
M00001624C:F01	4309	90.C4.sp6:130886.Seq
M00001624C:F01	4309	RTA00000186AF.e.22.1
M00001679A:A06	6660	90.F6.sp6:130924.Seq
M00001679A:A06	6660	122.B5.sp6:132089.Seq
M00001679A:A06	6660	RTA00000187AF.h.15.1
M00003759B:B09	697	90.G8.sp6:130938.Seq
M00003759B:B09	697	RTA00000188AF.d.6.1
M00003759B:B09	697	RTA00000188AF.d.6.1.Seq_THC178884
M00003844C:B11	6539	176.D9.sp6:134556.Seq
M00003844C:B11	6539	RTA00000189AF.d.22.1
M00003844C:B11	6539	90.B10.sp6:130880.Seq
M00003857A:G10	3389	90.A11.sp6:130869.Seq
M00003857A:G10	3389	RTA00000189AF.g.3.1

## cDNA Library ES7 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00003914C:F05	3900	99.E1.sp6:131278.Seq
M00003914C:F05	3900	RTA00000190AF.g.13.1
M00003922A:E06	23255	RTA00000190AF.j.4.1
M00003922A:E06	23255	99.F1.sp6:131290.Seq
M00003922A:E06	23255	RTA00000190AF.j.4.1.Seq_THC228776
M00003983A:A05	9105	99.C3.sp6:131256.Seq
M00003983A:A05	9105	RTA00000191AF.a.21.2
M00004028D:A06	6124	RTA00000191AR.e.2.3
M00004028D:A06	6124	99.D3.sp6:131268.Seq
M00004031A:A12	9061	RTA00000191AR.e.11.2
M00004031A:A12	9061	RTA00000191AR.e.11.3
M00004087D:A01	6880	RTA00000191AF.m.20.1
M00004087D:A01	6880	99.A5.sp6:131234.Seq
M00004108A:E06	4937	99.E5.sp6:131282.Seq
M00004108A:E06	4937	RTA00000191AF.p.21.1
M00004114C:F11	13183	123.D5.sp6:132305.Seq
M00004114C:F11	13183	RTA00000192AF.a.24.1
M00004114C:F11	13183	99.G5.sp6:131306.Seq

## cDNA Library ES8 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004146C:C11	5257	99.B6.sp6:131247.Seq
M00004146C:C11	5257	177.F5.sp6:134768.Seq
M00004146C:C11	5257	RTA00000192AF.f.3.1
M00004146C:C11	5257	RTA00000192AF.f.3.1.Seq_THC213833
M00004157C:A09	6455	RTA00000192AF.g.23.1
M00004157C:A09	6455	99.D6.sp6:131271.Seq
M00004157C:A09	6455	123.E7.sp6:132319.Seq
M00004172C:D08	11494	RTA00000192AF.j.6.1
M00004172C:D08	11494	99.G6.sp6:131307.Seq
M00004172C:D08	11494	177.E6.sp6:134757.Seq
M00004229B:F08	6455	RTA00000193AF.b.9.1
M00004229B:F08	6455	99.C8.sp6:131261.Seq

## cDNA Library ES9 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001466A:E07	4275	RTA00000120A.j.14.1
M00001531A:H11		89.F6.sp6:130732.Seq
M00001531A:H11		RTA00000123A.g.19.1
M00001551A:B10	6268	79.G9.sp6:130096.Seq
M00001551A:B10	6268	184.C12.sp6:135561.Seq
M00001551A:B10	6268	RTA00000126A.o.23.1
M00001552A:B12	307	RTA00000136A.o.4.2
M00001552A:B12	307	79.C7.sp6:130046.Seq
M00001556A:H01	15855	RTA00000184AF.j.1.1
M00001586C:C05	4623	RTA00000185AF.f.4.1
M00001604A:B10	1399	79.G8.sp6:130095.Seq
M00001604A:B10	1399	RTA00000129A.o.10.1
M00003879B:C11	5345	RTA00000189AF.l.19.1
M00003879B:C11	5345	90.B12.sp6:130882.Seq

## cDNA Library ES10 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001358C:C06		RTA00000177AF.o.4.3
M00001388D:G05	5832	80.F6.sp6:130273.Seq
M00001388D:G05	5832	RTA00000178AF.o.23.1
M00001394A:F01	6583	RTA00000179AF.d.13.1
M00001394A:F01	6583	172.B8.sp6:133896.Seq
M00001394A:F01	6583	80.H6.sp6:130297.Seq
M00001429A:H04	2797	RTA00000180AF.i.19.1
M00001447A:G03	10717	RTA00000181AF.d.10.1
M00001448D:C09	8	80.H10.sp6:130301.Seq
M00001448D:C09	8	RTA00000181AF.e.17.1
M00001448D:C09	8	100.B11.sp6:131444.Seq
M00001454D:G03	689	RTA00000181AR.l.22.1

## cDNA Library ES11 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00003975A:G11	12439	RTA00000190AF.o.24.1
M00003978B:G05	5693	RTA00000190AF.p.17.2.Seq_THC173318
M00003978B:G05	5693	RTA00000190AF.p.17.2
M00004059A:D06	5417	RTA00000191AF.h.19.1
M00004068B:A01	3706	99.C4.sp6:131257.Seq
M00004068B:A01	3706	RTA00000191AF.i.17.2
M00004205D:F06		99.E7.sp6:131284.Seq
M00004205D:F06		177.G7.sp6:134782.Seq
M00004205D:F06		RTA00000192AF.o.11.1
M00004212B:C07	2379	RTA00000192AF.p.8.1
M00004223A:G10	16918	RTA00000193AF.a.16.1

## cDNA Library ES12 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004223B:D09	7899	RTA00000193AF.a.17.1
M00004249D:G12		RTA00000193AF.c.22.1
M00004251C:G07		RTA00000193AF.d.2.1
M00004372A:A03	2030	RTA00000193AF.m.20.1

WO 99/33982  
cDNA Library ES13 - ATCC#  
Deposit Date - December 22, 1998

PCT/US98/27610

Clone Name	Cluster ID	Sequence Name
M00001340B:A06	17062	80.A1.sp6:130208.Seq
M00001340B:A06	17062	RTA00000177AF.b.8.4
M00001340D:F10	11589	80.B1.sp6:130220.Seq
M00001340D:F10	11589	RTA00000177AF.b.17.4
M00001341A:E12	4443	80.C1.sp6:130232.Seq
M00001341A:E12	4443	RTA00000177AF.b.20.4
M00001342B:E06	39805	80.D1.sp6:130244.Seq
M00001342B:E06	39805	RTA00000177AF.c.21.3
M00001346A:F09	5007	RTA00000177AF.g.2.1
M00001346A:F09	5007	80.H1.sp6:130292.Seq
M00001346D:G06	5779	RTA00000177AF.g.14.3
M00001346D:G06	5779	RTA00000177AF.g.14.1
M00001348B:B04	16927	80.E2.sp6:130257.Seq
M00001348B:B04	16927	RTA00000177AF.h.9.3
M00001348B:G06	16985	RTA00000177AF.h.10.1
M00001348B:G06	16985	80.F2.sp6:130269.Seq
M00001349B:B08	3584	RTA00000177AF.h.20.1
M00001349B:B08	3584	80.G2.sp6:130281.Seq
M00001350A:H01	7187	100.C2.sp6:131447.Seq
M00001350A:H01	7187	80.A3.sp6:130210.Seq
M00001350A:H01	7187	RTA00000177AF.i.8.2
M00001352A:E02	16245	RTA00000177AF.k.9.3
M00001352A:E02	16245	172.D2.sp6:133914.Seq
M00001352A:E02	16245	80.D3.sp6:130246.Seq
M00001355B:G10	14391	RTA00000177AF.m.17.3
M00001355B:G10	14391	80.G3.sp6:130282.Seq
M00001355B:G10	14391	172.H3.sp6:133963.Seq
M00001355B:G10	14391	100.E3.sp6:131472.Seq
M00001361D:F08	2379	80.C4.sp6:130235.Seq
M00001361D:F08	2379	RTA00000178AF.a.6.1
M00001365C:C10	40132	RTA00000178AF.c.7.1
M00001365C:C10	40132	80.F4.sp6:130271.Seq
M00001368D:E03		80.G4.sp6:130283.Seq
M00001368D:E03		RTA00000178AF.d.20.1
M00001370A:C09	6867	80.H4.sp6:130295.Seq
M00001370A:C09	6867	RTA00000178AF.e.12.1
M00001371C:E09	7172	100.A5.sp6:131426.Seq
M00001371C:E09	7172	RTA00000178AF.f.9.1
M00001371C:E09	7172	80.A5.sp6:130212.Seq
M00001378B:B02	39833	80.C5.sp6:130236.Seq
M00001378B:B02	39833	RTA00000178AF.i.23.1
M00001379A:A05	1334	80.D5.sp6:130248.Seq
M00001379A:A05	1334	RTA00000178AF.j.7.1
M00001380D:B09	39886	RTA00000178AF.j.24.1
M00001380D:B09	39886	80.E5.sp6:130260.Seq
M00001381D:E06		80.F5.sp6:130272.Seq
M00001381D:E06		RTA00000178AF.k.16.1
M00001382C:A02	22979	80.G5.sp6:130284.Seq
M00001382C:A02	22979	RTA00000178AF.k.22.1
M00001384B:A11		80.B6.sp6:130225.Seq
M00001384B:A11		RTA00000178AF.m.13.1
M00001386C:B12	5178	80.C6.sp6:130237.Seq

cDNA Library ES13 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001386C:B12	5178	RTA00000178AF.n.10.1
M00001387B:G03	7587	80.E6.sp6:130261.Seq
M00001387B:G03	7587	RTA00000178AF.n.24.1
M00001389A:C08	16269	RTA00000178AF.p.1.1
M00001389A:C08	16269	80.G6.sp6:130285.Seq
M00001396A:C03	4009	172.D8.sp6:133920.Seq
M00001396A:C03	4009	80.A7.sp6:130214.Seq
M00001396A:C03	4009	RTA00000179AF.e.20.1
M00001400B:H06		172.B9.sp6:133897.Seq
M00001400B:H06		80.B7.sp6:130226.Seq
M00001400B:H06		RTA00000179AF.j.13.1
M00001400B:H06		RTA00000179AF.j.13.1.Seq_THC105720
M00001402A:E08	39563	80.C7.sp6:130238.Seq
M00001402A:E08	39563	RTA00000179AF.k.20.1
M00001407B:D11	5556	RTA00000179AF.n.10.1
M00001407B:D11	5556	80.D7.sp6:130250.Seq
M00001410A:D07	7005	180.H5.sp6:136003.Seq
M00001410A:D07	7005	RTA00000179AF.o.22.1
M00001410A:D07	7005	80.F7.sp6:130274.Seq
M00001414A:B01		RTA00000180AF.a.9.1
M00001414A:B01		80.H7.sp6:130298.Seq
M00001414C:A07		80.A8.sp6:130215.Seq
M00001414C:A07		RTA00000180AF.a.11.1
M00001416A:H01	7674	79.C1.sp6:130040.Seq
M00001416A:H01	7674	RTA00000118A.g.9.1
M00001417A:E02	36393	RTA00000180AF.c.2.1
M00001417A:E02	36393	80.D8.sp6:130251.Seq
M00001423B:E07	15066	RTA00000180AF.e.24.1
M00001423B:E07	15066	80.H8.sp6:130299.Seq
M00001424B:G09	10470	80.A9.sp6:130216.Seq
M00001424B:G09	10470	RTA00000180AF.f.18.1
M00001425B:H08	22195	RTA00000180AF.g.7.1
M00001425B:H08	22195	80.B9.sp6:130228.Seq
M00001426B:D12		RTA00000180AF.g.22.1
M00001426B:D12		80.C9.sp6:130240.Seq
M00001426D:C08	4261	80.D9.sp6:130252.Seq
M00001426D:C08	4261	RTA00000180AF.h.5.1
M00001428A:H10	84182	100.G9.sp6:131502.Seq
M00001428A:H10	84182	RTA00000180AF.h.19.1
M00001428A:H10	84182	80.E9.sp6:130264.Seq
M00001449A:A12	5857	80.B11.sp6:130230.Seq
M00001449A:A12	5857	RTA00000118A.g.14.1
M00001449A:B12	41633	80.C11.sp6:130242.Seq
M00001449A:B12	41633	RTA00000118A.g.16.1
M00001449A:G10	36535	RTA00000181AF.f.5.1
M00001449A:G10	36535	80.D11.sp6:130254.Seq
M00001449A:G10	36535	100.D11.sp6:131468.Seq
M00001449C:D06	86110	RTA00000181AF.f.12.1
M00001449C:D06	86110	80.E11.sp6:130266.Seq
M00001450A:A02	39304	RTA00000118A.j.21.1.Seq_THC151859
M00001450A:A02	39304	RTA00000118A.j.21.1
M00001450A:A02	39304	79.F1.sp6:130076.Seq

cDNA Library ES13 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001450A:A02	39304	180.G9.sp6:135995.Seq
M00001450A:A11	32663	80.F11.sp6:130278.Seq
M00001450A:A11	32663	RTA00000118A.l.8.1
M00001450A:B12	82498	100.F11.sp6:131492.Seq
M00001450A:B12	82498	RTA00000118A.m.10.1
M00001450A:B12	82498	79.G1.sp6:130088.Seq
M00001450A:D08	27250	80.G11.sp6:130290.Seq
M00001450A:D08	27250	180.B10.sp6:135936.Seq
M00001450A:D08	27250	RTA00000181AF.g.10.1
M00001452A:B04	84328	RTA00000118A.p.10.1
M00001452A:B04	84328	79.A2.sp6:130017.Seq
M00001452A:B12	86859	RTA00000118A.p.8.1
M00001452A:B12	86859	79.B2.sp6:130029.Seq
M00001452A:F05	85064	RTA00000131A.m.23.1
M00001452A:F05	85064	79.D2.sp6:130053.Seq
M00001452C:B06	16970	80.H11.sp6:130302.Seq
M00001452C:B06	16970	100.C12.sp6:131457.Seq
M00001452C:B06	16970	RTA00000181AR.i.18.2
M00001453A:E11	16130	80.A12.sp6:130219.Seq
M00001453A:E11	16130	100.D12.sp6:131469.Seq
M00001453A:E11	16130	RTA00000119A.c.13.1
M00001453C:F06	16653	80.B12.sp6:130231.Seq
M00001453C:F06	16653	RTA00000181AF.k.5.3
M00001454A:A09	83103	RTA00000119A.e.24.2
M00001454A:A09	83103	79.G2.sp6:130089.Seq
M00001454B:C12	7005	121.D1.sp6:131917.Seq
M00001454B:C12	7005	RTA00000181AF.k.24.1
M00001454B:C12	7005	80.C12.sp6:130243.Seq
M00001455B:E12	13072	80.F12.sp6:130279.Seq
M00001455B:E12	13072	RTA00000181AR.m.5.2
M00001460A:F06	2448	89.A1.sp6:130667.Seq
M00001460A:F06	2448	RTA00000119A.j.21.1
M00001461A:D06	1531	89.C1.sp6:130691.Seq
M00001461A:D06	1531	RTA00000119A.o.3.1
M00001465A:B11	10145	79.F3.sp6:130078.Seq
M00001465A:B11	10145	RTA00000120A.g.12.1
M00001467A:B07	38759	89.F1.sp6:130727.Seq
M00001467A:B07	38759	RTA00000120A.m.12.3
M00001467A:D04	39508	RTA00000120A.o.2.1
M00001467A:D04	39508	89.G1.sp6:130739.Seq
M00001467A:E10	39442	89.A2.sp6:130668.Seq
M00001467A:E10	39442	RTA00000120A.o.21.1
M00001468A:F05	7589	RTA00000120A.p.23.1
M00001468A:F05	7589	89.B2.sp6:130680.Seq
M00001469A:A01		RTA00000121A.c.10.1
M00001469A:A01		89.C2.sp6:130692.Seq
M00001469A:C10	12081	89.D2.sp6:130704.Seq
M00001469A:C10	12081	RTA00000133A.d.14.2
M00001469A:H12	19105	89.E2.sp6:130716.Seq
M00001469A:H12	19105	RTA00000133A.e.15.1
M00001470A:C04	39425	89.G2.sp6:130740.Seq
M00001470A:C04	39425	RTA00000133A.f.1.1

cDNA Library ES13 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001471A:B01	39478	89.H2.sp6:130752.Seq
M00001471A:B01	39478	RTA00000133A.i.5.1
M00001487B:H06		RTA00000182AF.l.15.1
M00001487B:H06		89.B3.sp6:130681.Seq
M00001488B:F12		RTA00000182AF.l.20.1
M00001488B:F12		89.C3.sp6:130693.Seq
M00001494D:F06	7206	RTA00000182AF.o.15.1
M00001494D:F06	7206	89.E3.sp6:130717.Seq
M00001499B:A11	10539	RTA00000183AF.a.24.1
M00001499B:A11	10539	89.G3.sp6:130741.Seq
M00001499B:A11	10539	173.B5.SP6:134085.Seq
M00001500A:C05	5336	RTA00000183AF.b.13.1
M00001500A:C05	5336	89.H3.sp6:130753.Seq
M00001504A:E01		RTA00000183AF.c.24.1
M00001504A:E01		89.D4.sp6:130706.Seq
M00001504A:E01		RTA00000183AF.c.24.1.Seq_THC125912
M00001504C:A07	10185	RTA00000183AF.d.5.1
M00001504C:A07	10185	89.E4.sp6:130718.Seq
M00001505C:C05		89.H4.sp6:130754.Seq
M00001505C:C05		RTA00000183AF.e.1.1
M00001506D:A09		89.A5.sp6:130671.Seq
M00001506D:A09		RTA00000183AF.e.23.1
M00001506D:A09		121.G6.sp6:131958.Seq
M00001507A:H05	39168	RTA00000121A.l.10.1
M00001507A:H05	39168	89.B5.sp6:130683.Seq
M00001535A:F10	39423	79.C5.sp6:130044.Seq
M00001535A:F10	39423	RTA00000134A.k.22.1
M00001541A:H03	39174	79.E5.sp6:130068.Seq
M00001541A:H03	39174	RTA00000124A.n.13.1
M00001544A:G02	19829	79.H5.sp6:130104.Seq
M00001544A:G02	19829	RTA00000125A.h.24.4
M00001545A:D08	13864	RTA00000125A.m.9.1
M00001545A:D08	13864	79.B6.sp6:130033.Seq
M00001551A:F05	39180	RTA00000126A.n.8.2
M00001551A:F05	39180	79.A7.sp6:130022.Seq
M00001552A:D11	39458	RTA00000126A.p.15.2
M00001552A:D11	39458	79.D7.sp6:130058.Seq
M00001557A:F03	39490	RTA00000128A.b.4.1



cDNA Library ES14 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001511A:H06	39412	RTA00000133A.k.17.1
M00001511A:H06	39412	89.C5.sp6:130695.Seq
M00001512A:A09	39186	89.D5.sp6:130707.Seq
M00001512A:A09	39186	RTA00000121A.p.15.1
M00001512D:G09	3956	89.E5.sp6:130719.Seq
M00001512D:G09	3956	173.H5.SP6:134157.Seq
M00001512D:G09	3956	RTA00000183AF.g.3.1
M00001513B:G03		RTA00000183AF.g.9.1
M00001513B:G03		89.F5.sp6:130731.Seq
M00001513B:G03		RTA00000183AF.g.9.1.Seq_THC198280
M00001513C:E08	14364	RTA00000183AF.g.12.1
M00001513C:E08	14364	89.G5.sp6:130743.Seq
M00001514C:D11	40044	RTA00000183AF.g.22.1
M00001514C:D11	40044	RTA00000183AF.g.22.1.Seq_THC232899
M00001514C:D11	40044	89.H5.sp6:130755.Seq
M00001518C:B11	8952	89.A6.sp6:130672.Seq
M00001518C:B11	8952	RTA00000183AF.h.15.1
M00001528B:H04	8358	89.D6.sp6:130708.Seq
M00001528B:H04	8358	RTA00000183AF.i.5.1
M00001531A:D01	38085	RTA00000123A.e.15.1
M00001531A:D01	38085	89.E6.sp6:130720.Seq
M00001534A:C04	16921	RTA00000183AF.k.6.1
M00001534A:C04	16921	89.H6.sp6:130756.Seq
M00001534A:D09	5097	RTA00000134A.k.1.1
M00001534A:D09	5097	RTA00000134A.k.1.1.Seq_THC215869
M00001534C:A01	4119	RTA00000183AF.k.16.1
M00001534C:A01	4119	89.C7.sp6:130697.Seq
M00001535A:C06	20212	89.E7.sp6:130721.Seq
M00001535A:C06	20212	RTA00000134A.l.22.1.Seq_THC128232
M00001535A:C06	20212	RTA00000134A.l.22.1
M00001536A:B07	2696	RTA00000134A.m.13.1
M00001536A:B07	2696	89.F7.sp6:130733.Seq
M00001537A:F12	39420	89.H7.sp6:130757.Seq
M00001537A:F12	39420	RTA00000134A.o.23.1
M00001540A:D06	8286	89.B8.sp6:130686.Seq
M00001540A:D06	8286	RTA00000183AF.o.1.1
M00001542A:E06	39453	89.E8.sp6:130722.Seq
M00001542A:E06	39453	RTA00000135A.g.11.1
M00001544A:E06		RTA00000184AF.a.8.1
M00001544A:E06		173.G7.SP6:134147.Seq
M00001544A:E06		89.H8.sp6:130758.Seq
M00001545A:B02		89.B9.sp6:130687.Seq
M00001545A:B02		RTA00000135A.l.2.2
M00001548A:E10	5892	89.E9.sp6:130723.Seq
M00001548A:E10	5892	RTA00000184AF.d.11.1
M00001548A:E10	5892	RTA00000184AF.d.11.1.Seq_THC161896
M00001549C:E06	16347	89.H9.sp6:130759.Seq
M00001549C:E06	16347	RTA00000184AF.e.15.1
M00001550A:A03	7239	89.A10.sp6:130676.Seq
M00001550A:A03	7239	RTA00000126A.m.4.2
M00001550A:G01	5175	RTA00000184AF.f.3.1
M00001550A:G01	5175	89.B10.sp6:130688.Seq

WO 99/33982  
cDNA Library ES14 - ATCC#  
Deposit Date - December 22, 1998

PCT/US98/27610

Clone Name	Cluster ID	Sequence Name
M00001551A:G06	22390	RTA00000136A.j.13.1
M00001551A:G06	22390	89.C10.sp6:130700.Seq
M00001551C:G09	3266	RTA00000184AR.g.1.1
M00001551C:G09	3266	89.D10.sp6:130712.Seq
M00001553A:H06	8298	RTA00000127A.d.19.1
M00001553A:H06	8298	89.G10.sp6:130748.Seq
M00001553B:F12	4573	89.H10.sp6:130760.Seq
M00001553B:F12	4573	RTA00000184AF.h.9.1
M00001555A:B02	39539	RTA00000127A.i.21.1
M00001555A:B02	39539	89.B11.sp6:130689.Seq
M00001555A:C01	39195	89.C11.sp6:130701.Seq
M00001555A:C01	39195	RTA00000137A.c.16.1
M00001555D:G10	4561	RTA00000184AF.i.21.1
M00001555D:G10	4561	89.D11.sp6:130713.Seq
M00001556A:C09	9244	89.E11.sp6:130725.Seq
M00001556A:C09	9244	RTA00000127A.l.3.1
M00001556B:G02	11294	RTA00000184AF.j.6.1
M00001556B:G02	11294	89.A12.sp6:130678.Seq
M00001557B:H10	5192	173.E9.SP6:134125.Seq
M00001557B:H10	5192	RTA00000184AF.k.2.1
M00001557B:H10	5192	89.D12.sp6:130714.Seq
M00001557D:D09	8761	RTA00000184AF.k.12.1
M00001557D:D09	8761	89.E12.sp6:130726.Seq
M00001558B:H11	7514	RTA00000184AF.k.21.1
M00001558B:H11	7514	89.G12.sp6:130750.Seq
M00001559B:F01		89.H12.sp6:130762.Seq
M00001559B:F01		RTA00000184AF.l.11.1
M00001560D:F10	6558	90.A1.sp6:130859.Seq
M00001560D:F10	6558	RTA00000184AF.m.21.1
M00001566B:D11		RTA00000184AF.p.3.1
M00001566B:D11		90.D1.sp6:130895.Seq
M00001583D:A10	6293	RTA00000185AF.e.11.1
M00001583D:A10	6293	90.A2.sp6:130860.Seq
M00001590B:F03		RTA00000185AF.g.11.1
M00001590B:F03		90.C2.sp6:130884.Seq
M00001597D:C05	10470	RTA00000185AF.k.6.1
M00001597D:C05	10470	90.F2.sp6:130920.Seq
M00001598A:G03	16999	90.G2.sp6:130932.Seq
M00001598A:G03	16999	RTA00000185AF.k.9.1
M00001601A:D08	22794	RTA00000138A.b.5.1
M00001601A:D08	22794	90.H2.sp6:130944.Seq
M00001607A:E11	11465	RTA00000185AF.m.19.1
M00001607A:E11	11465	90.A3.sp6:130861.Seq
M00001608A:B03	7802	RTA00000185AF.n.5.1
M00001608A:B03	7802	90.B3.sp6:130873.Seq
M00001608B:E03	22155	RTA00000185AF.n.9.1
M00001608B:E03	22155	90.C3.sp6:130885.Seq
M00001608D:A11		RTA00000185AF.n.12.1
M00001608D:A11		90.D3.sp6:130897.Seq
M00001614C:F10	13157	RTA00000186AF.a.6.1
M00001614C:F10	13157	90.E3.sp6:130909.Seq
M00001617C:E02	17004	RTA00000186AF.b.21.1

cDNA Library ES14 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001617C:E02	17004	90.F3.sp6:130921.Seq
M00001619C:F12	40314	90.G3.sp6:130933.Seq
M00001619C:F12	40314	RTA00000186AF.c.15.1
M00001621C:C08	40044	RTA00000186AF.d.1.1
M00001621C:C08	40044	RTA00000186AF.d.1.1.Seq_THC232899
M00001621C:C08	40044	90.H3.sp6:130945.Seq
M00001621C:C08	40044	122.E1.sp6:132121.Seq
M00001623D:F10	13913	RTA00000186AF.e.6.1
M00001623D:F10	13913	90.A4.sp6:130862.Seq
M00001632D:H07		RTA00000186AF.h.14.1.Seq_THC112525
M00001632D:H07		RTA00000186AF.h.14.1
M00001632D:H07		90.E4.sp6:130910.Seq
M00001632D:H07		176.A3.sp6:134514.Seq
M00001644C:B07	39171	RTA00000186AF.l.7.1
M00001644C:B07	39171	90.F4.sp6:130922.Seq
M00001644C:B07	39171	217.A12.sp6:139369.Seq
M00001645A:C12	19267	RTA00000186AF.l.12.1.Seq_THC178183
M00001645A:C12	19267	176.G3.sp6:134586.Seq
M00001645A:C12	19267	RTA00000186AF.l.12.1
M00001645A:C12	19267	90.G4.sp6:130934.Seq
M00001648C:A01	4665	90.H4.sp6:130946.Seq
M00001648C:A01	4665	RTA00000186AF.m.3.1
M00001657D:C03	23201	RTA00000187AF.a.14.1
M00001657D:C03	23201	90.B5.sp6:130875.Seq
M00001657D:F08	76760	90.C5.sp6:130887.Seq
M00001657D:F08	76760	RTA00000187AF.a.15.1
M00001662C:A09	23218	RTA00000187AR.c.5.2
M00001662C:A09	23218	90.D5.sp6:130899.Seq
M00001663A:E04	35702	90.E5.sp6:130911.Seq
M00001663A:E04	35702	RTA00000187AR.c.15.2
M00001669B:F02	6468	90.F5.sp6:130923.Seq
M00001669B:F02	6468	RTA00000187AF.d.15.1
M00001670C:H02	14367	90.G5.sp6:130935.Seq
M00001670C:H02	14367	RTA00000187AF.e.8.1
M00001673C:H02	7015	90.H5.sp6:130947.Seq
M00001673C:H02	7015	RTA00000187AF.f.18.1
M00001675A:C09	8773	RTA00000187AF.f.24.1
M00001675A:C09	8773	90.A6.sp6:130864.Seq
M00001675A:C09	8773	RTA00000187AF.f.24.1.Seq_THC220002
M00001676B:F05	11460	RTA00000187AF.g.12.1
M00001676B:F05	11460	90.B6.sp6:130876.Seq
M00001676B:F05	11460	219.F2.sp6:139035.Seq
M00001677D:A07	7570	90.D6.sp6:130900.Seq
M00001677D:A07	7570	RTA00000187AF.g.24.1
M00001677D:A07	7570	RTA00000187AF.g.24.1.Seq_THC168636
M00001678D:F12	4416	90.E6.sp6:130912.Seq
M00001678D:F12	4416	RTA00000187AF.h.13.1
M00001679A:F10	26875	RTA00000187AF.i.1.1
M00001679A:F10	26875	90.A7.sp6:130865.Seq
M00001679B:F01	6298	90.B7.sp6:130877.Seq
M00001679B:F01	6298	RTA00000187AR.i.10.2
M00001680D:F08	10539	90.F7.sp6:130925.Seq

cDNA Library ES14 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00001680D:F08	10539	219.F6.sp6:139039.Seq
M00001680D:F08	10539	RTA00000187AF.l.7.1
M00001682C:B12	17055	90.G7.sp6:130937.Seq
M00001682C:B12	17055	RTA00000187AF.m.3.1
M00001682C:B12	17055	176.D6.sp6:134553.Seq
M00001688C:F09	5382	90.A8.sp6:130866.Seq
M00001688C:F09	5382	RTA00000187AF.m.23.2
M00001693C:G01	4393	RTA00000187AF.n.17.1
M00001693C:G01	4393	90.B8.sp6:130878.Seq
M00001716D:H05	67252	RTA00000187AF.o.6.1
M00001716D:H05	67252	90.C8.sp6:130890.Seq
M00003741D:C09	40108	90.D8.sp6:130902.Seq
M00003741D:C09	40108	RTA00000187AF.o.24.1
M00003747D:C05	11476	RTA00000187AF.p.19.1
M00003747D:C05	11476	90.E8.sp6:130914.Seq
M00003747D:C05	11476	RTA00000187AF.p.19.1.Seq_THC108482
M00003747D:C05	11476	219.H8.sp6:139065.Seq
M00003754C:E09		90.F8.sp6:130926.Seq
M00003754C:E09		RTA00000188AF.b.12.1
M00003761D:A09		RTA00000188AF.d.11.1
M00003761D:A09		90.H8.sp6:130950.Seq
M00003761D:A09		RTA00000188AF.d.11.1.Seq_THC212094
M00003762C:B08	17076	RTA00000188AF.d.21.1.Seq_THC208760
M00003762C:B08	17076	90.A9.sp6:130867.Seq
M00003762C:B08	17076	RTA00000188AF.d.21.1
M00003763A:F06	3108	RTA00000188AF.d.24.1
M00003763A:F06	3108	90.B9.sp6:130879.Seq
M00003774C:A03	67907	RTA00000188AF.g.11.1.Seq_THC123222
M00003774C:A03	67907	RTA00000188AF.g.11.1
M00003774C:A03	67907	90.C9.sp6:130891.Seq
M00003784D:D12		RTA00000188AF.i.8.1
M00003784D:D12		90.D9.sp6:130903.Seq
M00003839A:D08	7798	RTA00000189AF.c.18.1
M00003839A:D08	7798	90.A10.sp6:130868.Seq
M00003851B:D08		90.D10.sp6:130904.Seq
M00003851B:D08		RTA00000189AF.f.7.1
M00003851B:D10	13595	90.E10.sp6:130916.Seq
M00003851B:D10	13595	RTA00000189AF.f.8.1
M00003853A:D04	5619	90.F10.sp6:130928.Seq
M00003853A:D04	5619	RTA00000189AF.f.17.1
M00003853A:F12	10515	90.G10.sp6:130940.Seq
M00003853A:F12	10515	RTA00000189AF.f.18.1
M00003856B:C02	4622	90.H10.sp6:130952.Seq
M00003856B:C02	4622	RTA00000189AF.g.1.1
M00003857A:H03	4718	90.B11.sp6:130881.Seq
M00003857A:H03	4718	RTA00000189AF.g.5.1.Seq_THC196102
M00003857A:H03	4718	RTA00000189AF.g.5.1

cDNA Library ES15 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00003867A:D10		90.C11.sp6:130893.Seq
M00003867A:D10		RTA00000189AF.h.17.1
M00003871C:E02	4573	RTA00000189AF.j.12.1
M00003875C:G07	8479	90.G11.sp6:130941.Seq
M00003875C:G07	8479	RTA00000189AF.j.22.1
M00003875D:D11		90.H11.sp6:130953.Seq
M00003875D:D11		RTA00000189AF.j.23.1
M00003876D:E12	7798	90.A12.sp6:130870.Seq
M00003876D:E12	7798	RTA00000189AF.k.12.1
M00003906C:E10	9285	90.H12.sp6:130954.Seq
M00003906C:E10	9285	RTA00000190AF.d.7.1
M00003907D:A09	39809	99.A1.sp6:131230.Seq
M00003907D:A09	39809	RTA00000190AF.e.3.1.Seq_THC150217
M00003907D:A09	39809	RTA00000190AF.e.3.1
M00003907D:H04	16317	99.B1.sp6:131242.Seq
M00003907D:H04	16317	RTA00000190AF.e.6.1
M00003909D:C03	8672	RTA00000190AF.f.11.1
M00003909D:C03	8672	99.C1.sp6:131254.Seq
M00003968B:F06	24488	RTA00000190AF.n.16.1
M00003968B:F06	24488	99.C2.sp6:131255.Seq
M00003970C:B09	40122	RTA00000190AF.n.23.1
M00003970C:B09	40122	RTA00000190AF.n.23.1.Seq_THC109227
M00003970C:B09	40122	99.D2.sp6:131267.Seq
M00003974D:E07	23210	RTA00000190AF.o.20.1
M00003974D:E07	23210	RTA00000190AF.o.20.1.Seq_THC207240
M00003974D:E07	23210	99.E2.sp6:131279.Seq
M00003974D:H02	23358	RTA00000190AF.o.21.1.Seq_THC207240
M00003974D:H02	23358	RTA00000190AF.o.21.1
M00003974D:H02	23358	99.F2.sp6:131291.Seq
M00003981A:E10	3430	99.A3.sp6:131232.Seq
M00003981A:E10	3430	RTA00000191AF.a.9.1
M00003982C:C02	2433	RTA00000191AF.a.15.2
M00003982C:C02	2433	99.B3.sp6:131244.Seq
M00003982C:C02	2433	RTA00000191AF.a.15.2.Seq_THC79498
M00004028D:C05	40073	RTA00000191AF.e.3.1
M00004028D:C05	40073	99.E3.sp6:131280.Seq
M00004035C:A07	37285	99.H3.sp6:131316.Seq
M00004035C:A07	37285	RTA00000191AF.f.11.1
M00004035D:B06	17036	RTA00000191AF.f.13.1
M00004035D:B06	17036	99.A4.sp6:131233.Seq
M00004072A:C03		RTA00000191AF.j.9.1
M00004072A:C03		99.D4.sp6:131269.Seq
M00004081C:D10	15069	99.F4.sp6:131293.Seq
M00004081C:D10	15069	RTA00000191AF.l.6.1
M00004086D:G06	9285	99.H4.sp6:131317.Seq
M00004086D:G06	9285	RTA00000191AF.m.18.1
M00004105C:A04	7221	99.D5.sp6:131270.Seq
M00004105C:A04	7221	RTA00000191AF.p.9.1
M00004171D:B03	4908	RTA00000192AF.j.2.1
M00004171D:B03	4908	99.F6.sp6:131295.Seq
M00004185C:C03	11443	RTA00000192AF.l.13.2
M00004185C:C03	11443	123.A8.sp6:132272.Seq

cDNA Library ES15 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004185C:C03	11443	99.A7.sp6:131236.Seq
M00004191D:B11		RTA00000192AF.m.12.1
M00004191D:B11		99.B7.sp6:131248.Seq
M00004191D:B11		123.C8.sp6:132296.Seq
M00004197D:H01	8210	99.C7.sp6:131260.Seq
M00004197D:H01	8210	123.E8.sp6:132320.Seq
M00004197D:H01	8210	RTA00000192AF.n.13.1
M00004203B:C12	14311	99.D7.sp6:131272.Seq
M00004203B:C12	14311	RTA00000192AF.o.2.1
M00004214C:H05	11451	177.D8.sp6:134747.Seq
M00004214C:H05	11451	RTA00000192AF.p.17.1
M00004223D:E04	12971	RTA00000193AF.a.20.1
M00004223D:E04	12971	99.B8.sp6:131249.Seq
M00004269D:D06	4905	99.H8.sp6:131321.Seq
M00004269D:D06	4905	RTA00000193AF.e.14.1
M00004295D:F12	16921	99.D9.sp6:131274.Seq
M00004295D:F12	16921	RTA00000193AF.h.15.1
M00004296C:H07	13046	99.E9.sp6:131286.Seq
M00004296C:H07	13046	RTA00000193AF.h.19.1
M00004307C:A06	9457	RTA00000193AF.i.14.2
M00004307C:A06	9457	99.F9.sp6:131298.Seq
M00004307C:A06	9457	123.D11.sp6:132311.Seq
M00004312A:G03	26295	RTA00000193AF.i.24.2
M00004312A:G03	26295	99.G9.sp6:131310.Seq
M00004312A:G03	26295	RTA00000193AF.i.24.2.Seq_THC197345
M00004318C:D10	21847	RTA00000193AF.j.9.1
M00004318C:D10	21847	99.H9.sp6:131322.Seq
M00004359B:G02		RTA00000193AF.m.5.1.Seq_THC173318
M00004359B:G02		RTA00000193AF.m.5.1
M00004505D:F08		RTA00000194AF.b.19.1
M00004505D:F08		99.H10.sp6:131323.Seq
M00004692A:H08		99.B11.sp6:131252.Seq
M00004692A:H08		RTA00000194AF.c.24.1
M00004692A:H08		377.F4.sp6:141957.Seq
M00005180C:G03		RTA00000194AF.f.4.1

WO 99/33982  
cDNA Library ES16 - ATCC#  
Deposit Date - December 22, 1998

PCT/US98/27610

Clone Name	Cluster ID	Sequence Name
M00001346D:E03	6806	RTA00000177AF.g.13.3
M00001350A:B08		80.H2.sp6:130293.Seq
M00001350A:B08		RTA00000177AF.i.6.2
M00001357D:D11	4059	RTA00000177AF.n.18.3.Seq_THC123051
M00001357D:D11	4059	RTA00000177AF.n.18.3
M00001409C:D12	9577	RTA00000179AF.o.17.1
M00001409C:D12	9577	80.E7.sp6:130262.Seq
M00001418B:F03	9952	RTA00000180AF.c.20.1
M00001418B:F03	9952	RTA00000180AF.c.20.1.Seq_THC162284
M00001418B:F03	9952	80.E8.sp6:130263.Seq
M00001418D:B06	8526	RTA00000180AF.d.1.1
M00001421C:F01	9577	RTA00000180AF.d.23.1
M00001421C:F01	9577	80.G8.sp6:130287.Seq
M00001429B:A11	4635	RTA00000180AF.i.20.1
M00001432C:F06		RTA00000180AF.k.24.1
M00001439C:F08	40054	RTA00000180AF.p.10.1
M00001442C:D07	16731	RTA00000181AF.a.20.1
M00001442C:D07	16731	80.C10.sp6:130241.Seq
M00001443B:F01		80.D10.sp6:130253.Seq
M00001443B:F01		RTA00000181AF.b.7.1
M00001445A:F05	13532	80.E10.sp6:130265.Seq
M00001445A:F05	13532	RTA00000181AF.c.4.1
M00001446A:F05	7801	RTA00000181AF.c.21.1
M00001455A:E09	13238	RTA00000181AF.m.4.1
M00001455A:E09	13238	RTA00000181AF.m.4.1.Seq_THC140691
M00001460A:F12	39498	RTA00000119A.j.20.1
M00001481D:A05	7985	RTA00000182AR.j.2.1
M00001490B:C04	18699	RTA00000182AF.m.16.1
M00001490B:C04	18699	89.D3.sp6:130705.Seq
M00001500C:E04	9443	89.B4.sp6:130682.Seq
M00001500C:E04	9443	RTA00000183AF.c.1.1
M00001532B:A06	3990	89.G6.sp6:130744.Seq
M00001532B:A06	3990	RTA00000183AF.j.11.1
M00001534A:F09	5321	89.B7.sp6:130685.Seq
M00001534A:F09	5321	RTA00000183AF.k.8.1
M00001535A:B01	7665	RTA00000134A.l.19.1
M00001536A:C08	39392	89.G7.sp6:130745.Seq
M00001536A:C08	39392	RTA00000134A.m.16.1
M00001541A:F07	22085	RTA00000135A.e.5.2
M00001542B:B01		RTA00000183AF.p.4.1
M00001542B:B01		89.F8.sp6:130734.Seq
M00001544A:E03	12170	RTA00000125A.h.18.4
M00001545A:C03	19255	RTA00000135A.m.18.1
M00001545A:C03	19255	184.B10.sp6:135547.Seq
M00001545A:C03	19255	89.C9.sp6:130699.Seq
M00001548A:H09	1058	RTA00000126A.e.20.3.Seq_THC217534
M00001548A:H09	1058	RTA00000126A.e.20.3
M00001548A:H09	1058	79.F6.sp6:130081.Seq
M00001549A:B02	4015	RTA00000136A.e.12.1
M00001549A:B02	4015	79.G6.sp6:130093.Seq
M00001549A:D08	10944	RTA00000126A.h.17.2
M00001552B:D04	5708	RTA00000184AF.g.12.1

WO 99/33982  
cDNA Library ES16 - ATCC#  
Deposit Date - December 22, 1998

PCT/US98/27610

Clone Name	Cluster ID	Sequence Name
M00001552B:D04	5708	89.E10.sp6:130724.Seq
M00001552D:A01		89.F10.sp6:130736.Seq
M00001552D:A01		RTA00000184AF.g.22.1
M00001553D:D10	22814	RTA00000184AF.h.14.1
M00001553D:D10	22814	89.A11.sp6:130677.Seq
M00001558A:H05		RTA00000128A.c.20.1
M00001558A:H05		89.F12.sp6:130738.Seq
M00001561A:C05	39486	RTA00000128A.m.22.2
M00001561A:C05	39486	79.B8.sp6:130035.Seq
M00001564A:B12	5053	RTA00000184AF.o.12.1
M00001578B:E04	23001	RTA00000185AF.c.24.1
M00001579D:C03	6539	90.G1.sp6:130931.Seq
M00001579D:C03	6539	173.A12.SP6:134080.Seq
M00001579D:C03	6539	RTA00000185AF.d.11.1
M00001582D:F05		RTA00000185AF.d.24.1
M00001587A:B11	39380	RTA00000129A.e.24.1
M00001587A:B11	39380	79.E8.sp6:130071.Seq
M00001604A:F05	39391	RTA00000138A.c.3.1
M00001604A:F05	39391	79.A9.sp6:130024.Seq
M00001624A:B06	3277	RTA00000138A.l.5.1
M00001624A:B06	3277	217.E1.sp6:139406.Seq
M00001624A:B06	3277	90.B4.sp6:130874.Seq
M00001630B:H09	5214	90.D4.sp6:130898.Seq
M00001630B:H09	5214	122.C2.sp6:132098.Seq
M00001630B:H09	5214	RTA00000186AF.g.11.1
M00001651A:H01		RTA00000186AF.n.7.1
M00001651A:H01		90.A5.sp6:130863.Seq
M00001677C:E10	14627	RTA00000187AF.g.23.1
M00001679C:F01	78091	90.C7.sp6:130889.Seq
M00001679C:F01	78091	RTA00000187AF.j.6.1
M00001679C:F01	78091	176.G5.sp6:134588.Seq
M00001686A:E06	4622	RTA00000187AF.m.15.2
M00003796C:D05	5619	RTA00000188AF.l.9.1.Seq_THC167845
M00003796C:D05	5619	RTA00000188AF.l.9.1
M00003826B:A06	11350	RTA00000189AF.a.24.2
M00003826B:A06	11350	90.F9.sp6:130927.Seq
M00003833A:E05	21877	RTA00000189AF.b.21.1
M00003837D:A01	7899	90.H9.sp6:130951.Seq
M00003837D:A01	7899	RTA00000189AF.c.10.1
M00003846B:D06	6874	RTA00000189AF.e.9.1
M00003846B:D06	6874	90.C10.sp6:130892.Seq
M00003879B:D10	31587	RTA00000189AF.l.20.1
M00003879B:D10	31587	90.C12.sp6:130894.Seq
M00003879D:A02	14507	90.D12.sp6:130906.Seq
M00003879D:A02	14507	RTA00000189AR.l.23.2
M00003891C:H09		90.G12.sp6:130942.Seq
M00003891C:H09		RTA00000189AF.p.8.1
M00003912B:D01	12532	99.D1.sp6:131266.Seq
M00003912B:D01	12532	RTA00000190AF.g.2.1
M00004072B:B05	17036	RTA00000191AF.j.10.1
M00004081C:D12	14391	RTA00000191AF.l.7.1
M00004111D:A08	6874	RTA00000192AF.a.14.1



cDNA Library ES16 - ATCC#

Deposit Date - December 22, 1998

Clone Name	Cluster ID	Sequence Name
M00004111D:A08	6874	99.F5.sp6:131294.Seq
M00004121B:G01		177.H4.sp6:134791.Seq
M00004121B:G01		99.H5.sp6:131318.Seq
M00004121B:G01		RTA00000192AF.c.2.1
M00004138B:H02	13272	99.A6.sp6:131235.Seq
M00004138B:H02	13272	RTA00000192AF.e.3.1
M00004151D:B08	16977	RTA00000192AF.g.3.1
M00004169C:C12	5319	99.E6.sp6:131283.Seq
M00004169C:C12	5319	RTA00000192AF.i.12.1
M00004169C:C12	5319	123.F7.sp6:132331.Seq
M00004183C:D07	16392	RTA00000192AF.l.1.1
M00004183C:D07	16392	RTA00000192AF.l.1.1.Seq_THC202071
M00004230B:C07	7212	RTA00000193AF.b.14.1
M00004230B:C07	7212	99.D8.sp6:131273.Seq
M00004249D:F10		RTA00000193AF.c.21.1.Seq_THC222602
M00004249D:F10		RTA00000193AF.c.21.1
M00004275C:C11	16914	99.A9.sp6:131238.Seq
M00004275C:C11	16914	RTA00000193AF.f.5.1
M00004283B:A04	14286	RTA00000193AF.f.22.1
M00004285B:E08	56020	RTA00000193AF.g.2.1
M00004327B:H04		RTA00000193AF.j.20.1
M00004377C:F05	2102	RTA00000193AF.n.7.1
M00004384C:D02		RTA00000193AF.n.15.1
M00004384C:D02		RTA00000193AF.n.15.1.Seq_THC215687
M00004461A:B08		RTA00000194AR.a.10.2
M00004461A:B09		RTA00000194AF.a.11.1
M00004691D:A05		RTA00000194AF.c.23.1
M00004896A:C07		RTA00000194AF.d.13.1

The above material has been deposited with the American Type Culture Collection, Rockville, Maryland, under the accession number indicated. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for purposes of Patent Procedure. The deposit will be maintained for a period of 30 years following issuance of this patent, or for the enforceable life of the patent, whichever is greater. Upon issuance of the patent, the deposit will be available to the public from the ATCC without restriction.

This deposit is provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences herein. A license may

be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones

5           Where the ATCC deposit is composed of a pool of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single  
10 colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a  $T_m$  of approximately 80°C (assuming 2°C for each A or T and 4°C for  
15 each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide  
20 sequence.

**Table 1.** Sequence identification numbers, cluster ID, sequence name, and clone name

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
1	4635	RTA00000180AF.i.20.1	M00001429B:A11
2		RTA00000185AF.n.12.1	M00001608D:A11
3	4622	RTA00000187AF.m.15.2	M00001686A:E06
4	3706	RTA00000191AF.i.17.2	M00004068B:A01
5	36535	RTA00000181AF.f.5.1	M00001449A:G10
6	3990	RTA00000183AF.j.11.1	M00001532B:A06
7	5319	RTA00000192AF.i.12.1	M00004169C:C12
8	36393	RTA00000180AF.c.2.1	M00001417A:E02
9	2623	RTA00000183AF.a.6.1	M00001497A:G02
10	7587	RTA00000178AF.n.24.1	M00001387B:G03
11	7065	RTA00000137A.g.6.1	M00001557A:D02
12	10539	RTA00000187AF.l.7.1	M00001680D:F08
13	27250	RTA00000181AF.g.10.1	M00001450A:D08
14	5556	RTA00000179AF.n.10.1	M00001407B:D11
15		RTA00000192AF.m.12.1	M00004191D:B11
16	8761	RTA00000184AF.k.12.1	M00001557D:D09
17	4622	RTA00000189AF.g.1.1	M00003856B:C02
18	11460	RTA00000187AF.g.12.1	M00001676B:F05
19	16283	RTA00000120A.o.20.1	M00001467A:D08
20	3430	RTA00000191AF.a.9.1	M00003981A:E10
21	7065	RTA00000184AF.j.21.1	M00001557A:D02
22		RTA00000182AF.l.20.1	M00001488B:F12
23		RTA00000123A.g.19.1	M00001531A:H11
24	16918	RTA00000193AF.a.16.1	M00004223A:G10
25	16914	RTA00000193AF.f.5.1	M00004275C:C11
26	40108	RTA00000187AF.o.24.1	M00003741D:C09
27	14286	RTA00000193AF.f.22.1	M00004283B:A04
28	17004	RTA00000186AF.b.21.1	M00001617C:E02
29		RTA00000180AF.g.22.1	M00001426B:D12
30	13272	RTA00000192AF.e.3.1	M00004138B:H02
31		RTA00000194AF.f.4.1	M00005180C:G03
32	32663	RTA00000118A.l.8.1	M00001450A:A11
33		RTA00000180AF.a.9.1	M00001414A:B01
34	5832	RTA00000178AF.o.23.1	M00001388D:G05
35	7801	RTA00000181AF.c.21.1	M00001446A:F05
36	76760	RTA00000187AF.a.15.1	M00001657D:F08
37	40132	RTA00000178AF.c.7.1	M00001365C:C10
38		RTA00000183AF.e.1.1	M00001505C:C05
39	4016	RTA00000118A.c.4.1	M00001395A:C03
40	5382	RTA00000187AF.m.23.2	M00001688C:F09

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
41	5693	RTA00000190AF.p.17.2	M00003978B:G05
42	307	RTA00000136A.o.4.2	M00001552A:B12
43	39833	RTA00000178AF.i.23.1	M00001378B:B02
44		RTA00000193AF.m.5.1	M00004359B:G02
45	5325	RTA00000191AF.o.6.1	M00004093D:B12
46	5325	RTA00000191AF.o.6.2	M00004093D:B12
47	18957	RTA00000190AR.m.9.1	M00003958A:H02
48	39508	RTA00000120A.o.2.1	M00001467A:D04
49	22390	RTA00000136A.j.13.1	M00001551A:G06
50	12170	RTA00000125A.h.18.4	M00001544A:E03
51	4393	RTA00000187AF.n.17.1	M00001693C:G01
52	19	RTA00000182AF.b.7.1	M00001463C:B11
53		RTA00000193AF.c.21.1	M00004249D:F10
54	7899	RTA00000189AF.c.10.1	M00003837D:A01
55	40073	RTA00000191AF.e.3.1	M00004028D:C05
56	7005	RTA00000179AF.o.22.1	M00001410A:D07
57		RTA00000187AF.h.22.1	M00001679A:F06
58	18957	RTA00000190AF.m.9.2	M00003958A:H02
59	18957	RTA00000183AF.h.23.1	M00001528A:F09
60	16283	RTA00000182AF.c.22.1	M00001467A:D08
61	6974	RTA00000183AF.d.9.1	M00001504C:H06
62	2623	RTA00000183AF.b.14.1	M00001500A:E11
63	9105	RTA00000191AF.a.21.2	M00003983A:A05
64	13238	RTA00000181AF.m.4.1	M00001455A:E09
65	5749	RTA00000185AF.a.19.1	M00001571C:H06
66	6455	RTA00000193AF.b.9.1	M00004229B:F08
67	23001	RTA00000185AF.c.24.1	M00001578B:E04
68	6455	RTA00000192AF.g.23.1	M00004157C:A09
69	13595	RTA00000189AF.f.8.1	M00003851B:D10
70	39442	RTA00000120A.o.21.1	M00001467A:E10
71	17036	RTA00000191AF.f.13.1	M00004035D:B06
72		RTA00000183AF.g.9.1	M00001513B:G03
73	7005	RTA00000181AF.k.24.1	M00001454B:C12
74	6268	RTA00000126A.o.23.1	M00001551A:B10
75	16130	RTA00000119A.c.13.1	M00001453A:E11
76	23201	RTA00000187AF.a.14.1	M00001657D:C03
77	5321	RTA00000183AF.k.8.1	M00001534A:F09
78	13157	RTA00000186AF.a.6.1	M00001614C:F10
79	2102	RTA00000193AF.n.7.1	M00004377C:F05
80	1058	RTA00000126A.e.20.3	M00001548A:H09
81	40392	RTA00000180AF.j.8.1	M00001429D:D07
82		RTA00000183AF.e.23.1	M00001506D:A09
83	11476	RTA00000187AF.p.19.1	M00003747D:C05

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
84	3584	RTA00000177AF.h.20.1	M00001349B:B08
85	10470	RTA00000180AF.f.18.1	M00001424B:G09
86	39425	RTA00000133A.f.1.1	M00001470A:C04
87	5175	RTA00000184AF.f.3.1	M00001550A:G01
88	13576	RTA00000189AF.o.13.1	M00003885C:A02
89	7665	RTA00000134A.l.19.1	M00001535A:B01
90	16927	RTA00000177AF.h.9.3	M00001348B:B04
91	6660	RTA00000187AF.h.15.1	M00001679A:A06
92	2433	RTA00000191AF.a.15.2	M00003982C:C02
93	5097	RTA00000134A.k.1.1	M00001534A:D09
94	21847	RTA00000193AF.j.9.1	M00004318C:D10
95	3277	RTA00000138A.l.5.1	M00001624A:B06
96	5708	RTA00000184AF.g.12.1	M00001552B:D04
97	945	RTA00000178AR.a.20.1	M00001362C:H11
98	16269	RTA00000178AF.p.1.1	M00001389A:C08
99		RTA00000183AF.c.24.1	M00001504A:E01
100	16731	RTA00000181AF.a.20.1	M00001442C:D07
101	12439	RTA00000190AF.o.24.1	M00003975A:G11
102	3162	RTA00000177AF.j.12.3	M00001351B:A08
103		RTA00000194AF.b.19.1	M00004505D:F08
104		RTA00000193AF.n.15.1	M00004384C:D02
105		RTA00000186AF.n.7.1	M00001651A:H01
106	10717	RTA00000181AF.d.10.1	M00001447A:G03
107	4573	RTA00000189AF.j.12.1	M00003871C:E02
108		RTA00000186AF.h.14.1	M00001632D:H07
109	11443	RTA00000192AF.l.13.2	M00004185C:C03
110	5892	RTA00000184AF.d.11.1	M00001548A:E10
111	3162	RTA00000177AF.j.12.1	M00001351B:A08
112	10470	RTA00000185AF.k.6.1	M00001597D:C05
113	17055	RTA00000187AF.m.3.1	M00001682C:B12
114	2030	RTA00000193AF.m.20.1	M00004372A:A03
115	6558	RTA00000184AF.m.21.1	M00001560D:F10
116	23255	RTA00000190AF.j.4.1	M00003922A:E06
117	9577	RTA00000179AF.o.17.1	M00001409C:D12
118		RTA00000180AF.a.11.1	M00001414C:A07
119	8	RTA00000181AF.e.17.1	M00001448D:C09
120	67907	RTA00000188AF.g.11.1	M00003774C:A03
121	12081	RTA00000133A.d.14.2	M00001469A:C10
122	2448	RTA00000119A.j.21.1	M00001460A:F06
123	3389	RTA00000189AF.g.3.1	M00003857A:G10
124	39174	RTA00000124A.n.13.1	M00001541A:H03
125	24488	RTA00000190AF.n.16.1	M00003968B:F06
126	8210	RTA00000192AF.n.13.1	M00004197D:H01

SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
127		RTA00000135A.l.2.2	M00001545A:B02
128	40455	RTA00000190AF.m.10.2	M00003958C:G10
129	9577	RTA00000180AF.d.23.1	M00001421C:F01
130	13183	RTA00000192AF.a.24.1	M00004114C:F11
131	5214	RTA00000186AF.g.11.1	M00001630B:H09
132	67252	RTA00000187AF.o.6.1	M00001716D:H05
133	3108	RTA00000188AF.d.24.1	M00003763A:F06
134	2464	RTA00000178AF.n.18.1	M00001387A:C05
135	36313	RTA00000181AF.e.23.1	M00001448D:H01
136	23255	RTA00000177AF.e.14.3	M00001343D:H07
137	7985	RTA00000182AR.j.2.1	M00001481D:A05
138	8286	RTA00000183AF.o.1.1	M00001540A:D06
139	22195	RTA00000180AF.g.7.1	M00001425B:H08
140	4573	RTA00000184AF.h.9.1	M00001553B:F12
141	26875	RTA00000187AF.i.1.1	M00001679A:F10
142	7187	RTA00000177AF.i.8.2	M00001350A:H01
143	86859	RTA00000118A.p.8.1	M00001452A:B12
144	4623	RTA00000185AF.f.4.1	M00001586C:C05
145		RTA00000121A.c.10.1	M00001469A:A01
146	10185	RTA00000183AF.d.5.1	M00001504C:A07
147		RTA00000183AF.p.4.1	M00001542B:B01
148	15069	RTA00000191AF.l.6.1	M00004081C:D10
149	39304	RTA00000118A.j.21.1	M00001450A:A02
150	8672	RTA00000190AF.f.11.1	M00003909D:C03
151	13576	RTA00000177AF.g.16.1	M00001347A:B10
152	6293	RTA00000185AF.e.11.1	M00001583D:A10
153	16977	RTA00000192AF.g.3.1	M00004151D:B08
154	5345	RTA00000189AF.l.19.1	M00003879B:C11
155	4905	RTA00000193AF.e.14.1	M00004269D:D06
156	17036	RTA00000191AF.j.10.1	M00004072B:B05
157	5417	RTA00000191AF.h.19.1	M00004059A:D06
158	7172	RTA00000178AF.f.9.1	M00001371C:E09
159	40044	RTA00000186AF.d.1.1	M00001621C:C08
160	4386	RTA00000184AF.j.4.1	M00001556B:C08
161	40044	RTA00000183AF.g.22.1	M00001514C:D11
162	9685	RTA00000183AF.c.11.1	M00001501D:C02
163	22155	RTA00000185AF.n.9.1	M00001608B:E03
164	10515	RTA00000189AF.f.18.1	M00003853A:F12
165	6539	RTA00000185AF.d.11.1	M00001579D:C03
166	15066	RTA00000180AF.e.24.1	M00001423B:E07
167	4261	RTA00000180AF.h.5.1	M00001426D:C08
168	13864	RTA00000125A.m.9.1	M00001545A:D08
169	6539	RTA00000189AF.d.22.1	M00003844C:B11

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
170	11465	RTA00000185AF.m.19.1	M00001607A:E11
171	3266	RTA00000184AR.g.1.1	M00001551C:G09
172	102	RTA00000184AF.o.5.1	M00001563B:F06
173	16970	RTA00000181AR.i.18.2	M00001452C:B06
174	12971	RTA00000193AF.a.20.1	M00004223D:E04
175	5007	RTA00000177AF.g.2.1	M00001346A:F09
176	3765	RTA00000135A.d.1.1	M00001541A:D02
177	11294	RTA00000184AF.j.6.1	M00001556B:G02
178	3681	RTA00000131A.g.15.2	M00001449A:D12
179	9283	RTA00000181AR.m.21.2	M00001455D:F09
180	18699	RTA00000182AF.m.16.1	M00001490B:C04
181	86110	RTA00000181AF.f.12.1	M00001449C:D06
182	39648	RTA00000178AR.l.8.2	M00001383A:C03
183	7337	RTA00000123A.b.17.1	M00001528A:C04
184	1334	RTA00000178AF.j.7.1	M00001379A:A05
185	17076	RTA00000188AF.d.21.1	M00003762C:B08
186	22794	RTA00000138A.b.5.1	M00001601A:D08
187	39171	RTA00000186AF.l.7.1	M00001644C:B07
188	8551	RTA00000179AF.p.21.1	M00001412B:B10
189	5857	RTA00000118A.g.14.1	M00001449A:A12
190	9443	RTA00000183AF.c.1.1	M00001500C:E04
191	9457	RTA00000193AF.i.14.2	M00004307C:A06
192	7206	RTA00000182AF.o.15.1	M00001494D:F06
193	22979	RTA00000178AF.k.22.1	M00001382C:A02
194	40455	RTA00000190AR.m.10.1	M00003958C:G10
195	7221	RTA00000191AF.p.9.1	M00004105C:A04
196		RTA00000191AF.j.9.1	M00004072A:C03
197	7239	RTA00000126A.m.4.2	M00001550A:A03
198	31587	RTA00000189AF.l.20.1	M00003879B:D10
199	16317	RTA00000190AF.e.6.1	M00003907D:H04
200	13576	RTA00000189AR.o.13.1	M00003885C:A02
201	5779	RTA00000177AF.g.14.3	M00001346D:G06
202	6124	RTA00000191AR.e.2.3	M00004028D:A06
203	9952	RTA00000180AF.c.20.1	M00001418B:F03
204		RTA00000188AF.i.8.1	M00003784D:D12
205	5779	RTA00000177AF.g.14.1	M00001346D:G06
206	39490	RTA00000128A.b.4.1	M00001557A:F03
207	4416	RTA00000187AF.h.13.1	M00001678D:F12
208	4009	RTA00000179AF.e.20.1	M00001396A:C03
209	5336	RTA00000183AF.b.13.1	M00001500A:C05
210	39186	RTA00000121A.p.15.1	M00001512A:A09
211	40122	RTA00000190AF.n.23.1	M00003970C:B09
212	12532	RTA00000190AF.g.2.1	M00003912B:D01

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
213	8078	RTA00000177AR.l.13.1	M00001353A:G12
214	3900	RTA00000190AF.g.13.1	M00003914C:F05
215	7589	RTA00000120A.p.23.1	M00001468A:F05
216	8298	RTA00000127A.d.19.1	M00001553A:H06
217	4443	RTA00000177AF.b.20.4	M00001341A:E12
218	26295	RTA00000193AF.i.24.2	M00004312A:G03
219	3389	RTA00000183AF.m.19.1	M00001537B:G07
220	7015	RTA00000187AF.f.18.1	M00001673C:H02
221	8526	RTA00000180AF.d.1.1	M00001418D:B06
222	4665	RTA00000186AF.m.3.1	M00001648C:A01
223	1399	RTA00000129A.o.10.1	M00001604A:B10
224	9244	RTA00000127A.l.3.1	M00001556A:C09
225		RTA00000179AF.j.13.1	M00001400B:H06
226	82498	RTA00000118A.m.10.1	M00001450A:B12
227	35702	RTA00000187AR.c.15.2	M00001663A:E04
228	38759	RTA00000120A.m.12.3	M00001467A:B07
229	39648	RTA00000178AF.l.8.1	M00001383A:C03
230	19105	RTA00000133A.e.15.1	M00001469A:H12
231	85064	RTA00000131A.m.23.1	M00001452A:F05
232	9285	RTA00000191AF.m.18.1	M00004086D:G06
233	9285	RTA00000190AF.d.7.1	M00003906C:E10
234	39391	RTA00000138A.c.3.1	M00001604A:F05
235		RTA00000178AF.d.20.1	M00001368D:E03
236	39498	RTA00000119A.j.20.1	M00001460A:F12
237	7798	RTA00000189AF.k.12.1	M00003876D:E12
238	7798	RTA00000189AF.c.18.1	M00003839A:D08
239	19829	RTA00000125A.h.24.4	M00001544A:G02
240		RTA00000188AF.d.11.1	M00003761D:A09
241	4275	RTA00000120A.j.14.1	M00001466A:E07
242	22113	RTA00000125A.c.7.1	M00001542A:A09
243	40314	RTA00000186AF.c.15.1	M00001619C:F12
244	10944	RTA00000126A.h.17.2	M00001549A:D08
245	39809	RTA00000190AF.e.3.1	M00003907D:A09
246	22085	RTA00000135A.e.5.2	M00001541A:F07
247	19255	RTA00000135A.m.18.1	M00001545A:C03
248	14311	RTA00000192AF.o.2.1	M00004203B:C12
249	8479	RTA00000189AF.j.22.1	M00003875C:G07
250		RTA00000189AF.j.23.1	M00003875D:D11
251	4193	RTA00000184AF.e.13.1	M00001549B:F06
252	22814	RTA00000184AF.h.14.1	M00001553D:D10
253	39563	RTA00000179AF.k.20.1	M00001402A:E08
254	39420	RTA00000134A.o.23.1	M00001537A:F12
255	11589	RTA00000177AF.b.17.4	M00001340D:F10



WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
256	4937	RTA00000191AF.p.21.1	M00004108A:E06
257	39412	RTA00000133A.k.17.1	M00001511A:H06
258	4837	RTA00000185AR.k.3.2	M00001597C:H02
259	13046	RTA00000193AF.h.19.1	M00004296C:H07
260	4141	RTA00000177AF.p.20.3	M00001361A:A05
261	38085	RTA00000123A.e.15.1	M00001531A:D01
262		RTA00000189AF.p.8.1	M00003891C:H09
263	11451	RTA00000192AF.p.17.1	M00004214C:H05
264	14507	RTA00000189AR.l.23.2	M00003879D:A02
265	40054	RTA00000180AF.p.10.1	M00001439C:F08
266	39423	RTA00000134A.k.22.1	M00001535A:F10
267	39453	RTA00000135A.g.11.1	M00001542A:E06
268	10751	RTA00000187AF.k.7.1	M00001679D:D03
269	10751	RTA00000187AF.k.6.1	M00001679D:D03
270	78091	RTA00000187AF.j.6.1	M00001679C:F01
271	39539	RTA00000127A.i.21.1	M00001555A:B02
272		RTA00000182AF.l.15.1	M00001487B:H06
273		RTA00000194AF.d.13.1	M00004896A:C07
274		RTA00000128A.c.20.1	M00001558A:H05
275	9283	RTA00000181AR.m.22.2	M00001455D:F09
276	39168	RTA00000121A.l.10.1	M00001507A:H05
277	39458	RTA00000126A.p.15.2	M00001552A:D11
278	14391	RTA00000177AF.m.17.3	M00001355B:G10
279	39195	RTA00000137A.c.16.1	M00001555A:C01
280	7212	RTA00000193AF.b.14.1	M00004230B:C07
281	4015	RTA00000136A.e.12.1	M00001549A:B02
282	12977	RTA00000189AF.j.19.1	M00003875B:F04
283		RTA00000178AF.m.13.1	M00001384B:A11
284	14391	RTA00000191AF.l.7.1	M00004081C:D12
285		RTA00000194AF.c.23.1	M00004691D:A05
286		RTA00000181AF.b.7.1	M00001443B:F01
287	8358	RTA00000183AF.i.5.1	M00001528B:H04
288	1267	RTA00000125A.o.5.1	M00001546A:G11
289		RTA00000189AF.f.7.1	M00003851B:D08
290	16347	RTA00000184AF.e.15.1	M00001549C:E06
291	7899	RTA00000193AF.a.17.1	M00004223B:D09
292	2379	RTA00000178AF.a.6.1	M00001361D:F08
293	39478	RTA00000133A.i.5.1	M00001471A:B01
294	39392	RTA00000134A.m.16.1	M00001536A:C08
295	5053	RTA00000184AF.o.12.1	M00001564A:B12
296	16999	RTA00000185AF.k.9.1	M00001598A:G03
297	39180	RTA00000126A.n.8.2	M00001551A:F05
298	1037	RTA00000121A.f.8.1	M00001470A:B10

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
299	6867	RTA00000178AF.e.12.1	M00001370A:C09
300	10539	RTA00000183AF.a.24.1	M00001499B:A11
301	41633	RTA00000118A.g.16.1	M00001449A:B12
302	23218	RTA00000187AR.c.5.2	M00001662C:A09
303	39380	RTA00000129A.e.24.1	M00001587A:B11
304		RTA00000185AF.d.24.1	M00001582D:F05
305		RTA00000177AF.o.4.3	M00001358C:C06
306	6974	RTA00000184AF.a.15.1	M00001544B:B07
307		RTA00000185AF.g.11.1	M00001590B:F03
308	15855	RTA00000184AF.j.1.1	M00001556A:H01
309	84328	RTA00000118A.p.10.1	M00001452A:B04
310	10145	RTA00000120A.g.12.1	M00001465A:B11
311	39805	RTA00000177AF.c.21.3	M00001342B:E06
312		RTA00000187AF.h.23.1	M00001679A:F06
313	6298	RTA00000187AR.i.10.2	M00001679B:F01
314	14367	RTA00000187AF.e.8.1	M00001670C:H02
315		RTA00000193AF.c.22.1	M00004249D:G12
316	16921	RTA00000183AF.k.6.1	M00001534A:C04
317	1577	RTA00000184AF.i.23.1	M00001556A:F11
318	8773	RTA00000187AF.f.24.1	M00001675A:C09
319		RTA00000194AF.a.11.1	M00004461A:B09
320	39886	RTA00000178AF.j.24.1	M00001380D:B09
321	13532	RTA00000181AF.c.4.1	M00001445A:F05
322		RTA00000193AF.d.2.1	M00004251C:G07
323	5257	RTA00000192AF.f.3.1	M00004146C:C11
324	9061	RTA00000191AR.e.11.2	M00004031A:A12
325	19267	RTA00000186AF.l.12.1	M00001645A:C12
326	20212	RTA00000134A.l.22.1	M00001535A:C06
327	16653	RTA00000181AF.k.5.3	M00001453C:F06
328	16985	RTA00000177AF.h.10.1	M00001348B:G06
329	12977	RTA00000189AR.j.19.1	M00003875B:F04
330	9061	RTA00000191AR.e.11.3	M00004031A:A12
331		RTA00000194AR.a.10.2	M00004461A:B08
332	6468	RTA00000187AF.d.15.1	M00001669B:F02
333	16392	RTA00000192AF.l.1.1	M00004183C:D07
334	14627	RTA00000187AF.g.23.1	M00001677C:E10
335	6583	RTA00000179AF.d.13.1	M00001394A:F01
336	6806	RTA00000177AF.g.13.3	M00001346D:E03
337	9635	RTA00000137A.e.23.4	M00001557A:F01
338	689	RTA00000181AR.l.22.1	M00001454D:G03
339	4119	RTA00000183AF.k.16.1	M00001534C:A01
340	8952	RTA00000183AF.h.15.1	M00001518C:B11
341	2379	RTA00000192AF.p.8.1	M00004212B:C07

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
342	39486	RTA00000128A.m.22.2	M00001561A:C05
343	21877	RTA00000189AF.b.21.1	M00003833A:E05
344	6874	RTA00000192AF.a.14.1	M00004111D:A08
345	6874	RTA00000189AF.e.9.1	M00003846B:D06
346	37285	RTA00000191AF.f.11.1	M00004035C:A07
347		RTA00000193AF.j.20.1	M00004327B:H04
348	7674	RTA00000118A.g.9.1	M00001416A:H01
349	2797	RTA00000180AF.i.19.1	M00001429A:H04
350		RTA00000184AF.g.22.1	M00001552D:A01
351	7802	RTA00000185AF.n.5.1	M00001608A:B03
352	16921	RTA00000193AF.h.15.1	M00004295D:F12
353	11494	RTA00000192AF.j.6.1	M00004172C:D08
354	17062	RTA00000177AF.b.8.4	M00001340B:A06
355	16245	RTA00000177AF.k.9.3	M00001352A:E02
356	83103	RTA00000119A.e.24.2	M00001454A:A09
357	4309	RTA00000186AF.e.22.1	M00001624C:F01
358	13072	RTA00000181AR.m.5.2	M00001455B:E12
359	4059	RTA00000177AF.n.18.3	M00001357D:D11
360	5178	RTA00000178AF.n.10.1	M00001386C:B12
361	1120	RTA00000118A.p.15.3	M00001452A:D08
362	6420	RTA00000183AF.d.11.1	M00001504D:G06
363	13913	RTA00000186AF.e.6.1	M00001623D:F10
364		RTA00000192AF.c.2.1	M00004121B:G01
365	3956	RTA00000183AF.g.3.1	M00001512D:G09
366	14364	RTA00000183AF.g.12.1	M00001513C:E08
367	6880	RTA00000191AF.m.20.1	M00004087D:A01
368	84182	RTA00000180AF.h.19.1	M00001428A:H10
369	2790	RTA00000177AF.e.2.1	M00001343C:F10
370	4561	RTA00000184AF.i.21.1	M00001555D:G10
371	8847	RTA00000180AF.b.16.1	M00001416B:H11
372	56020	RTA00000193AF.g.2.1	M00004285B:E08
373	1531	RTA00000119A.o.3.1	M00001461A:D06
374	6420	RTA00000177AF.f.10.3	M00001345A:E01
375		RTA00000188AF.b.12.1	M00003754C:E09
376		RTA00000180AF.k.24.1	M00001432C:F06
377		RTA00000184AF.a.8.1	M00001544A:E06
378	2696	RTA00000134A.m.13.1	M00001536A:B07
379	260	RTA00000185AR.i.12.2	M00001594B:H04
380	11350	RTA00000189AF.a.24.2	M00003826B:A06
381	2428	RTA00000123A.l.21.1	M00001533A:C11
382	4313	RTA00000122A.n.3.1	M00001517A:B07
383		RTA00000184AF.p.3.1	M00001566B:D11
384	697	RTA00000188AF.d.6.1	M00003759B:B09

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
385	5619	RTA00000188AF.l.9.1	M00003796C:D05
386	4568	RTA00000122A.d.15.3	M00001513A:B06
387		RTA00000177AF.i.6.2	M00001350A:B08
388	5622	RTA00000178AF.a.11.1	M00001362B:D10
389	7514	RTA00000184AF.k.21.1	M00001558B:H11
390	5619	RTA00000189AF.f.17.1	M00003853A:D04
391	7570	RTA00000187AF.g.24.1	M00001677D:A07
392	23358	RTA00000190AF.o.21.1	M00003974D:H02
393	23210	RTA00000190AF.o.20.1	M00003974D:E07
394	5192	RTA00000184AF.k.2.1	M00001557B:H10
395	13538	RTA00000180AF.a.24.1	M00001415A:H06
396		RTA00000189AF.h.17.1	M00003867A:D10
397		RTA00000192AF.o.11.1	M00004205D:F06
398		RTA00000184AF.l.11.1	M00001559B:F01
399	4718	RTA00000189AF.g.5.1	M00003857A:H03
400	14929	RTA00000177AF.m.1.2	M00001353D:D10
401	4908	RTA00000192AF.j.2.1	M00004171D:B03
402		RTA00000178AF.k.16.1	M00001381D:E06
403		RTA00000194AF.c.24.1	M00004692A:H08
404	17732	RTA00000178AR.i.2.2	M00001376B:G06
405	17062	80.A1.sp6:130208.Seq	M00001340B:A06
406	11589	80.B1.sp6:130220.Seq	M00001340D:F10
407	4443	80.C1.sp6:130232.Seq	M00001341A:E12
408	39805	80.D1.sp6:130244.Seq	M00001342B:E06
409	2790	80.E1.sp6:130256.Seq	M00001343C:F10
410	23255	80.F1.sp6:130268.Seq	M00001343D:H07
411	6420	80.G1.sp6:130280.Seq	M00001345A:E01
412	5007	80.H1.sp6:130292.Seq	M00001346A:F09
413	13576	80.D2.sp6:130245.Seq	M00001347A:B10
414	16927	80.E2.sp6:130257.Seq	M00001348B:B04
415	16985	80.F2.sp6:130269.Seq	M00001348B:G06
416	3584	80.G2.sp6:130281.Seq	M00001349B:B08
417		80.H2.sp6:130293.Seq	M00001350A:B08
418	7187	80.A3.sp6:130210.Seq	M00001350A:H01
419	16245	80.D3.sp6:130246.Seq	M00001352A:E02
420	8078	80.E3.sp6:130258.Seq	M00001353A:G12
421	14929	80.F3.sp6:130270.Seq	M00001353D:D10
422	14391	80.G3.sp6:130282.Seq	M00001355B:G10
423	4141	80.B4.sp6:130223.Seq	M00001361A:A05
424	2379	80.C4.sp6:130235.Seq	M00001361D:F08
425	5622	80.D4.sp6:130247.Seq	M00001362B:D10
426	945	80.E4.sp6:130259.Seq	M00001362C:H11
427	40132	80.F4.sp6:130271.Seq	M00001365C:C10

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
428		80.G4.sp6:130283.Seq	M00001368D:E03
429	6867	80.H4.sp6:130295.Seq	M00001370A:C09
430	7172	80.A5.sp6:130212.Seq	M00001371C:E09
431	17732	80.B5.sp6:130224.Seq	M00001376B:G06
432	39833	80.C5.sp6:130236.Seq	M00001378B:B02
433	1334	80.D5.sp6:130248.Seq	M00001379A:A05
434	39886	80.E5.sp6:130260.Seq	M00001380D:B09
435		80.F5.sp6:130272.Seq	M00001381D:E06
436	22979	80.G5.sp6:130284.Seq	M00001382C:A02
437	39648	80.H5.sp6:130296.Seq	M00001383A:C03
438		80.B6.sp6:130225.Seq	M00001384B:A11
439	5178	80.C6.sp6:130237.Seq	M00001386C:B12
440	2464	80.D6.sp6:130249.Seq	M00001387A:C05
441	7587	80.E6.sp6:130261.Seq	M00001387B:G03
442	5832	80.F6.sp6:130273.Seq	M00001388D:G05
443	16269	80.G6.sp6:130285.Seq	M00001389A:C08
444	6583	80.H6.sp6:130297.Seq	M00001394A:F01
445	4009	80.A7.sp6:130214.Seq	M00001396A:C03
446		80.B7.sp6:130226.Seq	M00001400B:H06
447	39563	80.C7.sp6:130238.Seq	M00001402A:E08
448	5556	80.D7.sp6:130250.Seq	M00001407B:D11
449	9577	80.E7.sp6:130262.Seq	M00001409C:D12
450	7005	80.F7.sp6:130274.Seq	M00001410A:D07
451	8551	80.G7.sp6:130286.Seq	M00001412B:B10
452		80.H7.sp6:130298.Seq	M00001414A:B01
453		80.A8.sp6:130215.Seq	M00001414C:A07
454	13538	80.B8.sp6:130227.Seq	M00001415A:H06
455	8847	80.C8.sp6:130239.Seq	M00001416B:H11
456	36393	80.D8.sp6:130251.Seq	M00001417A:E02
457	9952	80.E8.sp6:130263.Seq	M00001418B:F03
458	9577	80.G8.sp6:130287.Seq	M00001421C:F01
459	15066	80.H8.sp6:130299.Seq	M00001423B:E07
460	10470	80.A9.sp6:130216.Seq	M00001424B:G09
461	22195	80.B9.sp6:130228.Seq	M00001425B:H08
462		80.C9.sp6:130240.Seq	M00001426B:D12
463	4261	80.D9.sp6:130252.Seq	M00001426D:C08
464	84182	80.E9.sp6:130264.Seq	M00001428A:H10
465	40392	80.H9.sp6:130300.Seq	M00001429D:D07
466	16731	80.C10.sp6:130241.Seq	M00001442C:D07
467		80.D10.sp6:130253.Seq	M00001443B:F01
468	13532	80.E10.sp6:130265.Seq	M00001445A:F05
469	8	80.H10.sp6:130301.Seq	M00001448D:C09
470	36313	80.A11.sp6:130218.Seq	M00001448D:H01

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
471	5857	80.B11.sp6:130230.Seq	M00001449A:A12
472	41633	80.C11.sp6:130242.Seq	M00001449A:B12
473	36535	80.D11.sp6:130254.Seq	M00001449A:G10
474	86110	80.E11.sp6:130266.Seq	M00001449C:D06
475	32663	80.F11.sp6:130278.Seq	M00001450A:A11
476	27250	80.G11.sp6:130290.Seq	M00001450A:D08
477	16970	80.H11.sp6:130302.Seq	M00001452C:B06
478	16130	80.A12.sp6:130219.Seq	M00001453A:E11
479	16653	80.B12.sp6:130231.Seq	M00001453C:F06
480	7005	80.C12.sp6:130243.Seq	M00001454B:C12
481	13072	80.F12.sp6:130279.Seq	M00001455B:E12
482	9283	80.G12.sp6:130291.Seq	M00001455D:F09
483	23255	100.C1.sp6:131446.Seq	M00001343D:H07
484	13576	100.E1.sp6:131470.Seq	M00001347A:B10
485	7187	100.C2.sp6:131447.Seq	M00001350A:H01
486	14391	100.E3.sp6:131472.Seq	M00001355B:G10
487	945	100.E4.sp6:131473.Seq	M00001362C:H11
488	7172	100.A5.sp6:131426.Seq	M00001371C:E09
489	39648	100.A6.sp6:131427.Seq	M00001383A:C03
490	84182	100.G9.sp6:131502.Seq	M00001428A:H10
491	8	100.B11.sp6:131444.Seq	M00001448D:C09
492	36535	100.D11.sp6:131468.Seq	M00001449A:G10
493	82498	100.F11.sp6:131492.Seq	M00001450A:B12
494	16970	100.C12.sp6:131457.Seq	M00001452C:B06
495	16130	100.D12.sp6:131469.Seq	M00001453A:E11
496	7005	121.D1.sp6:131917.Seq	M00001454B:C12
497		121.G6.sp6:131958.Seq	M00001506D:A09
498	18957	121.F7.sp6:131947.Seq	M00001528A:F09
499	40044	122.E1.sp6:132121.Seq	M00001621C:C08
500	5214	122.C2.sp6:132098.Seq	M00001630B:H09
501	6660	122.B5.sp6:132089.Seq	M00001679A:A06
502	13183	123.D5.sp6:132305.Seq	M00004114C:F11
503	6455	123.E7.sp6:132319.Seq	M00004157C:A09
504	5319	123.F7.sp6:132331.Seq	M00004169C:C12
505	11443	123.A8.sp6:132272.Seq	M00004185C:C03
506		123.C8.sp6:132296.Seq	M00004191D:B11
507	8210	123.E8.sp6:132320.Seq	M00004197D:H01
508	9457	123.D11.sp6:132311.Seq	M00004307C:A06
509	6420	172.E1.sp6:133925.Seq	M00001345A:E01
510	16245	172.D2.sp6:133914.Seq	M00001352A:E02
511	8078	172.C3.sp6:133903.Seq	M00001353A:G12
512	14929	172.D3.sp6:133915.Seq	M00001353D:D10
513	14391	172.H3.sp6:133963.Seq	M00001355B:G10

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
514	6583	172.B8.sp6:133896.Seq	M00001394A:F01
515	4009	172.D8.sp6:133920.Seq	M00001396A:C03
516		172.B9.sp6:133897.Seq	M00001400B:H06
517		176.A3.sp6:134514.Seq	M00001632D:H07
518	19267	176.G3.sp6:134586.Seq	M00001645A:C12
519	78091	176.G5.sp6:134588.Seq	M00001679C:F01
520	17055	176.D6.sp6:134553.Seq	M00001682C:B12
521	6539	176.D9.sp6:134556.Seq	M00003844C:B11
522		177.H4.sp6:134791.Seq	M00004121B:G01
523	5257	177.F5.sp6:134768.Seq	M00004146C:C11
524	11494	177.E6.sp6:134757.Seq	M00004172C:D08
525		177.G7.sp6:134782.Seq	M00004205D:F06
526	11451	177.D8.sp6:134747.Seq	M00004214C:H05
527	9283	173.D2.SP6:134106.Seq	M00001455D:F09
528	16283	173.F3.SP6:134131.Seq	M00001467A:D08
529	10539	173.B5.SP6:134085.Seq	M00001499B:A11
530	6420	173.F5.SP6:134133.Seq	M00001504D:G06
531	3956	173.H5.SP6:134157.Seq	M00001512D:G09
532		173.G7.SP6:134147.Seq	M00001544A:E06
533	1577	173.C9.SP6:134101.Seq	M00001556A:F11
534	9635	173.D9.SP6:134113.Seq	M00001557A:F01
535	5192	173.E9.SP6:134125.Seq	M00001557B:H10
536	6539	173.A12.SP6:134080.Seq	M00001579D:C03
537	945	180.C2.sp6:135940.Seq	M00001362C:H11
538	7005	180.H5.sp6:136003.Seq	M00001410A:D07
539	39304	180.G9.sp6:135995.Seq	M00001450A:A02
540	27250	180.B10.sp6:135936.Seq	M00001450A:D08
541	35555	184.A5.sp6:135530.Seq	M00001528A:C04
542	19255	184.B10.sp6:135547.Seq	M00001545A:C03
543	6268	184.C12.sp6:135561.Seq	M00001551A:B10
544	3277	217.E1.sp6:139406.Seq	M00001624A:B06
545	39171	217.A12.sp6:139369.Seq	M00001644C:B07
546	11460	219.F2.sp6:139035.Seq	M00001676B:F05
547	10539	219.F6.sp6:139039.Seq	M00001680D:F08
548	11476	219.H8.sp6:139065.Seq	M00003747D:C05
549	4016	79.A1.sp6:130016.Seq	M00001395A:C03
550	7674	79.C1.sp6:130040.Seq	M00001416A:H01
551	3681	79.E1.sp6:130064.Seq	M00001449A:D12
552	39304	79.F1.sp6:130076.Seq	M00001450A:A02
553	82498	79.G1.sp6:130088.Seq	M00001450A:B12
554	84328	79.A2.sp6:130017.Seq	M00001452A:B04
555	86859	79.B2.sp6:130029.Seq	M00001452A:B12
556	1120	79.C2.sp6:130041.Seq	M00001452A:D08

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
557	85064	79.D2.sp6:130053.Seq	M00001452A:F05
558	83103	79.G2.sp6:130089.Seq	M00001454A:A09
559	10145	79.F3.sp6:130078.Seq	M00001465A:B11
560	16283	79.H3.sp6:130102.Seq	M00001467A:D08
561	4568	79.D4.sp6:130055.Seq	M00001513A:B06
562	4313	79.F4.sp6:130079.Seq	M00001517A:B07
563	2428	79.A5.sp6:130020.Seq	M00001533A:C11
564	39423	79.C5.sp6:130044.Seq	M00001535A:F10
565	39174	79.E5.sp6:130068.Seq	M00001541A:H03
566	22113	79.F5.sp6:130080.Seq	M00001542A:A09
567	19829	79.H5.sp6:130104.Seq	M00001544A:G02
568	13864	79.B6.sp6:130033.Seq	M00001545A:D08
569	1058	79.F6.sp6:130081.Seq	M00001548A:H09
570	4015	79.G6.sp6:130093.Seq	M00001549A:B02
571	39180	79.A7.sp6:130022.Seq	M00001551A:F05
572	307	79.C7.sp6:130046.Seq	M00001552A:B12
573	39458	79.D7.sp6:130058.Seq	M00001552A:D11
574	39490	79.G7.sp6:130094.Seq	M00001557A:F03
575	39486	79.B8.sp6:130035.Seq	M00001561A:C05
576	39380	79.E8.sp6:130071.Seq	M00001587A:B11
577	1399	79.G8.sp6:130095.Seq	M00001604A:B10
578	39391	79.A9.sp6:130024.Seq	M00001604A:F05
579	6268	79.G9.sp6:130096.Seq	M00001551A:B10
580		377.F4.sp6:141957.Seq	M00004692A:H08
581	2448	89.A1.sp6:130667.Seq	M00001460A:F06
582	1531	89.C1.sp6:130691.Seq	M00001461A:D06
583	19	89.D1.sp6:130703.Seq	M00001463C:B11
584	38759	89.F1.sp6:130727.Seq	M00001467A:B07
585	39508	89.G1.sp6:130739.Seq	M00001467A:D04
586	16283	89.H1.sp6:130751.Seq	M00001467A:D08
587	39442	89.A2.sp6:130668.Seq	M00001467A:E10
588	7589	89.B2.sp6:130680.Seq	M00001468A:F05
589		89.C2.sp6:130692.Seq	M00001469A:A01
590	12081	89.D2.sp6:130704.Seq	M00001469A:C10
591	19105	89.E2.sp6:130716.Seq	M00001469A:H12
592	1037	89.F2.sp6:130728.Seq	M00001470A:B10
593	39425	89.G2.sp6:130740.Seq	M00001470A:C04
594	39478	89.H2.sp6:130752.Seq	M00001471A:B01
595		89.B3.sp6:130681.Seq	M00001487B:H06
596		89.C3.sp6:130693.Seq	M00001488B:F12
597	18699	89.D3.sp6:130705.Seq	M00001490B:C04
598	7206	89.E3.sp6:130717.Seq	M00001494D:F06
599	2623	89.F3.sp6:130729.Seq	M00001497A:G02



WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
600	10539	89.G3.sp6:130741.Seq	M00001499B:A11
601	5336	89.H3.sp6:130753.Seq	M00001500A:C05
602	2623	89.A4.sp6:130670.Seq	M00001500A:E11
603	9443	89.B4.sp6:130682.Seq	M00001500C:E04
604	9685	89.C4.sp6:130694.Seq	M00001501D:C02
605		89.D4.sp6:130706.Seq	M00001504A:E01
606	10185	89.E4.sp6:130718.Seq	M00001504C:A07
607	6974	89.F4.sp6:130730.Seq	M00001504C:H06
608	6420	89.G4.sp6:130742.Seq	M00001504D:G06
609		89.H4.sp6:130754.Seq	M00001505C:C05
610		89.A5.sp6:130671.Seq	M00001506D:A09
611	39168	89.B5.sp6:130683.Seq	M00001507A:H05
612	39412	89.C5.sp6:130695.Seq	M00001511A:H06
613	39186	89.D5.sp6:130707.Seq	M00001512A:A09
614	3956	89.E5.sp6:130719.Seq	M00001512D:G09
615		89.F5.sp6:130731.Seq	M00001513B:G03
616	14364	89.G5.sp6:130743.Seq	M00001513C:E08
617	40044	89.H5.sp6:130755.Seq	M00001514C:D11
618	8952	89.A6.sp6:130672.Seq	M00001518C:B11
619	35555	89.B6.sp6:130684.Seq	M00001528A:C04
620	18957	89.C6.sp6:130696.Seq	M00001528A:F09
621	8358	89.D6.sp6:130708.Seq	M00001528B:H04
622	38085	89.E6.sp6:130720.Seq	M00001531A:D01
623		89.F6.sp6:130732.Seq	M00001531A:H11
624	3990	89.G6.sp6:130744.Seq	M00001532B:A06
625	16921	89.H6.sp6:130756.Seq	M00001534A:C04
626	5321	89.B7.sp6:130685.Seq	M00001534A:F09
627	4119	89.C7.sp6:130697.Seq	M00001534C:A01
628	20212	89.E7.sp6:130721.Seq	M00001535A:C06
629	2696	89.F7.sp6:130733.Seq	M00001536A:B07
630	39392	89.G7.sp6:130745.Seq	M00001536A:C08
631	39420	89.H7.sp6:130757.Seq	M00001537A:F12
632	3389	89.A8.sp6:130674.Seq	M00001537B:G07
633	8286	89.B8.sp6:130686.Seq	M00001540A:D06
634	3765	89.C8.sp6:130698.Seq	M00001541A:D02
635	39453	89.E8.sp6:130722.Seq	M00001542A:E06
636		89.F8.sp6:130734.Seq	M00001542B:B01
637		89.H8.sp6:130758.Seq	M00001544A:E06
638	6974	89.A9.sp6:130675.Seq	M00001544B:B07
639		89.B9.sp6:130687.Seq	M00001545A:B02
640	19255	89.C9.sp6:130699.Seq	M00001545A:C03
641	1267	89.D9.sp6:130711.Seq	M00001546A:G11
642	5892	89.E9.sp6:130723.Seq	M00001548A:E10

WO 99/33982		
SEQ ID NO:	Cluster ID	Sequence Name
643	4193	89.G9.sp6:130747.Seq
644	16347	89.H9.sp6:130759.Seq
645	7239	89.A10.sp6:130676.Seq
646	5175	89.B10.sp6:130688.Seq
647	22390	89.C10.sp6:130700.Seq
648	3266	89.D10.sp6:130712.Seq
649	5708	89.E10.sp6:130724.Seq
650		89.F10.sp6:130736.Seq
651	8298	89.G10.sp6:130748.Seq
652	4573	89.H10.sp6:130760.Seq
653	22814	89.A11.sp6:130677.Seq
654	39539	89.B11.sp6:130689.Seq
655	39195	89.C11.sp6:130701.Seq
656	4561	89.D11.sp6:130713.Seq
657	9244	89.E11.sp6:130725.Seq
658	1577	89.F11.sp6:130737.Seq
659	4386	89.H11.sp6:130761.Seq
660	11294	89.A12.sp6:130678.Seq
661	5192	89.D12.sp6:130714.Seq
662	8761	89.E12.sp6:130726.Seq
663		89.F12.sp6:130738.Seq
664	7514	89.G12.sp6:130750.Seq
665		89.H12.sp6:130762.Seq
666	6558	90.A1.sp6:130859.Seq
667	102	90.B1.sp6:130871.Seq
668		90.D1.sp6:130895.Seq
669	5749	90.E1.sp6:130907.Seq
670	6539	90.G1.sp6:130931.Seq
671	6293	90.A2.sp6:130860.Seq
672		90.C2.sp6:130884.Seq
673	260	90.D2.sp6:130896.Seq
674	4837	90.E2.sp6:130908.Seq
675	10470	90.F2.sp6:130920.Seq
676	16999	90.G2.sp6:130932.Seq
677	22794	90.H2.sp6:130944.Seq
678	11465	90.A3.sp6:130861.Seq
679	7802	90.B3.sp6:130873.Seq
680	22155	90.C3.sp6:130885.Seq
681		90.D3.sp6:130897.Seq
682	13157	90.E3.sp6:130909.Seq
683	17004	90.F3.sp6:130921.Seq
684	40314	90.G3.sp6:130933.Seq
685	40044	90.H3.sp6:130945.Seq

PCT/US98/27610
Clone Name
M00001549B:F06
M00001549C:E06
M00001550A:A03
M00001550A:G01
M00001551A:G06
M00001551C:G09
M00001552B:D04
M00001552D:A01
M00001553A:H06
M00001553B:F12
M00001553D:D10
M00001555A:B02
M00001555A:C01
M00001555D:G10
M00001556A:C09
M00001556A:F11
M00001556B:C08
M00001556B:G02
M00001557B:H10
M00001557D:D09
M00001558A:H05
M00001558B:H11
M00001559B:F01
M00001560D:F10
M00001563B:F06
M00001566B:D11
M00001571C:H06
M00001579D:C03
M00001583D:A10
M00001590B:F03
M00001594B:H04
M00001597C:H02
M00001597D:C05
M00001598A:G03
M00001601A:D08
M00001607A:E11
M00001608A:B03
M00001608B:E03
M00001608D:A11
M00001614C:F10
M00001617C:E02
M00001619C:F12
M00001621C:C08

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
686	13913	90.A4.sp6:130862.Seq	M00001623D:F10
687	3277	90.B4.sp6:130874.Seq	M00001624A:B06
688	4309	90.C4.sp6:130886.Seq	M00001624C:F01
689	5214	90.D4.sp6:130898.Seq	M00001630B:H09
690		90.E4.sp6:130910.Seq	M00001632D:H07
691	39171	90.F4.sp6:130922.Seq	M00001644C:B07
692	19267	90.G4.sp6:130934.Seq	M00001645A:C12
693	4665	90.H4.sp6:130946.Seq	M00001648C:A01
694		90.A5.sp6:130863.Seq	M00001651A:H01
695	23201	90.B5.sp6:130875.Seq	M00001657D:C03
696	76760	90.C5.sp6:130887.Seq	M00001657D:F08
697	23218	90.D5.sp6:130899.Seq	M00001662C:A09
698	35702	90.E5.sp6:130911.Seq	M00001663A:E04
699	6468	90.F5.sp6:130923.Seq	M00001669B:F02
700	14367	90.G5.sp6:130935.Seq	M00001670C:H02
701	7015	90.H5.sp6:130947.Seq	M00001673C:H02
702	8773	90.A6.sp6:130864.Seq	M00001675A:C09
703	11460	90.B6.sp6:130876.Seq	M00001676B:F05
704	7570	90.D6.sp6:130900.Seq	M00001677D:A07
705	4416	90.E6.sp6:130912.Seq	M00001678D:F12
706	6660	90.F6.sp6:130924.Seq	M00001679A:A06
707		90.H6.sp6:130948.Seq	M00001679A:F06
708	26875	90.A7.sp6:130865.Seq	M00001679A:F10
709	6298	90.B7.sp6:130877.Seq	M00001679B:F01
710	78091	90.C7.sp6:130889.Seq	M00001679C:F01
711	10751	90.D7.sp6:130901.Seq	M00001679D:D03
712	10539	90.F7.sp6:130925.Seq	M00001680D:F08
713	17055	90.G7.sp6:130937.Seq	M00001682C:B12
714	5382	90.A8.sp6:130866.Seq	M00001688C:F09
715	4393	90.B8.sp6:130878.Seq	M00001693C:G01
716	67252	90.C8.sp6:130890.Seq	M00001716D:H05
717	40108	90.D8.sp6:130902.Seq	M00003741D:C09
718	11476	90.E8.sp6:130914.Seq	M00003747D:C05
719		90.F8.sp6:130926.Seq	M00003754C:E09
720	697	90.G8.sp6:130938.Seq	M00003759B:B09
721		90.H8.sp6:130950.Seq	M00003761D:A09
722	17076	90.A9.sp6:130867.Seq	M00003762C:B08
723	3108	90.B9.sp6:130879.Seq	M00003763A:F06
724	67907	90.C9.sp6:130891.Seq	M00003774C:A03
725		90.D9.sp6:130903.Seq	M00003784D:D12
726	11350	90.F9.sp6:130927.Seq	M00003826B:A06
727	7899	90.H9.sp6:130951.Seq	M00003837D:A01
728	7798	90.A10.sp6:130868.Seq	M00003839A:D08

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
729	6539	90.B10.sp6:130880.Seq	M00003844C:B11
730	6874	90.C10.sp6:130892.Seq	M00003846B:D06
731		90.D10.sp6:130904.Seq	M00003851B:D08
732	13595	90.E10.sp6:130916.Seq	M00003851B:D10
733	5619	90.F10.sp6:130928.Seq	M00003853A:D04
734	10515	90.G10.sp6:130940.Seq	M00003853A:F12
735	4622	90.H10.sp6:130952.Seq	M00003856B:C02
736	3389	90.A11.sp6:130869.Seq	M00003857A:G10
737	4718	90.B11.sp6:130881.Seq	M00003857A:H03
738		90.C11.sp6:130893.Seq	M00003867A:D10
739	12977	90.F11.sp6:130929.Seq	M00003875B:F04
740	8479	90.G11.sp6:130941.Seq	M00003875C:G07
741		90.H11.sp6:130953.Seq	M00003875D:D11
742	7798	90.A12.sp6:130870.Seq	M00003876D:E12
743	5345	90.B12.sp6:130882.Seq	M00003879B:C11
744	31587	90.C12.sp6:130894.Seq	M00003879B:D10
745	14507	90.D12.sp6:130906.Seq	M00003879D:A02
746	13576	90.F12.sp6:130930.Seq	M00003885C:A02
747		90.G12.sp6:130942.Seq	M00003891C:H09
748	9285	90.H12.sp6:130954.Seq	M00003906C:E10
749	39809	99.A1.sp6:131230.Seq	M00003907D:A09
750	16317	99.B1.sp6:131242.Seq	M00003907D:H04
751	8672	99.C1.sp6:131254.Seq	M00003909D:C03
752	12532	99.D1.sp6:131266.Seq	M00003912B:D01
753	3900	99.E1.sp6:131278.Seq	M00003914C:F05
754	23255	99.F1.sp6:131290.Seq	M00003922A:E06
755	24488	99.C2.sp6:131255.Seq	M00003968B:F06
756	40122	99.D2.sp6:131267.Seq	M00003970C:B09
757	23210	99.E2.sp6:131279.Seq	M00003974D:E07
758	23358	99.F2.sp6:131291.Seq	M00003974D:H02
759	3430	99.A3.sp6:131232.Seq	M00003981A:E10
760	2433	99.B3.sp6:131244.Seq	M00003982C:C02
761	9105	99.C3.sp6:131256.Seq	M00003983A:A05
762	6124	99.D3.sp6:131268.Seq	M00004028D:A06
763	40073	99.E3.sp6:131280.Seq	M00004028D:C05
764	37285	99.H3.sp6:131316.Seq	M00004035C:A07
765	17036	99.A4.sp6:131233.Seq	M00004035D:B06
766	3706	99.C4.sp6:131257.Seq	M00004068B:A01
767		99.D4.sp6:131269.Seq	M00004072A:C03
768	15069	99.F4.sp6:131293.Seq	M00004081C:D10
769	9285	99.H4.sp6:131317.Seq	M00004086D:G06
770	6880	99.A5.sp6:131234.Seq	M00004087D:A01
771	5325	99.C5.sp6:131258.Seq	M00004093D:B12

WO 99/33982			PCT/US98/27610
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
772	7221	99.D5.sp6:131270.Seq	M00004105C:A04
773	4937	99.E5.sp6:131282.Seq	M00004108A:E06
774	6874	99.F5.sp6:131294.Seq	M00004111D:A08
775	13183	99.G5.sp6:131306.Seq	M00004114C:F11
776		99.H5.sp6:131318.Seq	M00004121B:G01
777	13272	99.A6.sp6:131235.Seq	M00004138B:H02
778	5257	99.B6.sp6:131247.Seq	M00004146C:C11
779	6455	99.D6.sp6:131271.Seq	M00004157C:A09
780	5319	99.E6.sp6:131283.Seq	M00004169C:C12
781	4908	99.F6.sp6:131295.Seq	M00004171D:B03
782	11494	99.G6.sp6:131307.Seq	M00004172C:D08
783	11443	99.A7.sp6:131236.Seq	M00004185C:C03
784		99.B7.sp6:131248.Seq	M00004191D:B11
785	8210	99.C7.sp6:131260.Seq	M00004197D:H01
786	14311	99.D7.sp6:131272.Seq	M00004203B:C12
787		99.E7.sp6:131284.Seq	M00004205D:F06
788	12971	99.B8.sp6:131249.Seq	M00004223D:E04
789	6455	99.C8.sp6:131261.Seq	M00004229B:F08
790	7212	99.D8.sp6:131273.Seq	M00004230B:C07
791	4905	99.H8.sp6:131321.Seq	M00004269D:D06
792	16914	99.A9.sp6:131238.Seq	M00004275C:C11
793	16921	99.D9.sp6:131274.Seq	M00004295D:F12
794	13046	99.E9.sp6:131286.Seq	M00004296C:H07
795	9457	99.F9.sp6:131298.Seq	M00004307C:A06
796	26295	99.G9.sp6:131310.Seq	M00004312A:G03
797	21847	99.H9.sp6:131322.Seq	M00004318C:D10
798		99.H10.sp6:131323.Seq	M00004505D:F08
799		99.B11.sp6:131252.Seq	M00004692A:H08
800		99.D11.sp6:131276.Seq	M00005180C:G03
801	39304	RTA00000118A.j.21.1.Seq_THC151859	
802	2428	RTA00000123A.l.21.1.Seq_THC205063	
803	1058	RTA00000126A.e.20.3.Seq_THC217534	
804	5097	RTA00000134A.k.1.1.Seq_THC215869	
805	20212	RTA00000134A.l.22.1.Seq_THC128232	
806	23255	RTA00000177AF.e.14.3.Seq_THC228776	
807	2790	RTA00000177AF.e.2.1.Seq_THC229461	
808	6420	RTA00000177AF.f.10.3.Seq_THC226443	
809	4059	RTA00000177AF.n.18.3.Seq_THC123051	
810		RTA00000179AF.j.13.1.Seq_THC105720	
811	9952	RTA00000180AF.c.20.1.Seq_THC162284	
812	13238	RTA00000181AF.m.4.1.Seq_THC140691	
813	9685	RTA00000183AF.c.11.1.Seq_THC109544	
814		RTA00000183AF.c.24.1.Seq_THC125912	

WO 99/33982		PCT/US98/27610	
SEQ ID NO:	Cluster ID	Sequence Name	Clone Name
815	6420	RTA00000183AF.d.11.1.Seq_THC226443	
816	6974	RTA00000183AF.d.9.1.Seq_THC223129	
817	40044	RTA00000183AF.g.22.1.Seq_THC232899	
818		RTA00000183AF.g.9.1.Seq_THC198280	
819	5892	RTA00000184AF.d.11.1.Seq_THC161896	
820	40044	RTA00000186AF.d.1.1.Seq_THC232899	
821		RTA00000186AF.h.14.1.Seq_THC112525	
822	19267	RTA00000186AF.l.12.1.Seq_THC178183	
823	8773	RTA00000187AF.f.24.1.Seq_THC220002	
824	7570	RTA00000187AF.g.24.1.Seq_THC168636	
825	11476	RTA00000187AF.p.19.1.Seq_THC108482	
826		RTA00000188AF.d.11.1.Seq_THC212094	
827	17076	RTA00000188AF.d.21.1.Seq_THC208760	
828	697	RTA00000188AF.d.6.1.Seq_THC178884	
829	67907	RTA00000188AF.g.11.1.Seq_THC123222	
830	5619	RTA00000188AF.l.9.1.Seq_THC167845	
831	4718	RTA00000189AF.g.5.1.Seq_THC196102	
832	39809	RTA00000190AF.e.3.1.Seq_THC150217	
833	23255	RTA00000190AF.j.4.1.Seq_THC228776	
834	40122	RTA00000190AF.n.23.1.Seq_THC109227	
835	23210	RTA00000190AF.o.20.1.Seq_THC207240	
836	23358	RTA00000190AF.o.21.1.Seq_THC207240	
837	5693	RTA00000190AF.p.17.2.Seq_THC173318	
838	2433	RTA00000191AF.a.15.2.Seq_THC79498	
839	5257	RTA00000192AF.f.3.1.Seq_THC213833	
840	16392	RTA00000192AF.l.1.1.Seq_THC202071	
841		RTA00000193AF.c.21.1.Seq_THC222602	
842	26295	RTA00000193AF.i.24.2.Seq_THC197345	
843		RTA00000193AF.m.5.1.Seq_THC173318	
844		RTA00000193AF.n.15.1.Seq_THC215687	

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
2	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
3	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
4	<NONE>	<NONE>	<NONE>	BAR3_CHITE	BALBIANI RING PROTEIN 3 PRECURSOR>PIR2:S08167 Balbiani ring 3 protein - midge (Chironomus tentans)>GP:CTBR3_1 C;tentans balbiani ring 3 (BR3) gene	1
5	<NONE>	<NONE>	<NONE>	CYAA_PODAN	ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATASE) (ADENYL CYCLASE)>PIR2:JC4747 adenylate cyclase (EC 4.6.1.1) - Podospira anserina>GP:PANADCY_1 Podospira anserina adenyl cyclase gene, exons 1-4	1
6	<NONE>	<NONE>	<NONE>	VP03_HSVSA	PROBABLE MEMBRANE ANTIGEN 3 (TEGUMENT PROTEIN)>PIR2:C36806 hypothetical protein ORF3 - saimiriine herpesvirus 1 (strain 11)>GP:HSGEND_3 Herpesvirus saimiri complete genome DNA; ORF 03; similarity to ORF 75 and EBV BNRF1	0.97

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
7	<NONE>	<NONE>	<NONE>	ATFCA2_18	Arabidopsis thaliana DNA chromosome 4, ESSA 1 contig fragment No; 2; Hydroxyproline-rich glycoprotein homolog; Similarity to hydroxyproline-rich glycoprotein precursor-common tobacco	0.93
8	<NONE>	<NONE>	<NONE>	DHAL_ASPN G	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3) (ALDDH)>GP:ASNA LDAA_1 Aspergillus niger aldehyde dehydrogenase (aldA) gene, complete cds	0.9
9	<NONE>	<NONE>	<NONE>	NCU50264_1	Neurospora crassa two-component histidine kinase (nik-1) gene, 5' region and partial cds	0.86
10	<NONE>	<NONE>	<NONE>	NEUG_BOVI N	NEUROGRANIN (P17) (B-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT)>PIR2: A39034 neurogranin - bovine (fragment)	0.82
11	<NONE>	<NONE>	<NONE>	HUMBYSTIN _1	Homo sapiens bystin mRNA, complete cds	0.81
12	<NONE>	<NONE>	<NONE>	BTBMP1_1	Bos taurus BMP1 gene, partial sequence; Bone morphogenetic protein 1	0.69
13	<NONE>	<NONE>	<NONE>	TCCYSPROT _1	T;congolense mRNA for (prepro) cysteine proteinase	0.56
14	<NONE>	<NONE>	<NONE>	P60_LISIV	PROTEIN P60 PRECURSOR (INVASION-ASSOCIATED PROTEIN)>GP:LISIA PRELB_1 Listeria	0.15



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ivanovii extracellular protein homologue (iap) gene, complete cds	
15	<NONE>	<NONE>	<NONE>	HEX_ADE31	HEXON PROTEIN (LATE PROTEIN 2) (FRAGMENT)>PIR2: S37217 hexon protein - human adenovirus 31 (fragment)>GP:HSAT3 1H_1 H;sapiens adenovirus type 31 hexon gene; Hexon protein; Internal fragment containing hypervariable regions	0.15
16	<NONE>	<NONE>	<NONE>	HSU77493_1	Human Notch2 mRNA, partial cds; Transmembrane protein; hN	0.13
17	<NONE>	<NONE>	<NONE>	CYB_PARTE	CYTOCHROME B (EC 1.10.2.2)>PIR2:S07743 cytochrome b - Paramecium tetraurelia mitochondrion (SGC6)>GP:MIPAGE N_19 Paramecium aurelia mitochondrial complete genome; Apocytochrome b (AA 1-391)	0.078
18	<NONE>	<NONE>	<NONE>	HUMERB27_1	Human c-erbB-2 gene, exon 7; C-erb-2 protein	0.054
19	<NONE>	<NONE>	<NONE>	DMTRXIII_2	D;melanogaster DNA for trxl and trxlI genes; Trithorax protein trxl; Trithorax; putative>GP:DMTTHO RAX_2 D;melanogaster DNA for (putative) trithorax protein; Predicted trithorax protein	0.047

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
20	<NONE>	<NONE>	<NONE>	CELB0281_5	Caenorhabditis elegans cosmid B0281; Similar to reverse transcriptases	0.043
21	<NONE>	<NONE>	<NONE>	MOTY_VIBP A	SODIUM-TYPE FLAGELLAR PROTEIN MOTY PRECURSOR>GP:VP U06949_4 Vibrio parahaemolyticus BB22 RNase T (rnt) gene and flagellar motor component (motY) gene, complete cds	0.041
22	<NONE>	<NONE>	<NONE>	A56263	beta-galactosidase (EC 3.2.1.23) isozyme 12 - Arthrobacter sp. (strain B7)>GP:ASU17417_1 Arthrobacter sp; beta-galactosidase gene, complete cds	0.04
23	<NONE>	<NONE>	<NONE>	GSA_PSEAE	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE (EC 5.4.3.8) (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)>PIR2:S57898 glutamate 1-semialdehyde 2,1-aminomutase - Pseudomonas aeruginosa>GP:PAHE ML_1 P;aeruginosa hemL gene; Glutamate 1-sem	0.038
24	<NONE>	<NONE>	<NONE>	S16323	hypothetical protein - Arabidopsis thaliana>GP:ATHB1_1 A;thaliana homeobox gene Athb-1 mRNA; Open reading frame	0.035

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
25	<NONE>	<NONE>	<NONE>	IRS1_RAT	INSULIN RECEPTOR SUBSTRATE-1>PIR2:S16948 hypothetical protein IRS-1 - rat>GP:RNIRS1IRM_1 R;Norvegicus IRS-1 mRNA for insulin-receptor; During insulin stimulation, undergoes tyrosine phosphorylation and binds phosphatidylinositol 3-kinase	0.027
26	<NONE>	<NONE>	<NONE>	CEM02G9_2	Caenorhabditis elegans cosmid M02G9; M02G9;1; Similar to keratin like protein; cDNA EST yk308g11;5 comes from this gene; cDNA EST yk208e11;5 comes from this gene; cDNA EST yk208e11;3 comes	0.0088
27	<NONE>	<NONE>	<NONE>	S75490_3	competence region: iga=IgA protease, comA=transformation competence [Neisseria gonorrhoeae, MS11, Genomic, 3 genes, 2664 nt]	0.0041
28	<NONE>	<NONE>	<NONE>	EXTN_TOBA C	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)>PI R2:S06733 hydroxyproline-rich glycoprotein precursor - common tobacco>GP:NTEXT_1 Tobacco HRGPnt3 gene for extensin; Extensin (AA 1-620)	0.0025

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
29	<NONE>	<NONE>	<NONE>	HPCEGS_1	Hepatitis C virus complete genome sequence; Polyprotein	0.0014
30	<NONE>	<NONE>	<NONE>	HHVBC_4	Human hepatitis virus (genotype C, HMA) preS1, preS2, S, C, X, antigens, core antigen, X protein and polymerase	0.00093
31	<NONE>	<NONE>	<NONE>	HSLTGFBP4_1	Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4; Latent TGF-beta binding protein-4	0.00061
32	<NONE>	<NONE>	<NONE>	S74909	transposase - Synechocystis sp. (PCC 6803)>GP:D90909_10 8 Synechocystis sp; PCC6803 complete genome, 11/27, 1311235- 1430418; Transposase; ORF_ID:slr2062	0.00051
33	<NONE>	<NONE>	<NONE>	GRN_MOUSE	GRANULINS PRECURSOR (ACROGRANIN)>GP: MUSAP_1 Mouse gene for acrogranin precursor, complete cds	0.00022
34	<NONE>	<NONE>	<NONE>	CA21_MOUSE	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR>PIR2:A 43291 collagen alpha 2(I) chain precursor - mouse>GP:MMCOL1 A2_1 Mouse COL1A2 mRNA for pro-alpha-2(I) collagen	0.00016
35	<NONE>	<NONE>	<NONE>	MMMHC29N 7_2	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-	8.00E-05

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					alpha, palmitoyl-	
36	<NONE>	<NONE>	<NONE>	NFH_RAT	NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT)	2.40E-05
37	<NONE>	<NONE>	<NONE>	HUMVWFM_1	Human von Willebrand factor mRNA, 3' end; Von Willebrand factor prepropeptide	1.70E-05
38	<NONE>	<NONE>	<NONE>	CGHU2E	collagen alpha 2(XI) chain - human (fragment)	2.00E-06
39	<NONE>	<NONE>	<NONE>	A61183	hypothetical protein (sdsB region) - Pseudomonas sp.	4.90E-08
40	<NONE>	<NONE>	<NONE>	YM8L_YEAS T	HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION>PIR2:S5458 5 hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae)>GP:SC802 1X_4 S;cerevisiae chromosome XIII cosmid 8021; Unknown; YM8021;04, unknown, len: 622, CAI: 0;16,	1.50E-09
41	<NONE>	<NONE>	<NONE>	MTCY210_31	Mycobacterium tuberculosis cosmid Y210; Unknown; MTCY210;31, unknown, len: 299 aa, slight similarity to carboxykinases	3.10E-10

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
42	<NONE>	<NONE>	<NONE>	CEC01G10_5	Caenorhabditis elegans cosmid C01G10, complete sequence; C01G10;8; CDNA EST CEMSC45R comes from this gene>GP:CEC01G10_5 Caenorhabditis elegans cosmid C01G10; C01G10;8; CDNA EST CEMSC45R comes from this gene	2.30E-12
43	<NONE>	<NONE>	<NONE>	HSU15779_1	Human p70 (ST5) mRNA, alternatively spliced, complete cds; Differentially expressed; alternatively spliced	9.50E-14
44	<NONE>	<NONE>	<NONE>	MTCY210_31	Mycobacterium tuberculosis cosmid Y210; Unknown; MTCY210;31, unknown, len: 299 aa, slight similarity to carboxykinases	1.70E-17
45	U61403	Dictyostelium discoideum PrlA (prlA) mRNA, partial cds.	1	U93472_1	Danio rerio PPARB gene, partial cds; Nuclear receptor C domain	0.95
46	Z92832	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone F31D4; HTGS phase 1.	1	U93472_1	Danio rerio PPARB gene, partial cds; Nuclear receptor C domain	0.94
47	L36557	Oryza sativa (clone pRG3) repetitive element.	1	HSU61262_1	Human neogenin mRNA, complete cds	0.89

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
48	AF005898	Homo sapiens Na,K-ATPase beta-3 subunit pseudogene, complete sequence.	1	LRP1_CHICK	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR)>PIR2:A53102 LDL receptor-related protein / alpha-2-macroglobulin receptor precursor - chicken>GP:GGLRPA 2MR_1 G;gallus mRNA for LRP/alp	0.85
49	U18795	Saccharomyces cerevisiae chromosome V cosmid 9669, 8334, 8199, and lambda clone 1160.	1	NKC1_SQUA C	BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER 2 (NA-K-CL SYMPORTER)>PIR2:A53491 bumetanide-sensitive Na-K-Cl cotransporter - spiny dogfish>GP:SANKCC 1_1 Squalus acanthias bumetanide-sensitive Na-K-Cl cotransport protein (NKCC	0.73
50	AC002523	Homo sapiens; HTGS phase 1, 54 unordered pieces.	1	BXEN_CLOB O	BOTULINUM NEUROTOXIN TYPE E, NONTOXIC COMPONENT>GP:C LOENT120_1 C;botulinum gene for nontoxic component of progenitor toxin, complete cds	0.71

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
51	AC002345	*** SEQUENCING IN PROGRESS *** Genomic sequence from Human 17; HTGS phase 1, 10 unordered pieces.	1	P3K2_DICDI	PHOSPHATIDYLINO SITOL 3-KINASE 2 (EC 2.7.1.137) (PI3- KINASE) (PTDINS-3- KINASE) (PI3K)>GP:DDU23477 _1 Dictyostelium discoideum phosphatidylinositol- 4,5-diphosphate 3- kinase (PIK2) mRNA, complete cds	0.58
52	X14253	Human mRNA for cripto protein.	1	I55651	noradrenaline transporter - bovine>GP:BTU09198 _1 Bos taurus noradrenaline transporter mRNA, complete cds	0.55
53	U23516	Caenorhabditis elegans cosmid B0416.	1	I69024	MHC sex-limited protein - mouse (fragment)>GP:MUSM HC4AD_1 Mouse class III H2-Slp sex-limited protein gene, exons 1, 2 and 3; MHC sex-limited protein	0.47
54	AB006698	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19.	1	S81293_1	L1 {insertion sequence, provirus} [human papillomavirus type 6b HPV6b, KP4, Genomic Mutant, 121 nt]; Authors note this reading frame results from a 454 bp deletion and resulting	0.25
55	K03458	Human immunodeficiency virus type 1, isolate Zaire 6, vif, tat, rev, env, nef genes and 3' LTR.	1	S13383	hydroxyproline-rich glycoprotein - sorghum	0.24



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
56	B26794	T1O16TR TAMU Arabidopsis thaliana genomic clone T1O16.	1	RK34_PORP U	CHLOROPLAST 50S RIBOSOMAL PROTEIN L34>PIR2:S73111 ribosomal protein L34 - red alga (Porphyra purpurea) chloroplast>GP:PPU38 804_4 Porphyra purpurea chloroplast genome, complete sequence; 50S ribosomal protein L34	0.021
57	Z98950	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 507115; HTGS phase 1.	1	D41132	collagen-related protein 4 - Hydra magnipapillata (fragment)>PIR2:S219 32 mini-collagen - Hydra sp.>GP:HSNCOL4_1 Hydra N-COL 4 mRNA for mini-collagen; No start codon	0.02
58	U57057	Human WD protein IR10 mRNA, complete cds.	1	DMU15602_1	Drosophila melanogaster (zeste-white 4) mRNA, complete cds; Similar to C; elegans B0464;4 gene product, Swiss-Prot Accession Number Q03562	0.019
59	U57057	Human WD protein IR10 mRNA, complete cds.	1	CR2_MOUSE	COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)>PIR2:A4 3526 complement C3d/Epstein-Barr virus receptor 2 precursor - mouse>GP:MUSCR2A A_1 Murine complement receptor type 2 (CR2) mRNA, complete cds; Complement receptor type	0.0074

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
60	B65337	CIT-HSP-2021H21.TF CIT-HSP Homo sapiens genomic clone 2021H21.	1	A38096	perlecan precursor - human>GP:HUMHSP G2B_1 Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds	0.0051
61	U84722	Human vascular endothelial cadherin mRNA, complete cds.	1	HSTAFII13_1	H;sapiens mRNA for TAFII135; Subunit of RNA polymerase II transcription factor TFIID	0.0012
62	L41493	Avian rotavirus (strain turkey 1) genomic segment 4 outer capsid protein (VP8*) gene.	1	Y328_MYCP N	HYPOTHETICAL PROTEIN MG328 HOMOLOG>PIR2:S73 693 MG328 homolog P01_orf1033 - Mycoplasma pneumoniae (ATCC 29342) (SGC3)>GP:MPAE000 035_2 Mycoplasma pneumoniae from bases 442306 to 452472 (section 35 of 63) of the complete genome; MG328 homolog,	0.00015
63	D63139	Aeromonas sp. gene for chitinase, complete and partial cds.	1	MTCY16B7_3	Mycobacterium tuberculosis cosmid SCY16B7; Unknown; MTCY16B7;03, initiation factor, len: 900, similar at C-terminal half to eg IF2_BACSU P17889 initiation factor if-2 (716 aa), fasta	6.30E-05

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
64	J04974	Human alpha-2 type XI collagen mRNA (COL11A2).	1	GDF6_BOVIN	GROWTH/DIFFERENTIATION FACTOR GDF-6 PRECURSOR, (CARTILAGE-DERIVED MORPHOGENETIC PROTEIN 2) (CDMP-2) (FRAGMENT)>PIR2: B55452 cartilage-derived morphogenetic protein 2 precursor - bovine (fragment)>GP:BTU13661_1 Bos taurus cartilage-derived morph	1.00E-05
65	AC002394	Homo sapiens Chromosome 16 BAC clone CIT987-SKA-211C6 ~complete genomic sequence, complete sequence.	1	CELC14F11_6	Caenorhabditis elegans cosmid C14F11; Similar to aspartate aminotransferase; coded for by C; elegans cDNA CEMSF95FB; coded for by C; elegans cDNA yk41e4;3; coded for by C; elegans	4.60E-06
66	AB002312	Human mRNA for KIAA0314 gene, partial cds.	1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1)	1.00E-09
67	AC003085	Human BAC clone RG094H21 from 7q21-q22, complete sequence.	1	DP19_CAEEL	DPY-19 PROTEIN>PIR2:S44629 f22b7.10 protein - Caenorhabditis elegans>GP:CELF22B7_9 C; aenorhabditis elegans (Bristol N2) cosmid F22B7; Putative	4.20E-11
68	X55026	P.anserina complete mitochondrial genome.	1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1)	8.40E-12

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ASE 1)	
69	Z95399	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39B6; HTGS phase 1.	1	CER06B9_5	Caenorhabditis elegans cosmid R06B9, complete sequence; R06B9;b; Protein predicted using Genefinder; preliminary prediction	1.50E-24
70	AC002339	Arabidopsis thaliana chromosome II BAC T11A07 genomic sequence, complete sequence.	0.99	POLG_BVDV S	GENOME POLYPROTEIN>PIR1:A44217 genome polyprotein - bovine viral diarrhea virus (strain SD-1)>GP:BVDPOLYPR O_1 Bovine viral diarrhea virus polyprotein RNA, complete cds; Putative	1
71	Y08559	B.subtilis urease operon and downstream DNA.	0.99	LRP_CAEL	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN PRECURSOR (LRP)>PIR2:A47437 LDL-receptor-related protein - Caenorhabditis elegans>GP:CEF29D1 1_2 Caenorhabditis elegans cosmid F29D11, complete sequence; F29D11;1; Protein predicted using Genefi	1

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
72	U67548	Methanococcus jannaschii from bases 986219 to 996377 (section 90 of 150) of the complete genome.	0.99	YB60_YEAS T	HYPOTHETICAL 16.3 KD PROTEIN IN DUR1,2-NGR1 INTERGENIC REGION>PIR2:S4608 4 probable membrane protein YBR210w - yeast (Saccharomyces cerevisiae)>GP:SCYB R210W_1 S;cerevisiae chromosome II reading frame ORF YBR210w	1
73	U51645	Plasmodium falciparum cytidine triphosphate synthetase gene, complete cds.	0.99	HPSVRPL_1	Sin Nombre virus (NM H10) RNA L segment encoding RNA polymerase (L protein), complete cds; Viral RNA polymerase (L protein); Putative>GP:HPSVRP LA_1 Sin Nombre virus (NM R11) RNA L segment encoding RNA polymerase (L protein), complete cds; Vir	0.99
74	Z49889	Caenorhabditis elegans cosmid T06H11, complete sequence.	0.99	MUSHDPRO B_1	Mouse alternatively spliced HD protein mRNA, complete cds	0.021
75	Z69374	Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3 contains a pair of ESTs.	0.99	NCPR_YEAS T	NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)	0.017

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
76	Z35847	S.cerevisiae chromosome II reading frame ORF YBL086c.	0.99	CYPA_CAEE_L	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8) (PPIASE) (ROTAMASE) (CYCLOPHILIN-10)>GP:CEL B0252_4 Caenorhabditis elegans cosmid B0252; Similar to peptidyl-prolyl cis-trans isomerase (PPIASE) (CYCLOPHILIN)>GP:CEU34954_1 Caenorhabditis el	0.0044
77	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.99	CELR148_1	Caenorhabditis elegans cosmid R148; Contains similarity to drosophila DNA-binding protein K10 (NID:g8148); coded for by C; elegans cDNA yk118e11;5; coded for by C; elegans cDNA	0.0032
78	Y00324	Chicken vitellogenin gene 3' flanking region.	0.99	A56922	transcription factor shn - fruit fly (Drosophila melanogaster)	0.0023
79	M32659	D.melanogaster Shab11 protein mRNA, complete cds.	0.99	OMU25146_1	Oncorhynchus mykiss recombination activating protein 2 gene, partial cds	0.0017
80	Z69880	H.sapiens SERCA3 gene (partial).	0.99	M84D_DROME	MALE SPECIFIC SPERM PROTEIN MST84DD>PIR2:S25775 testis-specific protein Mst84Dd - fruit fly (Drosophila melanogaster)>GP:DM MST84D_4 D;melanogaster Mst84Da, Mst84Db, Mst84Dc and Mst84Dd genes for put; sperm protein	0.0011

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
81	M99166	Escherichia coli Trp repressor binding protein (wrbA) gene, complete cds.	0.99	MTU88962_1	Mycobacterium tuberculosis unknown protein gene, partial cds	6.50E-07
82	X99257	R.norvegicus mRNA for lamin C2.	0.99	MIU68729_1	Meloidogyne incognita cuticle preprocollagen (col-2) mRNA, complete cds; Putative	1.60E-09
83	AC002432	Human BAC clone RG317G18 from 7q31, complete sequence.	0.98	1FMDC	Foot and mouth disease virus type c-s8c1, chain C - foot and mouth disease virus type c-s8c1 expressed in hamster kidney cells	0.14
84	Z34799	Caenorhabditis elegans cosmid F34D10, complete sequence.	0.98	MMU57368_1	Mus musculus EGF repeat transmembrane protein mRNA, complete cds; Notch like repeats; notch 2	0.0028
85	B15207	344E15.TV CIT978SKA1 Homo sapiens genomic clone A-344E15.	0.98	POLG_HCVJ 6	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (NS5))>PI	0.00083

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
86	AC002412	*** SEQUENCING IN PROGRESS *** Human Chromosome X; HTGS phase 1, 2 unordered pieces.	0.98	KDG1_ARATH	DIACYLGLYCEROL KINASE 1 (EC 2.7.1.107) (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1)>PIR2:S71467 diacylglycerol kinase (EC 2.7.1.107) ATDGK1 - Arabidopsis thaliana>GP:ATHATD GK1_1 Arabidopsis thaliana mRNA for diacylglycerol kinase, complete c	0.00024
87	X57010	Human COL2A1 gene for collagen II alpha 1 chain, exons E2-E15.	0.98	D80005_1	Human mRNA for KIAA0183 gene, partial cds	5.90E-10
88	M83093	Neurospora crassa cAMP-dependent protein kinase (cot-1) gene, complete cds.	0.98	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME 1>GP:SPAC13A11_3 S;pombe chromosome 1 cosmid c13A11; Unknown; SPAC13A11;03, unknown, len: 210	3.00E-22
89	U96271	Helicobacter pylori heat shock protein 70 (hsp70) gene, complete cds.	0.97	SLMEN6_1	S;latifolia mRNA for Men-6 protein>GP:SLMEN6_1 S;latifolia mRNA for Men-6 protein	0.43
90	U49944	Caenorhabditis elegans cosmid C39E6.	0.97	RON_HUMAN	MACROPHAGE STIMULATING PROTEIN RECEPTOR PRECURSOR (EC 2.7.1.112)>PIR2:I38185 protein-tyrosine kinase (EC 2.7.1.112), receptor type ron - human>GP:HSRON_1 H;sapiens RON mRNA for tyrosine kinase; Putative	0.034



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
91	Y09255	B.cereus dnaI gene, partial.	0.97	CELT05C1_5	Caenorhabditis elegans cosmid T05C1; Coded for by C; elegans cDNA yk30f6;3; coded for by C; elegans cDNA yk34f10;3	0.00043
92	AC002413	*** SEQUENCING IN PROGRESS *** Human Chromosome X; HTGS phase 1, 2 unordered pieces.	0.96	CELC44E4_5	Caenorhabditis elegans cosmid C44E4; Weak similarity to the drosophila hyperplastic disc protein (GB:L14644); coded for by C; elegans cDNA yk49h6;5; coded for by C; elegans cDNA	1
93	U41625	Caenorhabditis elegans cosmid K03A1.	0.96	HMGC_HUMAN	HIGH MOBILITY GROUP PROTEIN HMGI-C>PIR2:JC2232 high mobility group I-C phosphoprotein - human>GP:HSHMGIC G5_1 Human high-mobility group phosphoprotein isoform I-C (HMGIC) gene, exon 5>GP:HSHMGICP_1 H;sapiens mRNA for HMGI-C protein>GP:HSHMGIC	1
94	Z82202	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34P24; HTGS phase 1.	0.96	YTH3_CAEE_L	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II>GP:CEC14A4_3 Caenorhabditis elegans cosmid C14A4, complete sequence; C14A4;3; Weak similarity with a B; Flavum translocation protein (Swiss Prot accession number P38376)	0.73

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
95	AL008734	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 324M8; HTGS phase 1.	0.96	S25299	extensin precursor (clone Tom L-4) - tomato>GP:TOMEXT ENB_1 L;esculentum extensin (class II) gene, complete cds	0.0004
96	L15388	Human G protein-coupled receptor kinase (GRK5) mRNA, complete cds.	0.96	HUMCOL7A1 X_1	Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds	4.60E-06
97	X97384	A.thaliana atran3 gene.	0.95	<NONE>	<NONE>	<NONE>
98	M62505	Human C5a anaphylatoxin receptor mRNA, complete cds.	0.95	RIPB_BRYDI	RIBOSOME-INACTIVATING PROTEIN BRYODIN (RRNA N-GLYCOSIDASE) (EC 3.2.2.22) (FRAGMENT)>PIR2: S16491 rRNA N-glycosidase (EC 3.2.2.22) bryodin - red bryony (fragment)	0.83
99	D28778	Cucumber mosaic virus RNA 1 for 1a, complete sequence.	0.95	POLS_RUBV M	STRUCTURAL POLYPROTEIN (CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2)>PIR1:GNWVR3 structural polyprotein - rubella virus (strain M33)>GP:TORUB24S_1 Rubella virus 24S subgenomic mRNA for structural proteins E1, E2 and C;	0.00037
100	AF016202	Homo sapiens immunoglobulin heavy chain CDR3 gene,	0.93	HSU79716_1	Human reelin (RELN) mRNA, complete cds	1

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		partial cds.				
101	Z68303	Caenorhabditis elegans cosmid ZK809, complete sequence.	0.93	HS5HT4SAR_1	H;sapiens mRNA for serotonin 4SA receptor (5-HT4SA-R)	0.87
102	X03049	E. coli DNA sequene 5' to origin of replication oriC.	0.93	S37594	mucin - human (fragment)	0.0019
103	M32659	D.melanogaster Shab11 protein mRNA, complete cds.	0.93	S38480	nonstructural protein - rubella virus>GP:RVM33NP_1 Rubella virus M33 RNA for a nonstructural protein; Nonstructural protein genes	2.30E-06
104	D88687	Human mRNA for KM-102-derived reductase-like factor, complete cds.	0.93	BAT3_HUMAN	LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3)>PIR2:A35098 MHC class III histocompatibility antigen HLA-B-associated transcript 3 - human>GP:HUMBAT3A_1 Human HLA-B-associated transcript 3 (BAT3) mRNA, complete cds>GP:HUMBAT3	8.70E-07
105	D16847	Mouse mRNA for stromal cell derived protein-1, complete cds.	0.93	S52796	prpL2 protein - human (fragment)>GP:HSPRP L2_1 H;sapiens mRNA for PRPL-2 protein	3.20E-08

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
106	D90915	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259.	0.92	YEK9_YEAS T	HYPOTHETICAL 53.9 KD PROTEIN IN AFG3-SEB2 INTERGENIC REGION>PIR2:S5047 7 hypothetical protein YER019w - yeast (Saccharomyces cerevisiae)>GP:SCE95 37_20 Saccharomyces cerevisiae chromosome V cosmid 9537, 9581, 9495, 9867, and lambda clone 5898	5.90E-05
107	AJ001101	Mus musculus mRNA for gC1qBP gene.	0.92	DMU58282_1	Drosophila melanogaster Bowel (bowl) mRNA, complete cds; Transcription factor; C2H2 zinc finger protein; zinc fingers have extensive sequence similarity to Drosophila odd-skipped	3.50E-05
108	X57108	Human gene for cerebroside sulfate activator protein, exons 10-14.	0.92	S69032	hypothetical protein YPR144c - yeast (Saccharomyces cerevisiae)>GP:YSCP9 659_17 Saccharomyces cerevisiae chromosome XVI cosmid 9659; Ypr144cp; Weak similarity near C-terminus to RNA Polymerase beta subunit (Swiss Prot; accession number P11213)	4.30E-21

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
109	D14635	Caenorhabditis elegans DNA for EMB-5.	0.91	YM13_YEAS_T	PUTATIVE ATP-DEPENDENT RNA HELICASE YMR128W>PIR2:S53058 probable membrane protein YMR128w - yeast (Saccharomyces cerevisiae)>GP:SC9553_4 S;cerevisiae chromosome XIII cosmid 9553; Unknown; YM9553;04, probable ATP-dependent RNA helicase, len:	0.69
110	B55500	CIT-HSP-387J2.TFB CIT-HSP Homo sapiens genomic clone 387J2.	0.91	U97553_79	Murine herpesvirus 68 strain WUMS, complete genome; Unknown	0.00016
111	X03049	E. coli DNA sequene 5' to origin of replication oriC.	0.9	POL_MLVAV	POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4))>PIR1:GNM VGV pol polyprotein - AKV murine leukemia virus	0.0019
112	U91327	Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.	0.89	JC5568	serine protease (EC 3.4.-.-) h1 - Serratia marcescens	1
113	X13295	Rat mRNA for alpha-2u globulin-related protein.	0.89	MNGPOLY_1	Mengo virus polyprotein genome, complete cds withe repeats	1
114	Z78415	Caenorhabditis elegans cosmid C17G1, complete sequence.	0.89	AB000121_1	Mouse mRNA for TBPIP, complete cds; TBP1 interacting protein	0.39

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
115	AC002308	*** SEQUENCING IN PROGRESS *** Human Chromosome 22q11 BAC Clone 1000e4; HTGS phase 1, 26 unordered pieces.	0.88	YLK2_CAEEL	HYPOTHETICAL 122.7 KD PROTEIN D1044.2 IN CHROMOSOME III>GP:CELD1044_4 Caenorhabditis elegans cosmid D1044	0.0037
116	AC002073	Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.	0.88	S28499	probable finger protein - rat>GP:RNZFP_1 R;norvegicus mRNA for putative zinc finger protein	1.10E-31
117	Z83848	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57A13; HTGS phase 1.	0.87	NDL_DROME	SERINE PROTEASE NUDEL PRECURSOR (EC 3.4.21.-)>PIR2:A57096 nudel protein precursor - fruit fly (Drosophila melanogaster)>GP:DM U29153_1 Drosophila melanogaster nudel (ndl) mRNA, complete cds; Serine protease; Soma dependent gene required matern	1
118	U23449	Caenorhabditis elegans cosmid K06A1.	0.87	AF023268_3	Homo sapiens clk2 kinase (CLK2), propin1, cotel, glucocerebrosidase (GBA), and metaxin genes, complete cds; metaxin pseudogene and glucocerebrosidase pseudogene; and thrombospondin3 (THBS3)	0.21
119	Z68181	H.vulgaris mRNA for elongation factor EF1-alpha.	0.87	RABCY450C_1	Rabbit cytochrome P-450 gene, clone pP-450PBc3, 3' end	0.14

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
120	AC000033	Homo sapiens chromosome 9, complete sequence.	0.87	VWF_CANF_A	VON WILLEBRAND FACTOR PRECURSOR>GP:DO GVWG_1 Canis familiaris von Willebrand factor mRNA, complete cds	0.036
121	U23449	Caenorhabditis elegans cosmid K06A1.	0.86	S48988_1	CRP-1=cystatin-related protein [rats, Wistar albino, mRNA Partial, 213 nt]; Cystatin-related protein; Method: conceptual translation supplied by author; This sequence comes from Fig;	0.64
122	Z89651	F.rubripes GSS sequence, clone 090124cD5.	0.86	CPU65981_1	Cryptosporidium parvum P-ATPase gene (CppA-E1) gene, complete cds; Putative calcium-ATPase	0.6
123	Z94055	Human DNA sequence from PAC 24M15 on chromosome 1. Contains tenascin-R (restrictin), EST.	0.86	GLTB_SYNY_3	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE 1 (EC 1.4.7.1) (FD-GOGAT)>PIR2:S6022 8 glutamate synthase (ferredoxin) (EC 1.4.7.1) gltB - Synechocystis sp. (PCC 6803)>GP:D90902_66 Synechocystis sp; PCC6803 complete genome, 4/27, 402290-524345; Gluta	0.03
124	Z49250	Human DNA sequence from cosmid HW2, Huntington's Disease Region, chromosome 4p16.3.	0.86	TRSCAPSID_1	Tobacco ringspot virus capsid protein gene, complete cds	3.00E-06

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
125	Z92855	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48C3; HTGS phase 1.	0.84	AE000809_8	Methanobacterium thermoautotrophicum from bases 161632 to 172569 (section 15 of 148) of the complete genome; Aspartyl-tRNA synthetase; Function Code:10;07 - Metabolism of	1
126	AC002340	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'TAMU' BAC 'T11J7' genomic sequence near marker 'm283'; HTGS phase 1, 2 unordered pieces.	0.83	CET01E8_3	Caenorhabditis elegans cosmid T01E8, complete sequence; T01E8;3; Similar to 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase; cDNA EST CEESG02F comes from this gene;	0.86
127	AL008716	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 206C7; HTGS phase 1.	0.83	HIVU51189_5	HIV-1 clone 93th253 from Thailand, complete genome; Tat protein	0.86
128	AC002340	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'TAMU' BAC 'T11J7' genomic sequence near marker 'm283'; HTGS phase 1, 2 unordered pieces.	0.83	S60257	meltrin alpha - mouse>GP:MUSMAB_1 Mouse mRNA for meltrin alpha, complete cds	0.0013



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
129	Z83848	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57A13; HTGS phase 1.	0.82	ARO1_PNEC A	PENTAFUNCTIONAL AROM POLYPEPTIDE (CONTAINS: 3-DEHYDROQUINATE SYNTHASE (EC 4.6.1.3), 3-DEHYDROQUINATE DEHYDRATASE (EC 4.2.1.10) (3-DEHYDROQUINASE), SHIKIMATE 5-DEHYDROGENASE (EC 1.1.1.25), SHIKIMATE KINASE (EC 2.7.1.71), AND EPSP SYNTHASE (E	0.0098
130	AF029308	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.	0.8	CELZK84_5	Caenorhabditis elegans cosmid ZK84; Final exon in repeat region; similar to long tandem repeat region of sialidase (SP:TCNA_TRYCR, P23253) and neurofilament H protein; coded for by C; elegans	2.00E-08
131	AC002458	Human BAC clone RG098M04 from 7q21-q22, complete sequence.	0.78	IGF2_PIG	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II)>GP:SSIGF2_1 S;scrofa mRNA IGF2 for insulin-like-growth factor 2; Insulin-like-growth factor 2 preproprotein	0.44
132	Z83843	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 368A4; HTGS phase 1.	0.78	PAR51A_1	P;tetraurelia 51A surface protein gene, complete cds	0.0014

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
133	X03021	Human gene for granulocyte-macrophage colony stimulating factor (GM-CSF).	0.78	CEF57B1_3	Caenorhabditis elegans cosmid F57B1, complete sequence; F57B1;3; Protein predicted using Genefinder; similar to collagen	2.20E-05
134	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w.	0.77	SYLM_SCHP O	PUTATIVE LEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.4) (LEUCINE--TRNA LIGASE)>PIR2:S6248 6 hypothetical protein SPAC4G8.09 - fission yeast (Schizosaccharomyces pombe)>GP:SPAC4G8_9 S;pombe chromosome I cosmid c4G8; Unknown; SPAC	0.96
135	Z74825	S.cerevisiae chromosome XV reading frame ORF YOL083w.	0.77	RNU59809_1	Rattus norvegicus mannose 6-phosphate/insulin-like growth factor II receptor (M6P/IGF2r) mRNA, complete cds; Also termed IGF-II/Man 6-P receptor, MPR, CI-MPR	0.01
136	U80445	Caenorhabditis elegans cosmid C50F2.	0.76	S28499	probable finger protein - rat>GP:RNZFP_1 R;norvegicus mRNA for putative zinc finger protein	1.10E-31
137	Z78545	Caenorhabditis elegans cosmid M03B6, complete sequence.	0.75	RRU73586_1	Rattus norvegicus Fanconi anemia group C mRNA, complete cds; Fanconi anemia group C protein; Similar to human FAC protein, GenBank Accession Numbers X66893 and X66894	0.023

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
138	Z97630	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1; HTGS phase 1.	0.74	HSMSHREC A_1	H;sapiens mRNA for MSH receptor; Author-given protein sequence is in conflict with the conceptual translation	0.036
139	AF007269	Arabidopsis thaliana BAC IG002N01.	0.71	HSU95090_1	Homo sapiens chromosome 19 cosmid F19541, complete sequence; F19541_1; Hypothetical (partial) protein similar to proline oxidase	0.16
140	AC002393	Mouse BAC284H12 Chromosome 6, complete sequence.	0.7	RNLTP2_1	Rattus norvegicus mRNA for LTBP-2 like protein; Latent TGF-beta binding protein-2 like protein	4.40E-05
141	B15232	344G8.TV CIT978SKA1 Homo sapiens genomic clone A-344G08.	0.67	DMSEVL2_2	Drosophila melanogaster sevenless mRNA; Put; sevenless protein (AA 1 - 2510)	0.41
142	D13748	Human mRNA for eukaryotic initiation factor 4A1.	0.66	MMU53563_1	Mus musculus Brg1 mRNA, partial cds; N-terminal region of the protein	0.00016
143	S45791	band 3-related protein=renal anion exchanger AE2 homolog [rabbits, New Zealand White, ileal epithelial cells, mRNA, 3964 nt].	0.66	POLS_RUBV R	STRUCTURAL POLYPROTEIN (CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2)>PIR1:GNWVRA structural polyprotein - rubella virus (strain RA27/3 vaccine)>GP:RUBCE2 1_1 Rubella virus RA27/3 RNA for capsid, E2 and E1 proteins; Poly	5.60E-05
144	M22462	Chicken protein p54 (ets-1)	0.66	HSHP8PROT _1	H;sapiens mRNA for HP8 protein; HP8	2.00E-06

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		mRNA, complete cds.			peptide	
145	U27999	Human clone pDEL52A11 HLA-C region cosmid 52 genomic survey sequence.	0.65	CA18_HUMAN	COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN)>PIR2:S15435 collagen alpha 1(VIII) chain precursor - human>GP:HSCOL8A1_1 Human COL8A1 mRNA for alpha 1(VIII) collagen	5.70E-06
146	M54787	N.crassa mating type a-1 protein (mt a-1) gene, exons 1-3.	0.64	I50717	vacuolar H <sup>+</sup> -ATPase A subunit - chicken (fragment)>GP:GGU22078_1 Gallus gallus vacuolar H <sup>+</sup> -ATPase A subunit gene, partial cds	0.0046
147	AC002094	Genomic sequence from Human 17, complete sequence.	0.63	PVPVA1_1	P;vivax pva1 gene	0.1
148	U32701	Haemophilus influenzae from bases 165345 to 176101 (section 16 of 163) of the complete genome.	0.63	FABG_HAEI_N	3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)>PIR2:D64051 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) - Haemophilus influenzae (strain Rd KW20)>GP:HIU32701_7 Haemophilus	2.00E-12
149	Z37159	T.brucei serum resistance associated (SRA) mRNA for VSG-like protein.	0.61	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
150	AF027865	Mus musculus Major Histocompatibility Locus class II region.	0.61	A56514	chromokinesin - chicken>GP:GGU18309_1 Gallus gallus chromokinesin mRNA, complete cds	0.045
151	U40938	Caenorhabditis elegans cosmid D1009.	0.61	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I>GP:SPAC13A11_3 S;pombe chromosome I cosmid c13A11; Unknown; SPAC13A11;03, unknown, len: 210	1.90E-24
152	I16670	Sequence 1 from patent US 5476781.	0.59	CELF21F8_7	Caenorhabditis elegans cosmid F21F8; Similar to eukaryotic aspartyl proteases	0.39
153	Z84468	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 299D3; HTGS phase 1.	0.59	CLG1_YEAST	CYCLIN-LIKE PROTEIN CLG1>PIR2:S37607 cyclin-like protein YGL215w - yeast (Saccharomyces cerevisiae)>GP:SCYG L215W_1 S;cerevisiae chromosome VII reading frame ORF YGL215w>GP:YSCC LG1CPR_1 Saccharomyces cerevisiae cyclin-like protein (CLG1) gene	0.0015
154	U00054	Caenorhabditis elegans cosmid K07E12.	0.57	<NONE>	<NONE>	<NONE>
155	M21207	Synthetic SV40 T antigen mutant pseudogene, 3' end.	0.57	1CJL2	cathepsin L (EC 3.4.22.15) mutant (F(78P)L, C25S, T110A, E176G, D178G), fragment 2 - human	0.43

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
156	AF020282	Dictyostelium discoideum DG2033 gene, partial cds.	0.56	AC002125_4	Homo sapiens DNA from chromosome 19-cosmid F25965, genomic sequence, complete sequence; F25965_5; Hypothetical 35;3 kDa protein similar to GTPase-activating proteins and orf3 from	0.6
157	M86352	Stigmatella aurantiaca reverse transcriptase (163 RT) gene, complete cds.	0.56	AC002398_4	Human DNA from chromosome 19-specific cosmid F25965, genomic sequence, complete sequence; F25965_3; Hypothetical 96 kDa human protein similar to alpha chimaerin; Hypothetical protein>GP:AC002398_4 Human DNA from chromosome 19-specific cosmi	4.50E-06
158	AC003101	*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HRPC41C23; HTGS phase 1, 33 unordered pieces.	0.54	<NONE>	<NONE>	<NONE>
159	B12117	F5L15-T7 IGF Arabidopsis thaliana genomic clone F5L15.	0.54	CEF32H2_5	Caenorhabditis elegans cosmid F32H2, complete sequence; F32H2;5; Similarity to Chicken fatty acid synthase (SW:P12276); cDNA EST yk16c2;5 comes from this gene; cDNA EST yk113h6;5 comes	1

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
160	AE000664	Mus musculus TCR beta locus from bases 250554 to 501917 (section 2 of 3) of the complete sequence.	0.54	CET01G9_6	Caenorhabditis elegans cosmid T01G9, complete sequence; T01G9;4; CDNA EST yk29b7;5 comes from this gene	0.84
161	B12117	F5L15-T7 IGF Arabidopsis thaliana genomic clone F5L15.	0.54	A39718	nicotinic acetylcholine receptor alpha chain - marbled electric ray (fragments)	0.27
162	Z71261	Caenorhabditis elegans cosmid F21C3, complete sequence.	0.5	KDGE_DROME	EYE-SPECIFIC DIACYLGLYCEROL KINASE (EC 2.7.1.107) (RETINAL DEGENERATION A PROTEIN) (DIGLYCERIDE KINASE) (DGK)->GP:DRODAG K_1 Fruit fly mRNA for diacylglycerol kinase, complete cds	4.60E-05
163	M61831	Human S-adenosylhomocysteine hydrolase (AHCY) mRNA, complete cds.	0.49	P2C2_ARATH	PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C)->PIR2:S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana>GP:ATHPP2 CA_1 Arabidopsis thaliana mRNA for protein phosphatase 2C	5.60E-08
164	U42608	Glycine max clathrin heavy chain mRNA, complete cds.	0.48	<NONE>	<NONE>	<NONE>

Table 2

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
165	Z93042	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 6B17; HTGS phase 1.	0.47	PYRD_BACS U	DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1) (DIHYDROOROTATE OXIDASE) (DHODEHASE)>PIR1:H39845 dihydroorotate oxidase (EC 1.3.3.1) - Bacillus subtilis>GPN:BSUB0009_25 Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200;	0.002
166	AC000044	Human Chromosome 22q13 Cosmid Clone p76e10, complete sequence.	0.47	MATK_MAR PO	PROBABLE INTRON MATURASE>PIR2:A05034 hypothetical protein 370i - liverwort (Marchantia polymorpha) chloroplast>GP:CHMP XX_21 Liverwort Marchantia polymorpha chloroplast genome DNA; ORF370i	0.0011
167	X51508	Rabbit mRNA for aminopeptidase N (partial).	0.47	S45361	LRR47 protein - fruit fly (Drosophila melanogaster)>GP:DM LRR47_1 D;melanogaster mRNA for LRR47	5.30E-07
168	Z67035	H.sapiens DNA segment containing (CA) repeat; clone AFM323yf1; single read.	0.45	JQ2246	22.5K cathepsin D inhibitor protein precursor - potato>GP:POTCATH D_1 Potato cathepsin D inhibitor protein mRNA, complete cds	0.79
169	Z93042	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 6B17; HTGS phase 1.	0.44	SMU31768_1	Schistosoma mansoni elastase gene, 3045 bp clone, complete cds	0.0022



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
170	L11172	Plasmodium falciparum RNA polymerase I gene, complete cds.	0.43	HUMPKD1G08_1	Homo sapiens polycystic kidney disease (PKD1) gene, exons 43-46; Polycystic kidney disease 1 protein	1
171	Z95889	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 211A9; HTGS phase 1.	0.43	A09811_1	R;norvegicus mRNA for BRL-3A binding protein; Author-given protein sequence is in conflict with the conceptual translation	0.00083
172	U32772	Haemophilus influenzae from bases 954819 to 966363 (section 87 of 163) of the complete genome.	0.43	YPT2_CAEE L	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III>PIR2:S44639 F37A4.2 protein - Caenorhabditis elegans>GP:CELF37A4_8 Caenorhabditis elegans cosmid F37A4	2.50E-28
173	Z99281	Caenorhabditis elegans cosmid Y57G11C, complete sequence.	0.42	PTU19464_1	Paramecium tetraurelia outer arm dynein beta heavy chain gene, complete cds	1
174	X04571	Human mRNA for kidney epidermal growth factor (EGF) precursor.	0.42	YEK9_YEAS T	HYPOTHETICAL 53.9 KD PROTEIN IN AFG3-SEB2 INTERGENIC REGION>PIR2:S50477 hypothetical protein YER019w - yeast (Saccharomyces cerevisiae)>GP:SCE9537_20 Saccharomyces cerevisiae chromosome V cosmid 9537, 9581, 9495, 9867, and lambda clone 5898	0.99

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
175	U32772	Haemophilus influenzae from bases 954819 to 966363 (section 87 of 163) of the complete genome.	0.41	YPT2_CAEE L	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III>PIR2:S44639 F37A4.2 protein - Caenorhabditis elegans>GP:CELF37A4_8 Caenorhabditis elegans cosmid F37A4	7.80E-21
176	AC002053	Human Chromosome 9p22 Cosmid Clone 92f5, complete sequence.	0.4	HSU33837_1	Human glycoprotein receptor gp330 precursor, mRNA, complete cds	1
177	U88309	Caenorhabditis elegans cosmid T23B3.	0.4	DROMTTGN C_1	Drosophila melanogaster mitochondrial cytochrome c oxidase subunit I (COI) gene, 5' end, Trp-, Cys-, and Tyr-tRNA genes, NADH dehydrogenase subunit 2 (ND2) gene, 3' end	0.99
178	M34025	Human fetal Ig heavy chain variable region (clone M44) mRNA, partial cds.	0.39	DNA2_YEAS T	DNA REPLICATION HELICASE DNA2>PIR2:S48904 probable purine nucleotide-binding protein YHR164c - yeast (Saccharomyces cerevisiae)>GPN:YSC H9986_3 Saccharomyces cerevisiae chromosome VIII cosmid 9986; Dna2p: DNA replication helicase; YHR164C>GP:	1
179	AC002395	Homo sapiens; HTGS phase 1, 127 unordered pieces.	0.39	VV_MUMPE	NONSTRUCTURAL PROTEIN V (NONSTRUCTURAL PROTEIN NS1)	0.11

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
180	AC003101	*** . SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HRPC41C23; HTGS phase 1, 33 unordered pieces.	0.39	YLK2_CAEE L	HYPOTHETICAL 122.7 KD PROTEIN D1044.2 IN CHROMOSOME III>GP:CELD1044_4 Caenorhabditis elegans cosmid D1044	0.0001
181	Z54335	Human DNA sequence from cosmid L17A9, Huntington's Disease Region, chromosome 4p16.3. Contains VNTR and a CpG island.	0.39	HUMNFAT3 A_1	Homo sapiens NF-AT3 mRNA, complete cds	1.60E-06
182	U95743	Homo sapiens chromosome 16 BAC clone CIT987-SK65D3, complete sequence.	0.38	CEZC434_6	Caenorhabditis elegans cosmid ZC434, complete sequence; ZC434;6; CDNA EST CEESO02F comes from this gene; cDNA EST CEES60F comes from this gene	0.18
183	AC001229	Sequence of BAC F5I14 from Arabidopsis thaliana chromosome 1, complete sequence.	0.34	HSOCAM_1	H;sapiens mRNA for immunoglobulin-like domain-containing 1 protein	0.051
184	X01703	Human gene for alpha-tubulin (b alpha 1).	0.33	NTC3_MOUS E	NEUROGENIC LOCUS NOTCH 3 PROTEIN>PIR2:S453 06 notch 3 protein - mouse>GP:MMNOTC_1 M;musculus mRNA for Notch 3	0.012

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
185	Z82189	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 170A21; HTGS phase 1.	0.31	LG106_3	Lemna gibba negatively light-regulated mRNA (Lg106); Second longest ORF (2)	0.27
186	Z98051	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4; HTGS phase 1.	0.3	S34960	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion (SGC6)>GP:MICO CN NR_3 Crithidia oncopelti mitochondrial ND4, ND5, COI, 12S ribosomal RNA genes for NADH dehydrogenase subunit 4/5, cytochrome oxidase subun	0.25
187	Z98749	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 449O17; HTGS phase 1.	0.3	SCKC_LEIQ H	CHARYBDOTOXIN (CHTX) (CHTX-LQ1)>PIR2:A60963 charybdotoxin 1 - scorpion (Leiurus quinquestriatus)>3D:2 CRD Charybdotoxin (nmr, 12 structures) - scorpion (Leiurus quinquestriatus)	0.12
188	X96763	C.albicans CDC4 gene.	0.29	CECC4_1	Caenorhabditis elegans cosmid CC4, complete sequence; CC4;a; Protein predicted using Genefinder; preliminary prediction	1.30E-17

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
189	U38804	Porphyra purpurea chloroplast genome, complete sequence.	0.28	HIVHCDR3C_1	Human immunodeficiency virus type 1 heavy-chain complementarity-determining region 3 mRNA (clone 11), partial cds; Heavy-chain complementarity-determining region 3 (CDR3) from HIV gp120->GP:HIVHCDR3I_1 Human immunodeficiency virus type 1 he	1
190	U20657	Human ubiquitin protease (Unph) proto-oncogene mRNA, complete cds.	0.28	HSU20657_1	Human ubiquitin protease (Unph) proto-oncogene mRNA, complete cds	5.60E-12
191	AC002037	Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.	0.27	VRP1_YEAS_T	VERPROLIN>GP:SC VERPRL_1 S;cerevisiae (A364) gene for verprolin	2.00E-11
192	U58748	Caenorhabditis elegans cosmid ZK180.	0.27	EXLP_TOBA_C	PISTIL-SECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP)>PIR2:JQ1696 pistil extensin-like protein precursor (clone pMG15) - common tobacco>GP:NTPMG15_1 N;tabacum mRNA for pistil extensin like protein	4.10E-12
193	Z68013	Caenorhabditis elegans cosmid W02H3, complete sequence.	0.26	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
194	AF017042	Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 5' end.	0.26	SPBC31F10_14	S.pombe chromosome II cosmid c31F10; Hypothetical protein; SPBC31F10;14c, unknown, len:1586aa, some similarity eg; to YJR140C, YJ9H_YEAST, P47171, involved in cell cycle regulation	1
195	B03174	cSRL-16e2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-16e2.	0.26	CELC30E1_7	Caenorhabditis elegans cosmid C30E1	0.38
196	X70810	E.gracilis chloroplast complete genome.	0.25	CEK10H10_8	Caenorhabditis elegans cosmid K10H10, complete sequence; K10H10;k; Protein predicted using Genefinder; preliminary prediction	0.98
197	U80024	Caenorhabditis elegans cosmid C18B10.	0.25	MMAF001794_1	Mus musculus Treacher Collins Syndrome protein (Tcof1) mRNA, complete cds; Putative nucleolar phosphoprotein; similar to Homo sapiens Treacher Collins syndrome TCOF1 protein encoded>GP:MMAF001794_1 Mus musculus Treacher Collins Syndrome p	0.017

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
198	AC000591	Drosophila melanogaster (subclone 9_g3 from P1 DS01486 (D32)) DNA sequence, complete sequence.	0.25	YHGE_ECOL I	HYPOTHETICAL 64.6 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (F574)>PIR2:E65135 hypothetical 64.6 kD protein in mrcA-pckA intergenic region - Escherichia coli (strain K-12)>GP:ECAE000415_7 Escherichia coli, mrcA, yrfE, yrfF, yrfG, yrfH, yrfI	0.00068
199	AC000591	Drosophila melanogaster (subclone 9_g3 from P1 DS01486 (D32)) DNA sequence, complete sequence.	0.25	YHGE_ECOL I	HYPOTHETICAL 64.6 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (F574)>PIR2:E65135 hypothetical 64.6 kD protein in mrcA-pckA intergenic region - Escherichia coli (strain K-12)>GP:ECAE000415_7 Escherichia coli, mrcA, yrfE, yrfF, yrfG, yrfH, yrfI	0.00068
200	Z99571	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 388N15; HTGS phase 1.	0.24	YA53_SCHP O	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I>GP:SPAC13A11_3 S;pombe chromosome I cosmid c13A11; Unknown; SPAC13A11;03, unknown, len: 210	0.017
201	U00672	Human interleukin-10 receptor mRNA, complete cds.	0.24	TFDP00900	- Polypeptides entry for factor Oct-2.5	1.00E-05

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
202	AC003061	*** SEQUENCING IN PROGRESS *** Mouse Chromosome 6 BAC clone b245c12; HTGS phase 2, 8 ordered pieces.	0.23	CG1_HUMAN	CG1 PROTEIN>GP:HSU46 023_1 Human Xq28 mRNA, complete cds; Orf	0.00078
203	AF009420	Homo sapiens microsatellite sequence in the HNF3a gene.	0.22	PN0675	collagen alpha 1(XVIII) chain - mouse (fragment)>GP:MUSC OLLAG_1 Mouse mRNA for collagen, partial cds	0.00072
204	B18861	F20C18-Sp6 IGF Arabidopsis thaliana genomic clone F20C18.	0.22	TFDP00659	- Polypeptides entry for factor PR	0.0003
205	U00672	Human interleukin-10 receptor mRNA, complete cds.	0.22	TFDP00900	- Polypeptides entry for factor Oct-2.5	1.00E-05
206	X52105	Dictyostelium discoideum SP60 gene for spore coat protein.	0.18	<NONE>	<NONE>	<NONE>
207	L07628	Saccharopolyspor a erythraea insertion sequence IS1136, copy B, 3' end.	0.17	D88764_1	Rana catesbeiana mRNA for alpha 2 type I collagen, complete cds	0.00021
208	Z49631	S.cerevisiae chromosome X reading frame ORF YJR131w.	0.16	YSCDAL1A_1	Saccharomyces cerevisiae alantoinase (DAL1) gene, complete cds	1
209	Z87893	F.rubripes GSS sequence, clone 043C17aB8.	0.16	CELC27A12_8	Caenorhabditis elegans cosmid C27A12; Partial CDS; this gene begins in the neighboring clone; coded for by C; elegans cDNA yk127f1;3; coded for by C; elegans cDNA yk127f1;5	1.30E-07



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
210	U92852	Rhoiptelea chiliantha maturase (matK) gene, chloroplast gene encoding chloroplast protein, complete cds.	0.15	SEU40259_5	Staphylococcus epidermidis trimethoprim resistance plasmid pSK639; Orf53	0.95
211	X62620	B.mori Abd-A gene homeobox.	0.15	ATAP22_36	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No; 2; Hypothetical protein; Similarity to NADH dehydrogenase, Chondrus crispus; MNOS:S59107	0.75
212	J02079	epstein-barr virus simple repeat array (ir3).	0.15	A38346	ultra-high-sulfur keratin 1 - mouse>GP:MUSSE1_1 Mouse serine 1 ultra high sulfur protein gene, complete cds; Putative	7.50E-05
213	M35027	Vaccinia virus, complete genome.	0.14	MTF1_FUSN U	MODIFICATION METHYLASE FNUDI (EC 2.1.1.73) (CYTOSINE-SPECIFIC METHYLTRANSFERASE FNUDI) (M.FNUDI)	0.87
214	AC003058	*** SEQUENCING IN PROGRESS *** Arabidopsis thaliana 'IGF' BAC 'F27F23' genomic sequence near marker 'CIC06E08'; HTGS phase 1, 8 unordered pieces.	0.14	HEXA_DICDI	BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL-BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE)>PIR2:A30766 beta-N-acetylhexosaminidase (EC 3.2.1.52) A precursor - slime mold (Dictyostelium	0.006

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					discoideum>GP:DDIN AGA_1 D;d	
215	AC001229	Sequence of BAC F5114 from Arabidopsis thaliana chromosome 1, complete sequence.	0.13	A49281	pol protein - simian T-cell lymphotropic virus type 1, STL V-1 (isolate Bab34) (fragment)>GP:STVB ABPOLA_1 Simian T-cell leukemia virus PCR derived (pol) gene, partial sequence BAB34POL; Bases 4779-4918 EMBL ATK numbering system; BAB34POL	0.77
216	U46067	Capra hircus beta-mannosidase mRNA, complete cds.	0.12	S70663	lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)>GP:EHU33 443_1 Entamoeba histolytica GalNAc lectin heavy subunit (hgl4) gene, partial cds; N-acetylgalactosamine adherence lectin heavy subunit	0.8
217	AC000380	*** SEQUENCING IN PROGRESS *** Human Chromosome 3 pac pDJ70i11; HTGS phase 1, 2 unordered pieces.	0.12	ATFCA8_19	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No; 8; Unnamed protein product	0.64

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
218	X61207	A.brasilense hisB, H, A, F and E genes for imidazole glycerolphosphate dehydratase, glutamine amidotransferase, phosphorybosilformimino-5-amino-phosphorybosil-4-imidazolecarboxamide isomerase, cyclase and phosphorybosil-AMP-cyclohydrolase.	0.12	OCCL02_1	O;circumcincta colost-2 gene; Cuticular collagen	0.0074
219	AF014259	HIV-1 Patient 1088 from Edinburgh, MA-p17 (gag) gene, partial cds.	0.11	DMU88570_1	Drosophila melanogaster CREB-binding protein homolog mRNA, complete cds; CBP	1
220	AC000636	Drosophila melanogaster (subclone 2_c11 from P1 DS07660 (D44)) DNA sequence, complete sequence.	0.11	A64829	hypothetical protein in dmsC 3' region - Escherichia coli (strain K-12)>GP:ECAE000192_1 Escherichia coli, ycaD, ycaK, pflA, pflB, focA genes from bases 944908 to 955952 (section 82 of 400) of the complete genome; Hypothetical protein in dmsC	0.051
221	AC002428	Human BAC clone GS039E22 from 5q31, complete sequence.	0.11	HSNMYC2_1	Human N-myc gene exon 2; Put; N-myc protein (aa 1-263) (953 is 1st base in codon)	0.00014
222	L40949	Homo sapiens (clone AT7-5eu) opioid-receptor-like protein mRNA, 5' end.	0.11	CEUNC93_2	C;elegans unc-93 gene; Protein 2	1.20E-13

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
223	AL008636	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 722E9; HTGS phase 1.	0.1	XELCOL2A1 A_1	Xenopus laevis alpha-1 collagen type II' mRNA, complete cds; Alpha-1 type II' collagen	2.60E-06
224	D86993	Human (lambda) DNA for immunoglobulin light chain.	0.1	CELM02B7_2	Caenorhabditis elegans cosmid M02B7	1.80E-09
225	AC002539	Homo sapiens chromosome 17, clone 195o20, complete sequence.	0.098	MTCY7D11_17	Mycobacterium tuberculosis cosmid Y7D11; Unknown; MTCY07D11;17c; unknown, len: 186 aa, FASTA best: Q10390 Y009_MYCTU hypothetical 31;0 KD protein MTCY190;09C (299 aa) opt: 355 z-score: 316;8	0.026
226	M88165	Human inter-alpha-trypsin inhibitor light chain (ITI) gene, exon 1.	0.096	A54161	ryanodine-binding protein alpha form - bullfrog>GP:D21070_1 Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RyR1), complete cds; Ryanodine receptor alpha isoform	1
227	Z92851	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39G8; HTGS phase 1.	0.082	CYA7_BOVIN	ADENYLATE CYCLASE, TYPE VII (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)	0.3

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
228	L00638	Arabidopsis thaliana ubiquitin conjugating enzyme exons 2-4.	0.072	NUCM_TRY BB	NADH-UBIQUINONE OXIDOREDUCTASE 49 KD SUBUNIT HOMOLOG (EC 1.6.5.3) (NADH DEHYDROGENASE SUBUNIT 7 HOMOLOG)>PIR2:A3 5693 NADH dehydrogenase (EC 1.6.99.3) chain 7 - Trypanosoma brucei mitochondrion (SGC6)	0.24
229	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds.	0.071	MMU65594_1	Mus musculus Brca2 mRNA, complete cds; Similar to human breast cancer susceptibility gene BRCA2; Allele: wild type; putative tumor suppressor	1
230	AF001549	Homo sapiens chromosome 16 BAC clone CIT987SK-270G1 complete sequence.	0.07	PM22_HUMAN	PERIPHERAL MYELIN PROTEIN 22 (PMP-22)>PIR2:JN0503 peripheral myelin protein 22 - human>GP:HUMGAS 3X_1 Human peripheral myelin protein 22 (GAS3) mRNA, complete cds>GP:HUMPMP22_1 Human peripheral myelin protein 22 mRNA, complete cds>GP:HUMPMP22	0.0078
231	L36829	Mus musculus alphaA-crystallin-binding protein I (AlphaA-CRYBP1) gene, complete cds.	0.066	<NONE>	<NONE>	<NONE>
232	AC000159	*** SEQUENCING IN PROGRESS *** Human BAC Clone 11q13;	0.058	CEZK863_1	Caenorhabditis elegans cosmid ZK863, complete sequence; ZK863;2; Similar to collagen	1

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HTGS phase 1, 10 unordered pieces.				
233	AC000159	*** SEQUENCING IN PROGRESS *** Human BAC Clone 11q13; HTGS phase 1, 10 unordered pieces.	0.058	CAC2_HAEC O	CUTICLE COLLAGEN 2C (FRAGMENT)>GP:H AECOL2C_1 H;contortus collagen 2C mRNA, 3'end	1.20E-08
234	Z23908	H. sapiens (D5S630) DNA segment containing (CA) repeat; clone AFM268zd9; single read.	0.057	VEU34999_1	Venezuelan equine encephalitis virus nonstructural and structural polyprotein genes, complete cds; Nonstructural polyprotein; Internal stop codon, readthrough occurs 5% of the time	0.0002
235	B21875	T3E8-Sp6 TAMU Arabidopsis thaliana genomic clone T3E8.	0.055	YRR2_CAEE L	HYPOTHETICAL 91.1 KD PROTEIN R144.2 IN CHROMOSOME III>GP:CELR144_7 Caenorhabditis elegans cosmid R144; Coded for by C; elegans cDNA CEESP84R; coded for by C; elegans cDNA yk23c4;5; coded for by C; elegans cDNA yk44f9;5; coded for by C; eleg	0.68
236	Z98303	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 140H19; HTGS phase 1.	0.048	AC002330_3	Arabidopsis thaliana BAC T10P11, complete sequence; Putative zinc-finger protein; C2H2 Zn-finger signature from position 80 to 100 [CEICNKGFRDQNL QLHRRGH]	0.99

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
237	D49911	Thermus thermophilus UvrA gene, complete cds.	0.044	APP1_MOUSE	AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP)>PIR2:A46362 amyloid precursor-like protein - mouse>GP:MUSAPLP_1 Mouse amyloid precursor-like protein mRNA, complete cds	8.90E-06
238	D49911	Thermus thermophilus UvrA gene, complete cds.	0.044	MMCOL18A1_1_2	Mus musculus alpha-1(XVIII) collagen (COL18A1) gene, exons 40-43, complete cds	1.60E-06
239	X78119	P.amygdalus, Batsch (Texas) prul mRNA.	0.042	CA44_HUMAN	COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR>PIR1:CGHU1B collagen alpha 4(IV) chain precursor - human>GP:HSCOL4A4_1 H;sapiens mRNA for collagen type IV alpha 4 chain; Type IV collagen alpha 4 chain	2.00E-06
240	U72877	Rana catesbeiana L-epinephrine transporter mRNA, complete cds.	0.041	YRR6_MYCAA	HYPOTHETICAL 33.0 KD PROTEIN IN LICA 3'REGION (ORF R6)>PIR2:S42125 hypothetical protein 3 - Mycoplasma capricolum (SGC3)>GP:MYCRP MH_6 M; capricolum rpmH, mpA and licA gene; Orf R6	0.0008
241	L39891	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds.	0.04	MUC2_HUMAN	MUCIN 2 (INTESTINAL MUCIN 2) (FRAGMENTS)	5.90E-05
242	L40390	Candida glabrata ERG3 gene, complete cds.	0.039	G01763	atrophin-1 - human>GP:HSU23851_1 Human atrophin-1 mRNA, complete cds	9.00E-07

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
243	B28113	T2L16TRB TAMU Arabidopsis thaliana genomic clone T2L16.	0.038	CELZK1248_14	Caenorhabditis elegans cosmid ZK1248	1.60E-18
244	AC000030	00175, complete sequence.	0.033	ATFCA8_40	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No; 8; Glycerol-3-phosphate permease homolog; Similarity to glycerol-3-phosphate permease - Haemophilus influenzae	0.63
245	B10738	F13G15-Sp6 IGF Arabidopsis thaliana genomic clone F13G15.	0.032	D87521_1	Mus musculus DNA-PKcs mRNA, complete cds	0.21
246	AF024503	Caenorhabditis elegans cosmid F31F4.	0.03	I38344	titin - human	1
247	Z49888	Caenorhabditis elegans cosmid F47A4, complete sequence.	0.027	KSU52064_1	Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds; Herpesvirus saimiri ORF73 homolog>GP:KSU756 98_78 Kaposi's sarcoma-associated herpesvirus long unique region, 80 putative ORF's and kaposin gene, complete cds; OR	3.40E-10
248	Z83822	Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.	0.025	GRSB_BACB R	GRAMICIDIN S SYNTHETASE II (GRAMICIDIN S BIOSYNTHESIS GRSB PROTEIN) (EC 6.-.-.)	1
249	Z94161	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone N102C10; HTGS	0.025	S16323	hypothetical protein - Arabidopsis thaliana>GP:ATHB1_1 A;thaliana homeobox gene Athb-1 mRNA; Open reading frame	0.0079



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		phase 1.				
250	AC002094	Genomic sequence from Human 17, complete sequence.	0.021	S57447	HPBR11-7 protein - human>GP:HSHPBR11 4_1 H;sapiens HPBR11-4 mRNA>GP:HSHPBR11 7_1 H;sapiens HPBR11-7 gene	8.20E-08
251	D79994	Human mRNA for KIAA0172 gene, partial cds.	0.021	CER10H10_1	Caenorhabditis elegans cosmid R10H10, complete sequence; R11A8;7; Protein predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc; No; S37771); cDNA EST CEESX25F comes from this gene;	7.00E-16
252	Z97635	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 438L4; HTGS phase 1.	0.017	CELW05H7_4	Caenorhabditis elegans cosmid W05H7	0.24
253	X84996	X.laevis mRNA for selenocysteine tRNA acting factor (Staf).	0.017	JN0786	integrin beta-4 chain precursor - mouse	0.088
254	AC002543	Human BAC clone RG300C03 from 7q31.2, complete sequence.	0.013	MZLMTCYT BT_1	Mendocellus isis mitochondrial NADH dehydrogenase, and cytochrome b genes, 3' end, and transfer RNA-Ser gene; This codes for the last 43 amino acids of NADH dehydrogenase subunit 1 followed	0.044

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
255	U10401	Caenorhabditis elegans cosmid T20B12.	0.012	MMMHC29N7_2	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-	0.069
256	L14593	Saccharomyces cerevisiae protein phosphatase (PTC1) gene, complete cds.	0.011	D86995_1	Human (gene 1) DNA for phosphatase 2C motif, partial cds	2.20E-14
257	U62317	Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence.	0.0093	P2Y8_XENLA	P2Y PURINOCEPTOR 8 (P2Y8)>GP:XLP2Y8_1 X;laevis mRNA for P2Y8 nucleotide receptor	0.89
258	D29655	Pig mRNA for UMP-CMP kinase, complete cds.	0.0075	AF004858_1	Mus musculus platelet activating factor receptor mRNA, partial cds; PAF-receptor	1
259	AF002992	Homo sapiens cosmid from Xq28, complete sequence.	0.0054	FBN1_BOVIN	FIBRILLIN 1 PRECURSOR>PIR2:A55567 fibrillin I - bovine>GP:BOVXAA AA_1 Bos taurus mRNA, complete cds; Putative	0.0004
260	B20752	T19M2-T7 TAMU Arabidopsis thaliana genomic clone T19M2.	0.0043	HSV11IEP_1	Feline herpesvirus type 1 gene for immediate early protein, complete cds; Feline herpesvirus type 1 immediate early protein	3.90E-05

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
261	AB006699	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22.	0.0037	YHV5_YEAS T	HYPOTHETICAL 143.6 KD PROTEIN IN SPO16-REC104 INTERGENIC REGION>PIR2:S4675 4 hypothetical protein YHR155w - yeast (Saccharomyces cerevisiae)>GPN:YSC H9666_15 Saccharomyces cerevisiae chromosome VIII cosmid 9666; Yhr155wp; Similar to Sip3p (Snf	0.077
262	Z99128	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 422H11; HTGS phase 1.	0.0032	ALU1_HUM AN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	0.0087
263	B21848	T2D2-Sp6 TAMU Arabidopsis thaliana genomic clone T2D2.	0.0031	B31794	mdm-1 protein (clone c103) - mouse	1.00E-05
264	L33853	Human germline immunoglobulin kappa chain variable region (Vk-IV subgroup) for anti-B-amyloid autoantibodies in Alzheimer's disease.	0.0027	B45550	cytochrome b homolog - Plasmodium yoelii	0.99
265	B36863	HS-1042-A1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=1 Row=K.	0.0027	YQK4_CAEE L	HYPOTHETICAL 64.3 KD PROTEIN C56G2.4 IN CHROMOSOME III>GP:CELC56G2_2 Caenorhabditis elegans cosmid C56G2	0.81

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
266	AC003041	*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 17, clone HCIT307A16; HTGS phase 1, 10 unordered pieces.	0.0024	GLB4_LAMSP	GIANT HEMOGLOBIN AIV CHAIN (FRAGMENT)>PIR2:S01810 hemoglobin AIV - tube worm (Lamellibrachia sp.) (fragment)	0.94
267	AC002315	Mouse BAC-146N21 Chromosome X contains iduronate-2-sulfatase gene; complete sequence.	0.0022	MG42_TARMA	SRV-RELATED PROTEIN MG42 (FRAGMENT)>PIR3:I51369 Sry-related sequence - Tarentola mauritanica (fragment)>GP:TELMG42DNA_1 Gecko MG42 gene, partial cds; Sry-related sequence	0.99
268	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	SCYJL204C_1	S;cerevisiae chromosome X reading frame ORF YJL204c	1
269	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	CEM199_3	Caenorhabditis elegans cosmid M199, complete sequence; M199;e; Protein predicted using Genefinder; preliminary prediction	0.97
270	AF016674	Caenorhabditis elegans cosmid C03H5.	0.0015	CEM199_3	Caenorhabditis elegans cosmid M199, complete sequence; M199;e; Protein predicted using Genefinder; preliminary prediction	0.97
271	Z54199	L.esculentum DNA Ailsa craig encoding l-aminocyclopropane-1-carboxylic acid oxidase.	0.0015	CELF20A1_5	Caenorhabditis elegans cosmid F20A1; Coded for by C; elegans cDNA yk9g1;3; coded for by C; elegans cDNA yk9g1;5; coded for by C; elegans cDNA CEESU55F;	0.11

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					weak similarity to putative	
272	Z99943	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 313L4; HTGS phase 1.	0.0014	CEK08F8_5	Caenorhabditis elegans cosmid K08F8, complete sequence; K08F8;5b	0.93
273	S81083	beta - ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta - ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein {alternatively spliced, exon 10 to 13 region} [human, Genomic, 1851 nt, segment 3 of 3].	0.0013	MTCY277_7	Mycobacterium tuberculosis cosmid Y277; Unknown; MTCY277;07c, unknown, len: 302	0.0001
274	Z82174	Human DNA sequence from cosmid B20F6 on chromosome 22q11.2-qter.	0.001	FBLA_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR>GP:HS FIBUA_1 H;sapiens mRNA for fibulin-1 A	0.00063
275	Z82215	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 6802; HTGS phase 1.	0.00079	BFR1_SCHPO	BREFELDIN A RESISTANCE PROTEIN>PIR2:S52239 hba2 protein - fission yeast (Schizosaccharomyces pombe)>GP:SPHBA2 GEN_1 S;pombe hba2 gene	0.15

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
276	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.00071	CX2_HEMHA	CYTOTOXIN 2 (TOXIN 12A)	0.32
277	Z82204	Human DNA sequence from clone J362G171.	0.00054	DMU34925_2	Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds	0.045
278	AC002530	Human BAC clone RG341D10 from 7p15-p21, complete sequence.	0.00053	CELT28F2_2	Caenorhabditis elegans cosmid T28F2; Weak similarity to HSP90	0.037
279	U91322	Human chromosome 16p13 BAC clone CIT987SK-276F8 complete sequence.	0.00051	CEW08D2_2	Caenorhabditis elegans cosmid W08D2, complete sequence; W08D2;3; Protein predicted using Genefinder>GP:CEW08D2_2 Caenorhabditis elegans cosmid W08D2; W08D2;3; Protein predicted using Genefinder	0.26
280	D16986	Human HepG2 partial cDNA, clone hmd2b09m5.	0.00037	POLG_PPVN A	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI- A) (EC 3.4.22.-) (49K PROTEINASE) (49	0.48
281	U91318	Human chromosome 16p13 BAC clone CIT987SK-962B4 complete	0.00031	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		sequence.				
282	M93406	Human dispersed Alu repeats and dispersed L1 repeat.	0.0003	VG8_SPV4	GENE 8 PROTEIN>PIR1:G8BP SV gene 8 protein - spiroplasma virus 4 (SGC3)	0.23
283	AC002398	Human DNA from chromosome 19-specific cosmid F25965, genomic sequence, complete sequence.	0.00021	HMCA_DROME	HOMEOTIC CAUDAL PROTEIN>PIR2:A263 57 homeotic protein Cad - fruit fly (Drosophila melanogaster)>GP:DR OCADA2_1 D;melanogaster caudal gene (cad) encoding a maternal and zygotic transcript, exon 2; Caudal protein>TFD:TFDP001 59 - Polypeptides en	0.021
284	AC002530	Human BAC clone RG341D10 from 7p15-p21, complete sequence.	0.0002	PL0009	complement C3d/Epstein-Barr virus receptor precursor - human	0.7
285	X01871	Yeast mitochondrial ori(o) repeat unit of petite mutant 5 (petite strain s-10/7/2).	0.00015	RVZMTCYT BT_1	Reventazonia sp; mitochondrial NADH dehydrogenase, and cytochrome b genes, 3' end, and transfer RNA-Ser gene; This codes for the last 43 amino acids of NADH dehydrogenase subunit 1 followed	0.73
286	U89984	Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.	0.00015	ACU89984_1	Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds; Similar to human transformation-	4.20E-13

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					sensitive protein: SwissProt Accession Number P31948	
287	AC002365	Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 174A6, U172D6, and U186B3 from Xp22, complete sequence.	0.00011	S10340	DNA-directed RNA polymerase (EC 2.7.7.6) - yeast ( <i>Kluyveromyces marxianus</i> var. <i>lactis</i> )	0.00062
288	AC002390	Human DNA from overlapping chromosome 19-specific cosmids R30072 and R28588, genomic sequence, complete sequence.	9.90E-05	D86603_1	Mouse mRNA for Bach protein 1, complete cds; Bach1	1
289	AC002980	Homo sapiens; HTGS phase 1, 34 unordered pieces.	9.20E-05	TRBKPCYB_1	<i>Trypanosoma brucei</i> kinetoplast apocytochrome b gene, complete cds	0.52
290	M99412	Human interleukin-8 receptor (IL8RB) gene, complete cds.	4.50E-05	S28832	microtubule-associated protein H1 (clone KS3.1) - longfin squid (fragment)	0.88
291	AC000120	Human BAC clone RG161K23 from 7q21, complete sequence.	4.00E-05	SXSCRBA_1	<i>Saxylosus</i> scrB and scrR genes; Sucrose repressor	0.99



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
292	AC003037	Homo sapiens; HTGS phase 1, 66 unordered pieces.	3.40E-05	S13569	hypothetical protein 5 - Lactococcus lactis subsp. lactis insertion sequence 1076>GP:LLTLE_1 Lactococcus lactis DNA for the transposon-like element on the lactose plasmid; ORF5 (AA 1 - 43)	0.018
293	Z81512	Caenorhabditis elegans cosmid F25C8, complete sequence.	2.40E-05	MUSDBPRC_1	Mus musculus DNA-binding protein Rc mRNA, complete cds; DNA binding protein Rc	1
294	B16681	343C3.TVB CIT978SKA1 Homo sapiens genomic clone A-343C03.	1.10E-05	COPP_YEAS_T	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP)>PIR2:B55123 coatomer complex beta' chain - yeast (Saccharomyces cerevisiae)>GPN:SCY GL137W_1 S;cerevisiae chromosome VII reading frame ORF YGL137w>GP:SCU11 237_1 Saccharomyces cerevisiae	0.081
295	Z16523	H. sapiens (D9S158) DNA segment containing (CA) repeat; clone AFM073yb11; single read.	1.00E-05	MMSEMF_1	M;musculus mRNA for semaphorin F; Smaphorin F	0.78
296	Z49704	S.cerevisiae chromosome XIII cosmid 8021.	5.60E-06	<NONE>	<NONE>	<NONE>
297	AC003071	Human BAC clone BK085E05 from 22q12.1-qter, complete sequence.	3.00E-06	HSRCAER_1	H;sapiens mRNA for red cell anion exchanger (EPB3, AE1, Band 3) 3' non-coding region	0.21

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
298	U20428	Human SNC19 mRNA sequence.	1.40E-06	HUMMUC2A_1	Human mucin-2 gene, partial cds	4.40E-06
299	U51903	Human RasGAP-related protein (IQGAP2) mRNA, complete cds.	6.60E-07	IQGA_HUMAN	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195)>PIR2:A54854 Ras GTPase activating-related protein - human>GP:HUMIQGA_1 Homo sapiens ras GTPase-activating-like protein (IQGAP1) mRNA, complete cds; Amino acid feature: IQ calmodulin-binding do	1.60E-14
300	AL000805	F.rubripes GSS sequence, clone 021G08aA1.	4.70E-07	MT13_MYTED	METALLOTHIONEIN 10-III (MT-10-III)>PIR2:S39418 metallothionein 10-III - blue mussel	2.20E-10
301	AC003016	Human BAC clone RG134C19 from 8q21, complete sequence.	4.30E-07	SPC57A10_5	S;pombe chromosome I cosmid c57A10; Unknown; SPAC57A10;05;c, unknown, len:606aa, similar to A; nidulans Q00659, sulfur metabolite repression control, (678aa), fasta scores, opt:1355,	0.00041
302	AC003089	Human BAC clone RG180F08A, complete sequence.	3.80E-07	HPBPRECK_1	Hepatitis B virus type 11 precore protein (pre-C region, C) gene, 5' end	0.41
303	AC002074	Human BAC clone GS056H18 from 7q31-q32, complete sequence.	2.40E-07	A47021_1	Sequence 23 from Patent WO9527787; Unnamed protein product; Author-given protein sequence is in conflict with the conceptual translation>GP:A51260_1 Sequence 23 from Patent WO9614416; Unnamed protein product; Author-given	0.0016

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					protein sequence is i	
304	U04980	Rattus norvegicus fetal troponin T 3 (fetal TnT3) mRNA, partial cds.	2.20E-07	HUMFSHD_1	Human facioscapulohumeral muscular dystrophy (FSHD) gene region, D4Z4 tandem repeat unit; ORF	3.30E-08
305	U68704	Human chromosome 21q22.3 P1-clone 3804 subclone 4-52.	2.00E-07	HHV6AGNM_96	Human herpesvirus-6 (HHV-6) U1102, variant A, complete virion genome; U88; Cys repeats; this loci is open in all six reading frames, part of IE-A	2.70E-05
306	U51583	Rattus norvegicus zinc finger homeodomain enhancer-binding protein-1 (Zfhep-1) mRNA, partial cds.	8.70E-08	AF005370_67	Alcelaphine herpesvirus 1 L-DNA, complete sequence; Putative immediate early protein; ORF73; similar to H; saimiri and KSHV ORF73	6.10E-07
307	M80206	Mus domesticus poliovirus receptor homolog (MPH) mRNA, complete cds.	8.10E-08	I53960	PRR2 alpha - human	1.70E-28
308	M60854	Human ribosomal protein S16 mRNA, complete cds.	5.70E-08	OLVPOL_1	Caprine arthritis encephalitis virus (isolate OVLV-N1) pol protein gene, 3' end of cds; Nt 2497-2695 from CAEV Co	0.27
309	U82828	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds.	1.50E-08	C40201	artifact-warning sequence (translated ALU class C) - human	0.00044

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
310	Z83836	Human DNA sequence from PAC 111J24 on chromosome 22q12-qter contains ESTs.	1.40E-08	HSU64473_1	Human rheumatoid arthritis synovium immunoglobulin heavy chain variable region mRNA, partial cds>GP:HSU64498_1 Human rheumatoid arthritis synovium immunoglobulin heavy chain variable region mRNA, partial cds	0.34
311	Z50029	Caenorhabditis elegans cosmid ZC504, complete sequence.	1.40E-08	MMU88984_1	Mus musculus NIK mRNA, complete cds	1.70E-50
312	AC002351	Homo sapiens; HTGS phase 1, 17 unordered pieces.	1.20E-08	D41132	collagen-related protein 4 - Hydra magnipapillata (fragment)>PIR2:S219 32 mini-collagen - Hydra sp.>GP:HSNCOL4_1 Hydra N-COL 4 mRNA for mini-collagen; No start codon	0.02
313	B65763	CIT-HSP-2023A12.TR CIT-HSP Homo sapiens genomic clone 2023A12.	3.60E-09	S18106	type II site-specific deoxyribonuclease (EC 3.1.21.4) Abri - Azospirillum brasilense	0.045
314	Z93021	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 516C23; HTGS phase 1.	2.00E-09	AB001684_134	Chlorella vulgaris C-27 chloroplast DNA, complete sequence; RNA polymerase gamma subunit	0.6
315	D88035	Rat mRNA for glycoprotein specific UDP-glucuronyltransferase, complete cds.	1.50E-09	D88035_1	Rat mRNA for glycoprotein specific UDP-glucuronyltransferase, complete cds	1.00E-33

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
316	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds.	1.30E-10	VGF1_IBVB	F1 PROTEIN>PIR1:VFIH B1 F1 protein - avian infectious bronchitis virus (strain Beaudette)>GP:IBACG B_1 Avian infectious bronchitis virus pol protein, spike protein, small virion-associated protein, membrane protein, and nucleocapsid protein gen	1
317	B04719	cSRL-42G12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-42G12.	7.90E-11	JC5238	galactosylceramide-like protein, GCP - human	0.31
318	M73506	Mouse Tcp-10c (t allele) gene.	2.80E-11	A39487	T-complex protein 10a (allele 129) - mouse	4.10E-16
319	U71148	Human Xq28 cosmids U225B5 and U236A12, complete sequence.	1.20E-11	A56547	sex-peptide precursor - Drosophila suzukii	0.4
320	Z95116	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 57G9; HTGS phase 1.	9.90E-13	ALU2_HUMAN	!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!	0.0017
321	M64795	Rat MHC class I antigen gene (RT1-u haplotype), complete cds.	1.70E-14	STC_DROME	SHUTTLE CRAFT PROTEIN>GP:DMU0 9306_1 Drosophila melanogaster shuttle craft protein (stc) mRNA, complete cds; C-terminal 222 amino acids encode a novel single- stranded DNA binding domain	1.40E-13

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
322	Y09036	H.sapiens NTRK1 gene, exon 17.	4.20E-15	AF010403_1	Homo sapiens ALR mRNA, complete cds; Alternatively spliced; similarity to ALL-1 and Drosophila trithorax	1
323	U12523	Rattus norvegicus ultraviolet B radiation-activated UV98 mRNA, partial sequence.	2.90E-15	SPBC30D10_4	S;pombe chromosome II cosmid c30D10; Hypothetical protein; SPBC30D10;04, unknown, len:148aa	2.40E-09
324	Z98755	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 76C18; HTGS phase 1.	2.20E-15	RPON_HAL MA	DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6)>PIR2:D41715 DNA-directed RNA polymerase II chain RPB10 homolog - Haloarcula marismortui>GP:HAL HMAENOA_4 H;marismortui tRNA-Leu, HL29, HmaL13, HmaS9, OrfMMV, OrfMNA, 2-phosphoglycerate dehydr	0.019
325	M86917	Human oxysterol-binding protein (OSBP) mRNA, complete cds.	1.60E-15	CEF14H8_2	Caenorhabditis elegans cosmid F14H8, complete sequence; F14H8;1; Similarity to Human oxysterol-binding protein (SW:OXYB_HUMAN)	2.10E-18
326	AC001231	Genomic sequence from Human 17, complete sequence.	1.30E-15	AC002397_3	Mouse BAC284H12 Chromosome 6, complete sequence; DRPLA	0.0016
327	AL008626	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1114G22; HTGS phase 1.	5.30E-16	TAU48227_1	Triticum aestivum soluble starch synthase mRNA, partial cds	5.90E-05

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
328	L04483	Human ribosomal protein S21 (RPS21) mRNA, complete cds.	7.60E-17	RS21_HUMAN	40S RIBOSOMAL PROTEIN S21>PIR2:S34108 ribosomal protein S21 - human>GP:SSZ84015_1 S;scrofa mRNA; expressed sequence tag (3'; clone c11g10); 40S ribosomal protein S21; Similar to human 40S ribosomal protein S21>GP:HUMRPS21X_1 Human ribosomal	1.40E-09
329	AB001899	Homo sapiens PACE4 gene, exon 2.	6.70E-17	LRP1_HUMAN	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER)>PIR2:S02392 LDL receptor-related protein precursor - human>GP:HSLDLRR_L_1 Human mRNA for LDL-recept	1
330	Z98755	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 76C18; HTGS phase 1.	4.40E-17	U97553_59	Murine herpesvirus 68 strain WUMS, complete genome; Ribonucleotide reductase large	0.06
331	AF017187	Homo sapiens LTR HERV-K repetitive element fragment ltr_19_9a sequence.	3.90E-18	D84255_1	Ovophis okinavensis mitochondrial DNA for NADH dehydrogenase subunit 1, partial cds, Ile-tRNA, Pro-tRNA, Phe-tRNA, Gln-tRNA, Met-tRNA and control region (D-loop region); This cds	0.007

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
332	B36252	HS-1038-A2-G01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 820 Col=2 Row=M.	3.10E-18	PGBM_MOUSE	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HSPG) (PERLECAN) (PLC)>PIR2:S18252 heparan sulfate proteoglycan - mouse>GP:MUSPERP A_1 Mouse perlecan mRNA, complete cds	0.00015
333	D78255	Mouse mRNA for PAP-1, complete cds.	2.70E-18	MUSPAP1_1	Mouse mRNA for PAP-1, complete cds	3.50E-18
334	AC003046	Human Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.	1.40E-18	CEC34F6_1	Caenorhabditis elegans cosmid C34F6; C34F6;1; CDNA EST yk46b12;5 comes from this gene; cDNA EST yk44c4;5 comes from this gene; cDNA EST yk46b12;3 comes from this gene	0.0015
335	AC003002	Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.	1.40E-18	MUSZFP0_1	Mouse mRNA for zinc finger protein, partial sequence	1.30E-19
336	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial.	3.40E-19	HS4U2IR2_1	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds; Nuclear antigen 2	2.00E-06
337	Z97876	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 295C6; HTGS	1.30E-19	AF003535_1	Homo sapiens L1 element ORF2-like protein gene, partial cds	7.00E-05



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		phase 1.				
338	M97159	Mouse (clone pIL2) B1 dispersed repeat unit.	1.10E-19	A26882	pIL2 hypothetical protein - rat (fragment)>GP:RATT DR_1 Rat growth and transformation-dependent mRNA, 3' end; Growth and transformation dependent protein	0.2
339	U30817	Bos taurus very-long-chain acyl-CoA dehydrogenase mRNA, nuclear gene encoding mitochondrial protein, complete cds.	4.70E-20	ACDV_RAT	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)>PIR2:A548 72 acyl-CoA dehydrogenase (EC 1.3.99.-) very-long-chain-specific precursor - rat>GP:RATVLCAD_1 Rat mRNA for very-long-chain Acyl-CoA dehydrogenase, compl	8.10E-25
340	Y11535	H.sapiens mRNA for SHOXb protein.	2.80E-20	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	0.00027
341	AL008730	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 487J7; HTGS phase 1.	7.10E-21	C40201	artifact-warning sequence (translated ALU class C) - human	0.001
342	U96629	Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.	5.30E-23	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	3.80E-10

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
343	U95743	Homo sapiens chromosome 16 BAC clone CIT987-SK65D3, complete sequence.	2.10E-24	UROM_HUMAN	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)>PIR2:A30452 uromodulin precursor - human>GP:HUMUMOD_1 Human uromodulin (Tamm-Horsfall glycoprotein) mRNA, complete cds; Uromodulin precursor	1
344	U15972	Mus musculus homeobox (Hoxa7) gene, complete cds.	4.00E-25	S20790	extensin - almond>GP:PAEXTS_1 P;amygdalus mRNA for extensin	0.34
345	U15972	Mus musculus homeobox (Hoxa7) gene, complete cds.	4.00E-25	CA24_CAEL	COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR>GP:CECOLA2IV_2 C;elegans a2(IV) collagen gene; Alternatively spliced transcript	0.1
346	Z66242	H.sapiens CpG island DNA genomic MseI fragment, clone 84a4, reverse read cpg84a4.rt1a.	4.80E-26	CEC35A5_8	Caenorhabditis elegans cosmid C35A5, complete sequence; C35A5;8; CDNA EST yk31f6;5 comes from this gene; cDNA EST yk38h1;3 comes from this gene; cDNA EST yk38h1;5 comes from this gene;	7.70E-19
347	L25331	Rattus norvegicus lysyl hydroxylase mRNA, complete cds.	3.90E-26	LYSH_CHICK	PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE)>PIR2:A23742 procollagen-lysine 5-dioxygenase (EC 1.14.11.4) precursor - chicken>GP:CHKLYH_1 Chicken lysyl	1.10E-43

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					hydroxylase mRNA, complete cds	
348	L81569	Drosophila melanogaster (subclone 2_d7 from P1 DS04260 (D68)) DNA sequence, complete sequence.	3.30E-26	CEL52B9_2	Caenorhabditis elegans cosmid C52B9; Coded for by C; elegans cDNA cm11d6; weakly similar to S; cervisiae PTM1 precursor (SP:P32857)	8.40E-29
349	U78082	Human RNA polymerase transcriptional regulation mediator (h-MED6) mRNA, complete cds.	2.30E-26	HSU78082_1	Human RNA polymerase transcriptional regulation mediator (h-MED6) mRNA, complete cds; H-Med6p	1.50E-16
350	U43381	Human Down Syndrome region of chromosome 21 DNA.	2.10E-28	HSMRNAEB_1	H;sapiens genomic DNA, integration site for Epstein-Barr virus; Hypothetical protein	0.18
351	D50416	Mouse mRNA for AREC3, complete cds.	2.50E-29	A29947	prostaglandin-endoperoxide synthase (EC 1.14.99.1) precursor - sheep>GP:SHPCOA_1 Sheep prostaglandin endoperoxide synthetase (cyclooxygenase), complete cds; Cyclooxygenase precursor (EC 1;14;99;1)	0.81

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
352	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds.	2.20E-29	CFU30222_1	Crithidia fasciculata fully edited ATPase subunit 6 (MURF4) mRNA, partial cds; Cryptogene	0.53
353	Z92826	Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone C18D11; HTGS phase 1.	1.10E-30	SPAC1B3_5	S;pombe chromosome I cosmid c1B3; Hypothetical protein; SPAC1B3;05, probable transcriptional regulator, len:630aa, similar eg; to YIL038C, NOT3_YEAST, P06102, general negative regulator,	3.20E-35
354	L09604	Homo sapiens differentiation-dependent A4 protein mRNA, complete cds.	3.70E-32	PVU72769_1	Phaseolus vulgaris PvPRP-12 (Pvprp1-12) mRNA, partial cds; Similar to cell wall proline rich protein>GP:PVU72769_1 Phaseolus vulgaris PvPRP-12 (Pvprp1-12) mRNA, partial cds; Similar to cell wall proline rich protein	0.00049
355	B42455	HS-1055-B2-G03-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 777 Col=6 Row=N.	1.30E-32	CEL T05H4_8	Caenorhabditis elegans cosmid T05H4; Similar to the beta transducin family; coded for by C; elegans cDNA yk156e11;3; coded for by C; elegans cDNA yk14c8;3; coded for by C; elegans cDNA	6.90E-14
356	AF001905	Homo sapiens cosmids E079, B0920 and A8 from Xq25 X-linked lymphoproliferative disease gene candidate region, complete sequence.	1.80E-33	I38344	titin - human	1

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
357	E03743	DNA sequence including male hormone dependent gene derived from hamster frankorgan.	1.10E-34	CELC03A7_2	Caenorhabditis elegans cosmid C03A7; Weak similarity to serotonin receptors	0.59
358	U31199	Human laminin gamma2 chain gene (LAMC2), exon 22 and flanking sequences.	1.20E-35	B44018	laminin B2t chain - human>GP:HSLAMB2 TB_1 H;sapiens mRNA for laminin	1.20E-14
359	D14678	Human mRNA for kinesin-related protein, partial cds.	2.00E-36	D49544_1	Mouse mRNA for KIFC1, complete cds	1.20E-23
360	AB000425	Porcine DNA for endopeptidase 24.16, exon 16 and complete cds.	8.20E-38	POL4_DROME	RETROVIRUS-RELATED POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) (TRANSPOSON 412)>PIR1:GNFF42 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 412>GP:DMRT412G_4	0.65
361	U39875	Rattus norvegicus EF-hand Ca2+-binding protein p22 mRNA, complete cds.	8.80E-42	I56333	apolipoprotein B - rat (fragment)>GP:RATA POLPB_1 Rattus norvegicus (clone rb9E) apolipoprotein B apoB mRNA, 3' end	0.23

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
362	L09647	Rattus norvegicus hepatocyte nuclear factor 3a (HNF-3 beta) mRNA, complete cds.	6.60E-42	HN3B_RAT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)>GP:RATHNF3B_1 Rattus norvegicus hepatocyte nuclear factor 3a (HNF-3 beta) mRNA, complete cds>TFD:TFDP01611 - Polypeptides entry for factor HNF-3 (beta)	8.10E-25
363	D25538	Human mRNA for KIAA0037 gene, complete cds.	4.10E-43	CELC34D4_1 2	Caenorhabditis elegans cosmid C34D4	0.018
364	Z56764	H.sapiens CpG island DNA genomic MseI fragment, clone 13f7, reverse read cpg13f7.rt1a.	1.40E-43	S75263	hypothetical protein - Synechocystis sp. (PCC 6803)>GP:D90904_29 Synechocystis sp; PCC6803 complete genome, 6/27, 630555-781448; Hypothetical protein; ORF_ID:sll0983	0.0028
365	AC002636	*** SEQUENCING IN PROGRESS *** Drosophila melanogaster (subclone 2_g4 from P1 DS03323 (D127)) DNA sequence; HTGS phase 2.	8.40E-44	DMU95760_1	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds; Notch pathway component; nuclear protein	3.40E-51
366	J05499	Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds.	8.00E-44	GLSL_RAT	GLUTAMINASE, LIVER ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)>GP:RATGAH_1 Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds	8.00E-29

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
367	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds.	5.00E-45	DMU95760_1	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds; Notch pathway component; nuclear protein	4.80E-45
368	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	4.10E-45	PTPK_HUMAN	PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP-KAPPA)>GP:HSPTPK AP_1 H;sapiens mRNA for phosphotyrosine phosphatase kappa; Human phosphotyrosine phosphatase kappa	4.70E-16
369	D17218	Human HepG2 3' region MboI cDNA, clone hmd3g02m3.	9.40E-47	MMU53563_1	Mus musculus Brg1 mRNA, partial cds; N-terminal region of the protein	0.00012
370	U78310	Homo sapiens pescadillo mRNA, complete cds.	8.10E-48	HSU78310_1	Homo sapiens pescadillo mRNA, complete cds	1.10E-21
371	AC000399	Genomic sequence from Mouse 9, complete sequence.	7.40E-48	KIP2_YEAST	KINESIN-LIKE PROTEIN KIP2>PIR1:C42640 kinesin-related protein KIP2 - yeast (Saccharomyces cerevisiae)>GP:SCKIP 2XVI_2 S;cerevisiae PEP4 and KIP2 genes encoding PEP4 proteinase (partial) and kinesin-related protein KIP2>GP:SCLACHX VI_17 S;cerev	0.14
372	AC002327	*** SEQUENCING IN PROGRESS *** Genomic sequence from Mouse 7; HTGS phase 1, 3	1.40E-48	CHKC1A205_1	Chicken alpha-2 type-1 collagen; amino acids - 16 to 3; Precollagen alpha-2	0.024

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		unordered pieces.				
373	X67016	H.sapiens mRNA for amphiglycan.	9.00E-49	CED2085_2	Caenorhabditis elegans cosmid D2085, complete sequence; D2085;1; Similar to glutamine-dependent carbamoyl-phosphate synthase, aspartate carbamoyltransferase, dihydroorotase; cDNA EST cm16f3>GP:CED2085_2 Caenorhabditis elegans cosmid D2085; D	0.14
374	L10409	Mouse fork head related protein (HNF-3beta) mRNA, complete cds.	1.50E-49	MMU04197_1	Mus musculus HNF3 beta transcription factor (HNF3b) mRNA, partial cds; Sequence of this partial cDNA begins in the first third of the conserved HNF3/forkhead DNA binding domain	1.20E-30
375	U01139	Mus musculus B6D2F1 clone 2C11B mRNA.	1.20E-49	SPBC3D5_14	S;pombe chromosome II cosmid c3D5; Unknown; SPBC3D5;14c, unknown; partial; serine rich, len:309aa, similar eg; to YNL283C, YN23_YEAST, P53832, hypothetical 52;3 kd protein, (503aa),	0.00091
376	Z82170	Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat.	9.00E-50	BSU55043_3	Bacillus subtilis plasmid pPOD2000 Rep, RapAB, RapA, ParA, ParB, and ParC genes, complete cds; ORF3	0.025



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
377	Z99289	Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 142L7; HTGS phase 1.	7.70E-50	A64431	hypothetical protein MJ1050 - Methanococcus jannaschii>GP:MJU67548_2 Methanococcus jannaschii from bases 986219 to 996377 (section 90 of 150) of the complete genome; M; jannaschii predicted coding region MJ1050; Identified by GeneMark; putativ	5.60E-05
378	X98260	H.sapiens mRNA for M-phase phosphoprotein, mpp11.	6.20E-50	ZRF1_MOUSE	ZUOTIN RELATED FACTOR>GP:MMU53208_1 Mus musculus zuotin related factor (ZRF1) mRNA, complete cds; Similar to DnaJ encoded by GenBank Accession Number L16953	3.90E-30
379	M18981	Human prolactin receptor-associated protein (PRA) gene, complete cds.	9.00E-52	S106_HUMAN	CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTH FACTOR-INDUCIBLE PROTEIN 2A9) (S100 CALCIUM-BINDING PROTEIN A6)>PIR1:BCHUY calcyclin - human>GP:HUMCACY_1 Human calcyclin gene, complete cds>GP:HUMCACYA_1 Human prolactin recept	8.80E-24
380	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds.	1.60E-53	S33015	hypothetical protein - human herpesvirus 4	0.00088

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
381	U53225	Human sorting nexin 1 (SNX1) mRNA, complete cds.	1.80E-55	G02522	sorting nexin 1 - human>GP:HSU53225_1 Human sorting nexin 1 (SNX1) mRNA, complete cds	9.20E-50
382	Z92844	Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.	6.50E-56	D14487_1	Lentinus edodes Le;MFB1 mRNA, complete cds	1
383	D87450	Human mRNA for KIAA0261 gene, partial cds.	4.30E-56	D87450_1	Human mRNA for KIAA0261 gene, partial cds; Similar to D;melanogaster parallel sister chromatids protein	4.30E-30
384	AC002301	*** SEQUENCING IN PROGRESS *** Human chromosome +16p11.2 BAC clone CIT987SK-A-328A3; HTGS phase 2, 1 ordered pieces.	9.80E-57	S62328	kinesin-like DNA binding protein KID - human>GP:HUMKID_1 Human mRNA for Kid (kinesin-like DNA binding protein), complete cds	2.60E-27
385	L29766	Homo sapiens epoxide hydrolase (EPHX) gene, complete cds.	7.30E-57	HSBCTCF4_1	Homo sapiens mRNA for hTCF-4	2.30E-05
386	U58884	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin.	3.30E-58	MMU58884_1	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds; similar to Human Drebrin; SH3-containing protein; similar to human drebrin	6.00E-43
387	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial.	9.50E-59	RNY15054_1	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial; 70 kD tumor-specific antigen	4.70E-45

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
388	AC000406	*** SEQUENCING IN PROGRESS *** Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22; HTGS phase 1, 17 unordered pieces.	7.40E-59	<NONE>	<NONE>	<NONE>
389	L42612	Homo sapiens keratin 6 isoform K6f (KRT6F) mRNA, complete cds.	3.60E-59	KRHUEA	keratin, type II cytoskeletal - human (fragment)>GP:HSKE RA_1 Human messenger fragment encoding cytoskeletal keratin (type II); mRNA from cultured epidermal cells from human foreskin>GP:HUMKE R56K_1 Human 56k cytoskeletal type II keratin mRNA	7.60E-30
390	L29766	Homo sapiens epoxide hydrolase (EPHX) gene, complete cds.	2.70E-60	EGR2_HUMAN	EARLY GROWTH RESPONSE PROTEIN 2 (EGR-2) (KROX-20 PROTEIN) (AT591)>GP:HUMEG R2A_1 Human early growth response 2 protein (EGR2) mRNA, complete cds>TFD:TFDP00485 - Polypeptides entry for factor Egr-2	7.80E-06
391	L08758	Mus musculus homeobox protein (Hox A10) gene, 5' end of cds.	1.40E-60	PAALGYGE N_1	P;aeruginosa algY gene; Alginate lyase	0.00031
392	I29058	Sequence 3 from patent US 5576423.	4.20E-61	JC5106	stromal cell-derived factor 2 - human>GP:D50645_1 Human mRNA for SDF2, complete cds; Stroma cell-derived	1.50E-32

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					factor-2	
393	I29058	Sequence 3 from patent US 5576423.	4.20E-61	JC5106	stromal cell-derived factor 2 - human>GP:D50645_1 Human mRNA for SDF2, complete cds; Stroma cell-derived factor-2	1.50E-32
394	U46067	Capra hircus beta-mannosidase mRNA, complete cds.	1.90E-62	CHU46067_1	Capra hircus beta-mannosidase mRNA, complete cds	2.70E-39
395	U40747	Mus musculus formin binding protein 11 mRNA, partial cds.	6.90E-63	S64713	formin binding protein 11 - mouse (fragment)>GP:MMU40747_1 Mus musculus formin binding protein 11 mRNA, partial cds; FBP 11; Formin binding protein 11; tandem WWP/WW domains separated by 15 amino acid linker	3.00E-46
396	M36164	Human glyceraldehyde-3-phosphate dehydrogenase mRNA, 3' flank.	1.10E-63	BHT1UL_12	Bovine herpesvirus type 1 UL22-35 genes; UL26;5>GP:BHU31809_2 Bovine herpesvirus 1 maturational proteinase (UL26) gene, complete cds, and scaffold protein (UL26;5) gene, complete cds	0.003
397	Y09036	H.sapiens NTRK1 gene, exon 17.	7.30E-65	MMU39060_1	Mus musculus glucocorticoid receptor interacting protein 1 (GRIP1) mRNA, complete cds; Hormone-dependent interaction with hormone binding domains of steroid receptors;	0.0054

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					transactivation	
398	U17901	Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.	2.70E-70	JC4239	phospholipase A2-activating protein - rat	8.40E-17
399	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.	1.70E-74	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4>PIR2:A54803 microtubule-associated motor KIF4 - mouse>GP:MUSKIF4_1 Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds; ATP-binding site: base980-1037, motor domain: base732-1781, alpha-helical co	1.10E-44
400	AF007860	Xenopus laevis xl-Mago mRNA, complete cds.	4.60E-75	AF007862_1	Mus musculus mm-Mago mRNA, complete cds; Similar to Drosophila melanogaster Mago protein	6.50E-68
401	I45565	Sequence 15 from patent US 5637463.	2.30E-82	RNU57391_1	Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds; Putative FceRI gamma ITAM interacting protein; SH2 domain-containing protein B; Method: conceptual	9.90E-42

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
402	U29156	Mus musculus eps15R mRNA, complete cds.	1.00E-85	MMU29156_1	Mus musculus eps15R mRNA, complete cds; Involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author	4.90E-62
403	U70139	Mus musculus putative CCR4 protein mRNA, partial cds.	1.00E-85	MMU70139_1	Mus musculus putative CCR4 protein mRNA, partial cds; Similar to yeast transcription factor CCR4; transcriptional readthrough occurs with transcription being initiated at the IAP and continues	7.20E-66
404	U82626	Rattus norvegicus basement membrane-associated chondroitin proteoglycan Bamacan mRNA, complete cds.	7.60E-96	RNU82626_1	Rattus norvegicus basement membrane-associated chondroitin proteoglycan Bamacan mRNA, complete cds; Chondroitin sulfate proteoglycan; CSPG	8.20E-58

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
405	L09604	Homo sapiens differentiation-dependent A4 protein mRNA, complete cds.	2.00E-35	<NONE>	<NONE>	<NONE>
406	AB000516	Homo sapiens mRNA for DSIF p160, complete cds	0.41	POLG_TUMVQ	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; VPG PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI-A)	2.9
407	Z94753	Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cu <sup>++</sup> -transporting P-type ATPase exons 22, 23 and STS	0.004	<NONE>	<NONE>	<NONE>
408	AB011123	Homo sapiens mRNA for KIAA0551 protein, partial cds	0	MI15_CAEEL	Q23356 caenorhabditis elegans. serine/threonine-protein kinase mig-15 (ec 2.7.1.-). 11/98	2.00E-51
409	D17218	Human HepG2 3' region MboI cDNA, clone hmd3g02m3	e-123	NARG_BACSU	NITRATE REDUCTASE ALPHA CHAIN (EC 1.7.99.4)	9.9
410	M95098	Bos taurus lysozyme gene (cow 2), complete cds	1.1	HAIR_MOUSE	HAIRLESS PROTEIN	8.00E-10

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
411	Z60048	H.sapiens CpG DNA, clone 187a9, reverse read cpg187a9.rt1a .	4.00E-54	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	4.00E-21
412	Z48975	P.magnus gene for protein urPAB	0.014	YPT2_CAEEL	HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III	2.00E-12
413	AJ001296	Notophthalmus viridescens mRNA for cytokeratin 8	0.37	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	5.00E-21
414	J03831	Xenopus laevis (clone pXEC1.3) C protein mRNA, complete cds.	0.37	PDR5_YEAST	SUPPRESSOR OF TOXICITY OF SPORIDESMIN	3.3
415	AB007157	Homo sapiens gene for ribosomal protein S21, partial cds	e-142	RS21_HUMAN	40S RIBOSOMAL PROTEIN S21	0.002
416	X86340	H.sapiens C7 gene, exon 13	3.3	STC_DROME	SHUTTLE CRAFT PROTEIN	4.3
417	U12404	Human Csa-19 mRNA, complete cds.	0	R10A_PIG	60S RIBOSOMAL PROTEIN L10A (CSA-19) (FRAGMENT)	9.00E-57
418	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8.00E-08	<NONE>	<NONE>	<NONE>
419	M80198	Human FKBP-12 pseudogene, clone lambda-512, 5' flank and complete cds.	5.00E-14	RCO1_NEUCR	TRANSCRIPTIONAL REPRESSOR RCO-1	0.008
420	AF052573	Homo sapiens DNA polymerase eta (POLH) mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
421	AF035940	Homo sapiens MAGOH mRNA, complete cds	e-131	MGN_DROME	MAGO NASHI PROTEIN	4.00E-39
422	AF054994	Homo sapiens clone 23832 mRNA sequence	0.12	<NONE>	<NONE>	<NONE>



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
423	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-05	<NONE>	<NONE>	<NONE>
424	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
425	D43952	Mouse gene for reticulocalbin, exon1 and promoter region	0.36	<NONE>	<NONE>	<NONE>
426	X68553	C.elegans repetitive DNA sequence	0.4	TCB1_RABIT	T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11)	0.11
427	M83314	Tomato phenylalanine ammonia lyase (pal) gene, complete cds and promoter region.	3.3	SMB2_HUMAN	DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1)	0.65
428	AF070636	Homo sapiens clone 24686 mRNA sequence	5.00E-23	<NONE>	<NONE>	<NONE>
429	<NONE>	<NONE>	<NONE>	IQGA_HUMAN	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195)	2.00E-06
430	AF068627	Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds	5.00E-04	LOX1_LENCU	LIPOXYGENASE (EC 1.13.11.12)	9.9
431	AF020043	Homo sapiens chromosome-associated polypeptide	0	YJH4_YEAST	HYPOTHETICAL 141.3 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION	4.00E-16
432	K00046	ross river virus 26s subgenomic rna and junction region.	0.12	CUL2_HUMAN	CULLIN HOMOLOG 2 (CUL-2)	7.4

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
433	AF005664	Homo sapiens properdin (PFC) gene, complete cds	0.005	UL88_HCMVA	PROTEIN UL88	5.8
434	Z70705	H.sapiens mRNA (fetal brain cDNA com5)	2.00E-05	PH87_YEAST	INORGANIC PHOSPHATE TRANSPORTER PHO87	1.5
435	U29156	Mus musculus eps15R mRNA, complete cds.	e-125	EP15_HUMAN	EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN)	1.00E-13
436	AE000750	Aquifex aeolicus section 82 of 109 of the complete genome	0.37	<NONE>	<NONE>	<NONE>
437	U49169	Dictyostelium discoideum V-ATPase A subunit (vatA) mRNA, complete cds	0.12	VCAP_HSV6U	MAJOR CAPSID PROTEIN (MCP)	5.6
438	AF032871	Homo sapiens uncoupling protein 3 (UCP3) gene, exon 1 and partial exon 2	0.13	WEE1_SCHPO	MITOSIS INHIBITOR PROTEIN KINASE WEE1 (EC 2.7.1.-)	3.7
439	AB000425	Porcine DNA for endopeptidase 24.16, exon 16 and complete cds	4.00E-32	<NONE>	<NONE>	<NONE>
440	U51037	Mus musculus 11-zinc-finger transcription factor	0.04	<NONE>	<NONE>	<NONE>
441	AF032456	Homo sapiens ubiquitin conjugating enzyme G2	e-110	<NONE>	<NONE>	<NONE>
442	AF009288	Homo sapiens clone HEB8 Cri-du-chat region mRNA	2.00E-14	LMG1_HUMAN	LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN)	8.1

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
443	AF024578	Homo sapiens type-1 protein phosphatase skeletal muscle glycogen targeting subunit (PPP1R3) gene, exon 4, and complete cds	1.1	<NONE>	<NONE>	<NONE>
444	M24486	Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-11.	0	DACHA	<NONE>	4.00E-58
445	X96400	P.tetraulera alpha-51D gene	0.37	<NONE>	<NONE>	<NONE>
446	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
447	X84996	X.laavis mRNA for selenocysteine tRNA acting factor (Staf)	0.12	POL_MLVRD	POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4))	2.00E-08
448	AF019980	Dictyostelium discoideum ZipA (zipA) gene, partial cds	3.4	HMDL_BRAFL	HOMEBOX PROTEIN DLL HOMOLOG	0.23
449	X78424	D.carota (Queen Anne's Lace) Inv*Dc2 gene, 3432bp	0.38	<NONE>	<NONE>	<NONE>
450	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
451	X89886	P.patens mRNA for 5-aminolevulinate dehydratase	1.1	CKR6_HUMAN	C-C CHEMOKINE RECEPTOR TYPE 6 (C-C CKR-6) (CCR6)	9.9
452	U67471	Methanococcus jannaschii section 13 of 150 of the complete genome	0.12	YR72_ECOLI	HYPOTHETICAL 53.2 KD PROTEIN (ORF2) (RETRON EC67)	5.8
453	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	1.00E-62	YOJ8_CAEEL	HYPOTHETICAL 51.6 KD PROTEIN ZK353.8 IN CHROMOSOME III	1.7

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
454	U70667	Human Fas-ligand associated factor 1 mRNA, partial cds	0	YKB2_YEAST	HYPOTHETICAL 69.1 KD PROTEIN IN PUT3-CCE1 INTERGENIC REGION	3.00E-09
455	M95858	Bos taurus recoverin mRNA, complete cds.	0.35	GIDA_MYCGE	GLUCOSE INHIBITED DIVISION PROTEIN A	1.4
456	U67594	Methanococcus jannaschii section 136 of 150 of the complete genome	0.36	<NONE>	<NONE>	<NONE>
457	X06747	Human hnRNP core protein A1	3.00E-31	<NONE>	<NONE>	<NONE>
458	Z65575	H.sapiens CpG DNA, clone 47c5, reverse read cpg47c5.rt1a .	1.3	<NONE>	<NONE>	<NONE>
459	X88893	C.jacchus intron 4 of visual pigment gene	5.00E-15	<NONE>	<NONE>	<NONE>
460	M57426	Maize stripe virus RNA 3 nonstructural protein	0.33	DSC2_MOUSE	DESMOCOLLIN 2A/2B PRECURSOR (EPITHELIAL TYPE 2 DESMOCOLLIN)	6.5
461	X01638	Yeast TEF1 gene for elongation factor EF-1 alpha	1.1	PPOL_DROME	POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (PARP)	3.5
462	M60064	S.typhimurium glutamate 1-semialdehyde aminotransferase (hemL) gene, complete cds.	1.1	EPB4_MOUSE	EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) KINASE 2) (TYROSINE KINASE MYK- 1)	2.5
463	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.36	ACHG_XENLA	ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR	1.5
464	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	2.00E-58	VG13_BPML5	GENE 13 PROTEIN (GP13)	2.5

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
465	M77235	Human cardiac tetrodotoxin-insensitive voltage-dependent sodium channel alpha subunit (HH1) mRNA, complete cds.	3.8	ZPBOC1	<NONE>	6.9
466	M58330	C.maltosa autonomously replicating sequence.	0.004	EPB4_MOUSE	EPHRIN TYPE-B RECEPTOR 4 PRECURSOR (EC 2.7.1.112) KINASE 2) (TYROSINE KINASE MYK- 1)	2.4
467	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.35	ACHG_XENLA	ACETYLCHOLINE RECEPTOR PROTEIN, GAMMA CHAIN PRECURSOR	2.4
468	L10106	Mus musculus protein tyrosine phosphate mRNA, complete cds.	7.00E-59	VGLI_PRVRI	GLYCOPROTEIN GP63 PRECURSOR	4.3
469	U65939	Azotobacter vinelandii GTPase (ftsA) gene, partial cds, and ATP binding protein (ftsZ) gene, complete cds	1.1	TRUA_BACSP	Q45557 bacillus sp. (strain ksm-64). trna pseudouridine synthase a (ec 4.2.1.70) (pseudouridylate synthase i) (pseudouridine synthase i) (uracil hydrolyase). 11/98	0.001
470	U51037	Mus musculus 11-zinc-finger transcription factor	0.041	<NONE>	<NONE>	<NONE>
471	M32685	Human platelet glycoprotein IIIa, exon 14.	3.6	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
472	U82691	Phrynocephalus raddei CAS 179770 NADH dehydrogenase subunit 1 (ND1), partial cds, tRNA-Gln, tRNA-Ile and tRNA-Met, NADH dehydrogenase subunit 2 tRNA-Cys and tRNA-Tyr and c...	1.1	<NONE>	<NONE>	<NONE>
473	D85430	Mouse Murr1 mRNA, exon	0.12	EPA5_CHICK	EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112)	2.5
474	U20661	Dictyostelium discoideum unknown internal repeat protein gene, complete cds, and unknown orf1, orf2 and orf3 genes, partial cds	0.36	YHL1_EBV	HYPOTHETICAL BHLF1 PROTEIN	4.00E-04
475	X56537	Human novel homeobox mRNA for a DNA binding protein	0.04	FA5_HUMAN	COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR)	9.5
476	U32843	Haemophilus influenzae Rd section 158 of 163 of the complete genome	5	<NONE>	<NONE>	<NONE>
477	U67554	Methanococcus jannaschii section 96 of 150 of the complete genome	0.36	<NONE>	<NONE>	<NONE>
478	AB004244	Narke japonica mRNA for Nj-synaphin 1b, complete cds	1.1	NIA1_ORYSA	NITRATE REDUCTASE 1 (EC 1.6.6.1) (NR1)	1.00E-07
479	AF075079	Homo sapiens full length insert cDNA YQ80A08	1.00E-12	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
480	AE000723	Aquifex aeolicus section 55 of 109 of the complete genome	1	YKK0_YEAST	HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION	9.1
481	X73902	H.sapiens mRNA for nicein B2 chain	0	LMG2_HUMAN	LAMININ GAMMA-2 CHAIN PRECURSOR	3.00E-93
482	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-10	P53_CRIGR	CELLULAR TUMOR ANTIGEN P53	5.7
483	AL010240	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-64, complete sequence	1.2	<NONE>	<NONE>	<NONE>
484	U49919	Arabidopsis thaliana lupeol synthase mRNA, complete cds	0.54	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	6.00E-10
485	AF077618	Homo sapiens p73 gene, exon 3	0.39	MYOD_MOUSE	MYOBLAST DETERMINATION PROTEIN 1	2.1
486	AF054994	Homo sapiens clone 23832 mRNA sequence	0.13	<NONE>	<NONE>	<NONE>
487	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
488	AF068627	Mus musculus DNA cytosine-5 methyltransferase 3B2 (Dnmt3b) mRNA, alternatively spliced, complete cds	5.00E-04	ACE2_YEAST	METALLOTHIONE IN EXPRESSION ACTIVATOR	1.5
489	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-07	RINI_PIG	RIBONUCLEASE INHIBITOR	0.19

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
490	L77886	Human protein tyrosine phosphatase mRNA, complete cds	1.00E-21	VS48_TBRVS	SATELLITE RNA 48 KD PROTEIN	1.6
491	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	5.00E-04	CRP3_LIMPO	C-REACTIVE PROTEIN 3.3 PRECURSOR	3.5
492	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	EPA5_CHICK	EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112)	2.7
493	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-09	<NONE>	<NONE>	<NONE>
494	U28153	Caenorhabditis elegans UNC-76 (unc-76) gene, complete cds.	0.37	<NONE>	<NONE>	<NONE>
495	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.37	NCPR_YEAST	NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR)	7.00E-05
496	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.013	YMB3_CAEEL	PROBABLE INTEGRIN ALPHA CHAIN F54G8.3 PRECURSOR	3.3
497	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	<NONE>	<NONE>	<NONE>
498	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-10	<NONE>	<NONE>	<NONE>
499	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	VGLY_LYCVW	GLYCOPROTEIN POLYPROTEIN PRECURSOR (CONTAINS: GLYCOPROTEINS G1 AND G2)	3.2



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
500	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-06	HR78_DROME	NUCLEAR HORMONE RECEPTOR HR78 (DHR78) (NUCLEAR RECEPTOR XR78E/F)	2.5
501	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-10	MYSH_BOVIN	MYOSIN I HEAVY CHAIN-LIKE PROTEIN (MIHC) (BRUSH BORDER MYOSIN I) (BBMI)	4.00E-04
502	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-04	BAL_HUMAN	BILE-SALT-ACTIVATED LIPASE PRECURSOR (EC 3.1.1.3) (EC 3.1.1.13) (BAL) (BILE-SALT-STIMULATED LIPASE) (BSSL) (ESTERASE) (PANCREATIC LYSOPHOSPHOLIPASE)	2.6
503	AF080399	Drosophila melanogaster mitotic checkpoint control protein kinase BUB1 (Bub1) mRNA, complete cds	1.1	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88)	2.00E-23
504	U59706	Gallus gallus alternatively spliced AMPA glutamate receptor, isoform GluR2 flop, (GluR2) mRNA, partial cds.	0.014	<NONE>	<NONE>	<NONE>
505	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>
506	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-04	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
507	AF100661	Caenorhabditis elegans cosmid H20E11	0.38	<NONE>	<NONE>	<NONE>
508	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-11	CA1A_HUMAN	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR	0.024
509	U47322	Cloning vector DNA, complete sequence.	2.00E-38	COA1_SV40	COAT PROTEIN VP1	6.2
510	AF031924	Homo sapiens homeobox transcription factor barx2	e-156	CCMA_HAEIN	HEME EXPORTER PROTEIN A (CYTOCHROME C-TYPE BIOGENESIS ATP-BINDING PROTEIN CCMA)	3.5
511	AF010484	Homo sapiens ICI YAC 91A12, right end sequence	3.00E-10	<NONE>	<NONE>	<NONE>
512	Z63829	H.sapiens CpG DNA, clone 90h2, forward read cpg90h2.fl1a .	5.00E-22	NFIR_MESAU	NUCLEAR FACTOR 1 CLONE PNF1/RED1 (NF-1) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN)	2.4
513	Z35094	H.sapiens mRNA for SURF-2	5.00E-97	SUR2_HUMAN	SURFEIT LOCUS PROTEIN 2	1.00E-46
514	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	<NONE>	<NONE>	<NONE>
515	D38417	Mouse mRNA for arylhydrocarbon receptor, complete cds	e-154	TEGU_EBV	LARGE TEGUMENT PROTEIN	3.4
516	L10911	Homo sapiens splicing factor (CC1.4) mRNA, complete cds.	e-117	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
517	X17093	Human HLA-F gene for human leukocyte antigen F	0.009	YEN1_SCHPO	O13695 schizosaccharomyces pombe (fission yeast). hypothetical 52.9 kd serine-rich protein c11g7.01 in chromosome i. 11/98	5.4
518	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_HUMAN	OXYSTEROL-BINDING PROTEIN	1.00E-40
519	X55038	Mouse mCENP-B gene for centromere autoantigen B	0.001	YNW7_YEAST	HYPOTHETICAL 68.8 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION	3.00E-04
520	AB018323	Homo sapiens mRNA for KIAA0780 protein, partial cds	3.00E-41	LBR_CHICK	LAMIN B RECEPTOR	2.3
521	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-10	CA25_HUMAN	PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR	0.002
522	X03558	Human mRNA for elongation factor 1 alpha subunit	0	EF11_HUMAN	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	e-110
523	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-11	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	8.00E-07
524	AB014591	Homo sapiens mRNA for KIAA0691 protein, complete cds	0	NOT2_YEAST	GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 2	8.00E-05
525	AB019488	Homo sapiens DNA for TRKA, exon 17 and complete cds	0	TRKA_HUMAN	HIGH AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR PROTEIN (P140-TRKA)	2.00E-27

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
526	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-15	CNG4_BOVIN	240K PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) MODULATORY SUBUNIT))	0.018
527	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-06	HMZ1_DROME	ZERKNUELLT PROTEIN 1 (ZEN-1)	0.88
528	J03750	Mouse single stranded DNA binding protein p9 mRNA, complete cds.	e-135	P15_HUMAN	ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14)	3.00E-21
529	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-12	RS5_DROME	40S RIBOSOMAL PROTEIN S5	0.42
530	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rtl.a.	8.00E-61	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	4.00E-15
531	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3.00E-60	<NONE>	<NONE>	<NONE>
532	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.00E-11	<NONE>	<NONE>	<NONE>
533	U50535	Human BRCA2 region, mRNA sequence CG006	4.00E-12	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	1.1
534	X92841	H.sapiens MICA gene	1.00E-55	LIN1_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6.00E-09

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
535	U60337	Homo sapiens beta-mannosidase mRNA, complete cds	0	NODC_BRAEL	N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)	1.4
536	M21731	Human lipocortin-V mRNA, complete cds.	e-169	ANX5_HUMAN	ANNEXIN V (LIPOCORTIN V) (ENDONEXIN II) (CALPHOBINDIN I) (CBP-I) (PLACENTAL ANTICOAGULANT PROTEIN I) (PAP-I) ANTICOAGULANT -ALPHA) (VAC-ALPHA) (ANCHORIN CII)	1.00E-05
537	Y08013	S.salar DNA segment containing GT repeat	0.006	<NONE>	<NONE>	<NONE>
538	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
539	M98502	Mus musculus protein encoding twelve zinc finger proteins (pMLZ-4) mRNA, complete cds.	2.00E-17	DYNA_CHICK	DYNACTIN, 117 KD ISOFORM	7.4
540	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	HXA3_HAEIN	HEME:HEMOPEXIN-BINDING PROTEIN PRECURSOR	2.6
541	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-13	AMO_KLEAE	AMINE OXIDASE PRECURSOR (EC 1.4.3.6) (MONAMINE OXIDASE) (TYRAMINE OXIDASE)	1.5
542	AF083322	Homo sapiens centriole associated protein CEP110 mRNA, complete cds	e-133	CA34_HUMAN	PROCOLLAGEN ALPHA 3(IV) CHAIN PRECURSOR	1.5
543	J03746	Human glutathione S-transferase mRNA, complete cds.	e-170	GTM1_HUMAN	GLUTATHIONE S-TRANSFERASE, MICROSOMAL (EC 2.5.1.18)	5.00E-39

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
544	U67522	Methanococcus jannaschii section 64 of 150 of the complete genome	0.37	A1AA_HUMAN	ALPHA-1A ADRENERGIC RECEPTOR	4.3
545	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	<NONE>	<NONE>	<NONE>
546	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
547	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
548	D87001	Human (lambda) DNA for immunoglobulin light chain	0.35	VAL3_TYLCU	AL3 PROTEIN (C3 PROTEIN)	3.2
549	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-08	TEGU_HSV11	LARGE TEGUMENT PROTEIN (VIRION PROTEIN UL36)	0.004
550	D16991	Human HepG2 partial cDNA, clone hmd2d01m5	8.00E-09	PTM1_YEAST	PROTEIN PTM1 PRECURSOR	0.033
551	M34025	Human fetal Ig heavy chain variable region	3.2	<NONE>	<NONE>	<NONE>
552	M98502	Mus musculus protein encoding twelve zinc finger proteins (pMLZ-4) mRNA, complete cds.	5.00E-14	<NONE>	<NONE>	<NONE>
553	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
554	Z78730	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15C3	3.00E-20	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	5.00E-06
555	U74496	Human chromosome 4q35 subtelomeric sequence	8.00E-08	ICP4_VZVD	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP4	0.39

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
556	U39875	Rattus norvegicus EF-hand Ca <sup>2+</sup> -binding protein p22 mRNA, complete cds.	2.00E-56	YHFK_ECOLI	HYPOTHETICAL 79.5 KD PROTEIN IN CRP-ARGD INTERGENIC REGION (O696)	9.8
557	U65416	Human MHC class I molecule (MICB) gene, complete cds	0.12	<NONE>	<NONE>	<NONE>
558	AG000037	Homo sapiens genomic DNA, 21q region, clone: 9H11A22	5.00E-25	<NONE>	<NONE>	<NONE>
559	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-05	<NONE>	<NONE>	<NONE>
560	AB007918	Homo sapiens mRNA for KIAA0449 protein, partial cds	0.015	VGLE_HSV11	GLYCOPROTEIN E PRECURSOR	2.2
561	U58884	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin	1.00E-73	YCV2_YEAST	HYPOTHETICAL 13.8 KD PROTEIN IN PWP2-SUP61 INTERGENIC REGION	2.6
562	AB007878	Homo sapiens KIAA0418 mRNA, complete cds	e-110	GLU2_MAIZE	GLUTELIN 2 PRECURSOR (ZEIN-GAMMA) (27 KD ZEIN)	0.72
563	AF065482	Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds	0	YJD6_YEAST	HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC REGION	1.4
564	U27873	Stealth virus 1 clone 3B11 T7	0.002	SYN1_HUMAN	SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1)	1.6
565	L38951	Homo sapiens importin beta subunit mRNA, complete cds	2.00E-68	VP2_BRD	STRUCTURAL CORE PROTEIN VP2	1.1
566	AF007155	Homo sapiens clone 23763 unknown mRNA, partial cds	e-165	YOHI_AZOVI	HYPOTHETICAL 33.2 KD PROTEIN IN IBPB 5'REGION	7.5

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
567	Z56295	H.sapiens CpG DNA, clone 10c2, forward read cpg10c2.ft1a .	0.12	A1AB_CANFA	ALPHA-1B ADRENERGIC RECEPTOR (FRAGMENT)	0.85
568	Z83792	G.gallus microsatellite DNA (LEI0222)	0.12	<NONE>	<NONE>	<NONE>
569	U11820	Feline immunodeficiency virus USIL2489_7B gag polyprotein (gag) gene, complete cds, polymerase polyprotein (pol) gene, partial cds, vif protein (vif), complete cds, and envelope glycoprotein (env), complete cds, complete g...	1.1	<NONE>	<NONE>	<NONE>
570	M18065	Mouse 18S and 28S ribosomal DNA, 5' hypervariable (Vr) region, clone M1.	6.00E-04	CC40_YEAST	CELL DIVISION CONTROL PROTEIN 40	3.7
571	AF053645	Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exons 3 through 10	2.00E-07	YMQ4_CAEEL	HYPOTHETICAL 25.8 KD PROTEIN K02D10.4 IN CHROMOSOME III	4.3
572	X04588	Human 2.5 kb mRNA for cytoskeletal tropomyosin TM30(nm)	0	<NONE>	<NONE>	<NONE>
573	AC001159	Homo sapiens (subclone 1_h9 from PAC H92) DNA sequence	5.00E-04	XYND_CELFI	ENDO-1,4-BETA-XYLANASE D PRECURSOR (EC 3.2.1.8)	7.3
574	Z60625	H.sapiens CpG DNA, clone 2c10, forward read cpg2c10.ft1aa .	4.00E-13	<NONE>	<NONE>	<NONE>
575	AF070640	Homo sapiens clone 24781	e-164	<NONE>	<NONE>	<NONE>



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		mRNA sequence				
576	Y11306	Homo sapiens mRNA for hTCF-4	2.00E-48	TCF1_HUMAN	T-CELL-SPECIFIC TRANSCRIPTION FACTOR 1 (TCF-1)	2.00E-15
577	X65279	pWE15 cosmid vector DNA	7.00E-69	OCLN_POTTR	Q28793 potorous tridactylus (potoroo). occludin. 11/98	0.71
578	M10296	Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.	0.001	LMB1_HYDAT	LAMININ BETA-1 CHAIN PRECURSOR (FRAGMENTS)	1.9
579	X53744	Canine mRNA for 68kDA subunit of signal recognition particle (SRP68)	e-162	SR68_CANFA	SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68)	5.00E-16
580	AF086438	Homo sapiens full length insert cDNA clone ZD80G11	2.00E-04	<NONE>	<NONE>	<NONE>
581	U15140	Mycobacterium bovis ribosomal proteins IF-1 complete cds, and S4 (rpsD) gene, partial cds	1.3	<NONE>	<NONE>	<NONE>
582	D13292	Human mRNA for ryudocan core protein	e-166	RSP4_ARATH	40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG)	1.4
583	S71022	neoplasm-related C140 product [human, thyroid carcinoma cells, mRNA, 670 nt]	9.00E-30	RL6_HUMAN	60S RIBOSOMAL PROTEIN L6 (TAX-RESPONSIVE ELEMENT BINDING PROTEIN 107) (TAXREB107)	5.6
584	L20934	Anopheles gambiae complete mitochondrial genome	0.014	<NONE>	<NONE>	<NONE>
585	Z49269	H.sapiens gene for chemokine HCC-1.	1.1	AMY1_DICTH	ALPHA-AMYLASE 1 (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	2.5

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
586	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-04	<NONE>	<NONE>	<NONE>
587	AF029893	Homo sapiens i-beta-1,3-N-acetylglucosaminyltransferase mRNA, complete cds	0.13	HEMO_PIG	HEMOPEXIN PRECURSOR (HYALURONIDASE) (EC 3.2.1.35)	3.5
588	J05109	T.thermophila calcium-binding 25 kDa (TCBP 25) protein gene, complete cds.	0.014	<NONE>	<NONE>	<NONE>
589	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-04	<NONE>	<NONE>	<NONE>
590	AF060246	Mus musculus strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	1.00E-83	SCRB_PEDPE	SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) (SUCRASE)	10
591	Y11966	B.aphidicola (host T.suberi) plasmid pBTs1 genes leuA, hspA, repA2, repA1, leuB, leuC, leuD, leuA	0.37	<NONE>	<NONE>	<NONE>
592	U20428	Human SNC19 mRNA sequence	1.00E-64	YY22_MYCTU	HYPOTHETICAL 30.8 KD PROTEIN CY49.22	0.29
593	AF043084	Lycopersicon esculentum ethylene receptor homolog (ETR1) mRNA, complete cds	0.37	KNIR_DROME	ZYGOTIC GAP PROTEIN KNIRPS	9.9
594	X65279	pWE15 cosmid vector DNA	5.00E-66	COA1_SV40	COAT PROTEIN VP1	0.001
595	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial	0.041	UL88_HSV7J	PROTEIN U59	5.8

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds				
596	M91452	Sus scrofa ryanodine receptor (RYP1) gene, complete cds.	3.2	<NONE>	<NONE>	<NONE>
597	U77327	Human Ki-1/57 intracellular antigen mRNA, partial cds	e-158	GAT1_CHICK	ERYTHROID TRANSCRIPTION FACTOR (GATA-1) (ERYF1)	1.2
598	U77327	Human Ki-1/57 intracellular antigen mRNA, partial cds	0	RPB7_ARATH	DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 5)	6.2
599	Y16964	Saccharomyces sp. mitochondrial DNA for OLI1 gene, strain CID1	0.37	NMD5_YEAST	NONSENSE-MEDIATED MRNA DECAY PROTEIN 5	1.9
600	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-06	<NONE>	<NONE>	<NONE>
601	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-08	<NONE>	<NONE>	<NONE>
602	AF091046	Brugia pahangi nuclear hormone receptor (bhr-1) gene, partial cds	1.1	INVO_PONPY	INVOLUCRIN	0.23
603	M87339	Human replication factor C, 37-kDa subunit mRNA, complete cds	0	AC12_HUMAN	ACTIVATOR 1 37 KD SUBUNIT (REPLICATION FACTOR C 37 KD SUBUNIT) (A1 37 KD SUBUNIT) (RF-C 37 KD SUBUNIT) (RFC37)	1.00E-38
604	D28116	Human genes for collagen type IV alpha 5 and 6, exon 1 and exon	0.39	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		1'				
605	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	<NONE>	<NONE>	<NONE>
606	AE001149	Borrelia burgdorferi (section 35 of 70) of the complete genome	0.13	<NONE>	<NONE>	<NONE>
607	X14168	Human pLC46 with DNA replication origin	6.00E-16	Z136_HUMAN	ZINC FINGER PROTEIN 136	0.31
608	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.r1a .	7.00E-90	HN3B_RAT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-19
609	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.043	PGCV_MOUSE	VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (PG-M)	3.5
610	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	7.00E-07	CA11_CHICK	PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR	0.4
611	AB007956	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487	e-106	RRPB_CVMA5	RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B)	9.7
612	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
613	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-05	UL52_EBV	HELICASE/PRIMASE COMPLEX PROTEIN (PROBABLE DNA REPLICATION PROTEIN BSLF1)	5.9
614	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	3.00E-71	POLG_PVYHU	GENOME POLYPROTEIN (CONTAINS: N-TERMINAL PROTEIN; HELPER COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); 42-50 KD PROTEIN; CYTOPLASMIC INCLUSION PROTEIN (CI); 6 KD PROTEIN; NUCLEAR INCLUSION PROTEIN A (NI- A) (EC 3.4.22.-) (49K PROTEINASE) (49	4.3
615	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-09	VP3_ROTPO	INNER CORE PROTEIN VP3	7.7
616	J05499	Rattus norvegicus L-glutamine amidohydrolase mRNA, complete cds	e-143	GLSL_RAT	GLUTAMINASE, LIVER ISOFORM PRECURSOR (EC 3.5.1.2) (GLS)	7.00E-67
617	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.37	Y642_METJA	HYPOTHETICAL PROTEIN MJ0642	5.8
618	M21191	Human aldolase pseudogene mRNA, complete cds.	1.00E-32	LIN1_NYCCO	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	6.00E-17
619	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	NUCM_BOVIN	NADH-UBIQUINONE OXIDOREDUCTASE 49 KD SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-49KD) (CI-49KD)	0.044

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
620	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.005	HEMZ_RHOCA	FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE)	4.4
621	AF041428	Homo sapiens ribosomal protein s4 X isoform gene, complete cds	0.002	<NONE>	<NONE>	<NONE>
622	X07158	Chironomus thummi DNA for Cla repetitive element	0.13	<NONE>	<NONE>	<NONE>
623	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-04	<NONE>	<NONE>	<NONE>
624	AF100470	Rattus norvegicus ribosome attached membrane protein 4 (RAMP4) mRNA, complete cds	1.00E-53	<NONE>	<NONE>	<NONE>
625	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds	2.00E-38	<NONE>	<NONE>	<NONE>
626	M13452	Human lamin A mRNA, 3'end.	6.00E-16	<NONE>	<NONE>	<NONE>
627	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.014	ACDV_RAT	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD)	4.00E-20
628	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
629	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
630	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
631	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
632	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-05	YS83_CAEEL	HYPOTHETICAL 86.9 KD PROTEIN ZK945.3 IN CHROMOSOME II	0.65
633	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	NRP_MOUSE	NEUROPILIN PRECURSOR (A5 PROTEIN)	2.7
634	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-05	Y4JN_RHISN	HYPOTHETICAL 16.3 KD PROTEIN Y4JN	5.9
635	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-05	<NONE>	<NONE>	<NONE>
636	X64707	H.sapiens BBC1 mRNA	e-179	RL13_HUMAN	60S RIBOSOMAL PROTEIN L13 (BREAST BASIC CONSERVED PROTEIN 1)	5.00E-40
637	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-08	<NONE>	<NONE>	<NONE>
638	X14168	Human pLC46 with DNA replication origin	5.00E-14	SP3_HUMAN	TRANSCRIPTION FACTOR SP3 (SPR-2) (FRAGMENT)	0.19
639	X90999	H.sapiens mRNA for Glyoxalase II	9.00E-20	GLO2_HUMAN	HYDROXYACYLG LUTATHIONE HYDROLASE (EC 3.1.2.6)	0.007
640	AF083322	Homo sapiens centriole associated protein CEP110 mRNA, complete cds	9.00E-51	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	0.005

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
641	Z12002	M.musculus Pvt-1 mRNA.	0.36	CP5F_CANTR	CYTOCHROME P450 LIA6 (ALKANE-INDUCIBLE) (EC 1.14.14.1) (P450-ALK3)	5.6
642	M10206	R.sphaeroides reaction center L subunit (complete cds) and M subunit (5' end) genes.	1.1	YGR1_YEAST	HYPOTHETICAL 34.8 KD PROTEIN IN SUT1-RCK1 INTERGENIC REGION	0.006
643	K02668	E. coli ddl gene encoding D-alanine:D-alanine ligase and ftsQ and ftsA genes, complete cds, and ftsZ gene, 5' end.	3.3	ANKB_HUMAN	ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID)	7.00E-07
644	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
645	X53616	C.domesticus calnexin (pp90) mRNA	1.1	<NONE>	<NONE>	<NONE>
646	X57010	Human COL2A1 gene for collagen II alpha 1 chain, exons E2-E15	3.3	PRIO_PIG	MAJOR PRION PROTEIN PRECURSOR (PRP)	1.9
647	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	1.1	UL07_HSV2H	PROTEIN UL7	7.3
648	X52956	Human CAMII-psi3 calmodulin retropseudogene	0.37	PRTP_EBV	PROBABLE PROCESSING AND TRANSPORT PROTEIN	7.5
649	M93425	Human protein tyrosine phosphatase (PTP-PEST) mRNA, complete cds.	0	PTNC_HUMAN	PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1)	e-107
650	L47615	Mus musculus DNA-binding protein (Fli-1) gene, 5' end of cds.	0.13	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	2.00E-07
651	U60337	Homo sapiens beta-mannosidase mRNA, complete	0	GIL1_ENTHI	GALACTOSE-INHIBITABLE LECTIN 170 KD	0.22



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		cds			SUBUNIT	
652	U08813	Oryctolagus cuniculus Na <sup>+</sup> /glucose cotransporter-related protein mRNA, complete cds.	1.00E-22	NAG1_HUMAN	SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER)	0.1
653	Y00282	Human mRNA for ribophorin II	2.00E-78	RIB2_HUMAN	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 63 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (RIBOPHORIN II)	5.00E-19
654	D10051	Human gene for 92-kDa type IV collagenase, 5'-flanking region	0.014	TAGB_DICDI	PRESTALK-SPECIFIC PROTEIN TAGB PRECURSOR (EC 3.4.21.-)	7.6
655	M29930	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17.	8.00E-08	<NONE>	<NONE>	<NONE>
656	U78310	Homo sapiens pescadillo mRNA, complete cds	0	YG2S_YEAST	HYPOTHETICAL 69.9 KD PROTEIN IN MIC1-SRB5 INTERGENIC REGION	0.002
657	X68792	S.coelicolor A3(2) promoter sequence pth270	3.2	YBS0_YEAST	HYPOTHETICAL 27.0 KD PROTEIN IN VAL1-HSP26 INTERGENIC REGION	0.073
658	U50535	Human BRCA2 region, mRNA sequence CG006	4.00E-12	ALU1_HUMAN	!!!! ALU SUBFAMILY J WARNING ENTRY !!!!	1.2

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
659	U15522	Sus scrofa clone pvg1a Ig heavy chain variable VDJ region mRNA, partial cds.	3.2	Z165_HUMAN	ZINC FINGER PROTEIN 165	3.2
660	M20918	C.thummi piger haemoglobin (Hb) gene DNA, complete cds.	0.12	YT25_CAEEL	HYPOTHETICAL 59.9 KD PROTEIN B0304.5 IN CHROMOSOME II	0.033
661	U60337	Homo sapiens beta-mannosidase mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
662	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.001	ENV_MLVFP	ENV POLYPROTEIN PRECURSOR (CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN)	3.3
663	M97287	Human MAR/SAR DNA binding protein (SATB1) mRNA, complete cds. > :: gb 158691 158691 Sequence 1 from patent US 5652340	0	SAT1_HUMAN	DNA-BINDING PROTEIN SATB1 (SPECIAL AT-RICH SEQUENCE BINDING PROTEIN 1)	2.00E-20
664	L42612	Homo sapiens keratin 6 isoform K6f (KRT6F) mRNA, complete cds	e-168	K2C4_BOVIN	KERATIN, TYPE II CYTOSKELETAL 59 KD, COMPONENT IV	4.00E-10
665	U17901	Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.	e-152	PLAP_MOUSE	PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP)	4.00E-13
666	M73047	Homo sapiens tripeptidyl peptidase II mRNA, complete cds.	0	MERT_STRLI	MERCURIC TRANSPORT PROTEIN (MERCURY ION TRANSPORT PROTEIN)	4.4

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
667	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	0	RL9_HUMAN	60S RIBOSOMAL PROTEIN L9	2.00E-11
668	X98330	H.sapiens mRNA for ryanodine receptor 2	1.1	HS74_MOUSE	HEAT SHOCK 70 KD PROTEIN AGP-2	0.034
669	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.002	RPC2_DROME	DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE	1.1
670	AF069250	Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds	7.00E-80	LEGB_PEA	LEGUMIN B (FRAGMENT)	0.011
671	Z71419	S.cerevisiae chromosome XIV reading frame ORF YNL143c	1.1	FOCD_ECOLI	OUTER MEMBRANE USHER PROTEIN FOCD PRECURSOR	9.7
672	AF044965	Homo sapiens polio virus related protein 2 gene, alpha isoform, exon 6 and partial cds	e-167	PVR_MOUSE	POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR	1.00E-12
673	X65319	Cloning vector pCAT-Enhancer	2.00E-80	S106_HUMAN	CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) CALCIUM-BINDING PROTEIN A6)	3.00E-15
674	D29655	Pig mRNA for UMP-CMP kinase, complete cds	e-103	V319_ASFB7	J319 PROTEIN	4.3
675	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	VEGR_RAT	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 PRECURSOR RECEPTOR FLT) (FLT-1)	3.3

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
676	D90217	S. cerevisiae gene for YmL33, mitochondrial ribosomal proteins of large subunit	2.00E-07	MALY_ECOLI	MALY PROTEIN (EC 2.6.1.-)	5.6
677	AF038952	Homo sapiens cofactor A protein mRNA, complete cds	e-160	T1CA_MOUSE	TCPI-CHAPERONIN COFACTOR A	4.00E-19
678	Z96950	Gorilla gorilla DNA sequence orthologous to the human Xp:Yp telomere-junction region	5.00E-14	YHBZ_ECOLI	HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION (F390)	3.3
679	D50418	Mouse mRNA for AREC3, partial cds	2.00E-79	CYGX_RAT	OLFACTORY GUANYLYL CYCLASE GC-D PRECURSOR (EC 4.6.1.2)	1.1
680	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	8.00E-08	P2C2_SCHPO	PROTEIN PHOSPHATASE 2C HOMOLOG 2 (EC 3.1.3.16)	1.00E-04
681	AL010280	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-106, complete sequence	0.12	<NONE>	<NONE>	<NONE>
682	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	5.00E-04	VSM2_TRYBB	VARIANT SURFACE GLYCOPROTEIN MITAT 1.2 PRECURSOR (VSG 221)	4.3
683	U00238	Homo sapiens glutamine PRPP amidotransferase (GPAT) mRNA, complete cds	0	<NONE>	<NONE>	<NONE>
684	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.005	PRPR_SALTY	PROPIONATE CATABOLISM OPERON REGULATORY PROTEIN	1.5

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
685	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-07	YAND_SCHPO	HYPOTHETICAL 30.4 KD PROTEIN C3H1.13 IN CHROMOSOME I	0.38
686	D25538	Human mRNA for KIAA0037 gene, complete cds	0	<NONE>	<NONE>	<NONE>
687	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	A1AA_RAT	ALPHA-1A ADRENERGIC RECEPTOR (RA42)	4.4
688	L26956	Mesocricetus auratus stearyl-CoA desaturase sequence including male hormone dependent gene derived from hamster frankorgan	4.00E-33	<NONE>	<NONE>	<NONE>
689	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
690	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	YO93_CAEEL	HYPOTHETICAL 58.5 KD PROTEIN T20B12.3 IN CHROMOSOME III	2.00E-08
691	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	8.00E-09	<NONE>	<NONE>	<NONE>
692	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_RABIT	OXYSTEROL-BINDING PROTEIN	1.00E-34
693	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-04	UFO2_MAIZE	FLAVONOL 3-O-GLUCOSYLTRANSFERASE (EC 2.4.1.91)	3.1

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
694	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	5.00E-04	<NONE>	<NONE>	<NONE>
695	U34954	Caenorhabditis elegans cyclophilin isoform 10	5.00E-24	CYPA_CAEEL	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 10 (EC 5.2.1.8)	2.00E-29
696	AB011167	Homo sapiens mRNA for KIAA0595 protein, partial cds	0	RFX5_HUMAN	BINDING REGULATORY FACTOR	2.1
697	U03886	Human GS2 mRNA, complete cds.	2.00E-28	SKD1_MOUSE	SKD1 PROTEIN	4.00E-17
698	AF086275	Homo sapiens full length insert cDNA clone ZD45C02	3.00E-41	SPT7_YEAST	TRANSCRIPTIONAL ACTIVATOR SPT7	0.82
699	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	CA1E_HUMAN	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR	1.1
700	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-11	E434_ADECC	Q65962 canine adenovirus type 1 (strain cll). early e4 31 kd protein. 11/98	4.4
701	L17340	Drosophila melanogaster germline transcription factor gene, complete cds.	3.3	CISY_TETTH	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7) (14 NM FILAMENT-FORMING PROTEIN)	9.7
702	X58170	M.musculus mRNA for t-Complex Tcp-10a gene	2.00E-45	PME2_LYCES	PECTINESTERASE 2 PRECURSOR (EC 3.1.1.11) (PECTIN METHYLESTERASE) (PE 2)	7.4
703	Z96207	H.sapiens telomeric DNA sequence, clone 12PTEL049, read 12PTELOO049.se	8.00E-08	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		q				
704	X58430	Human Hox1.8 gene	e-146	HXAA_HUMAN	HOMEODOMAIN PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL)	4.00E-05
705	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	6.00E-06	YN39_SYNP7	HYPOTHETICAL 9.2 KD PROTEIN IN CYST-CYSR INTERGENIC REGION (ORF 81)	0.89
706	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	MYSH_BOVIN	MYOSIN I HEAVY CHAIN-LIKE PROTEIN (MIHC) (BRUSH BORDER MYOSIN I) (BBMI)	0.001
707	M19961	Human cytochrome c oxidase subunit Vb (coxVb) mRNA, complete cds.	e-123	OTHU5B	<NONE>	3.00E-30
708	X68380	M.musculus gene for cathepsin D, exon 3	5.00E-04	42_MOUSE	ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN)	9.9
709	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	1.00E-11	TCPA_DROME	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)	4.3
710	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-10	<NONE>	<NONE>	<NONE>
711	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	4.00E-12	<NONE>	<NONE>	<NONE>
712	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
713	AB018323	Homo sapiens mRNA for KIAA0780 protein, partial cds	3.00E-41	LBR_CHICK	LAMIN B RECEPTOR	3.4
714	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	6.00E-06	YM8L_YEAST	HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION	3.00E-08
715	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	4.00E-13	PSC_DROME	POSTERIOR SEX COMBS PROTEIN	0.6
716	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	7.00E-07	IRKX_RAT	INWARD RECTIFIER POTASSIUM CHANNEL BIR9 (KIR5.1)	5.4
717	AC001038	Homo sapiens (subclone 2_h2 from P1 H49) DNA sequence	8.00E-09	MGMT_YEAST	METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE	0.48
718	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-11	YWDE_BACSU	HYPOTHETICAL 19.9 KD PROTEIN IN SACA-UNG INTERGENIC REGION PRECURSOR	1.8
719	U01139	Mus musculus B6D2F1 clone 2C11B mRNA.	e-110	GSC_DROME	HOMEBOX PROTEIN GOOSECOID	7.2
720	AB017430	Homo sapiens mRNA for kinesin-like DNA binding protein, complete cds	0	YBAV_ECOLI	HYPOTHETICAL 12.7 KD PROTEIN IN HUPB-COF INTERGENIC REGION	0.17
721	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.001	CPCF_SYNP2	PHYCOCYANOBILIN LYASE BETA SUBUNIT (EC 4.1.1.1)	2.4
722	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-10	<NONE>	<NONE>	<NONE>



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
723	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.04	YKK7_CAEEL	HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III	0.057
724	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	8.00E-08	H5_CAIMO	HISTONE H5	0.39
725	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	3.00E-09	DED1_YEAST	PUTATIVE ATP-DEPENDENT RNA HELICASE DED1	0.5
726	J04617	Human elongation factor EF-1-alpha gene, complete cds. > :: dbj E02629 E02629 DNA of human polypeptide chain elongation factor-1 alpha	5.00E-36	ALU7_HUMAN	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	0.84
727	X54859	Porcine TNF-alpha and TNF-beta genes for tumour necrosis factors alpha and beta, respectively.	3.3	Z165_HUMAN	ZINC FINGER PROTEIN 165	5.6
728	D49911	Thermus thermophilus UvrA gene, complete cds	0.014	CC48_CAPAN	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG	9.9
729	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-06	CA25_HUMAN	PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR	0.011
730	D15057	Human mRNA for DAD-1, complete cds	0	DAD1_HUMAN	DEFENDER AGAINST CELL DEATH 1 (DAD-1)	8.00E-16
731	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	6.00E-06	ANFD_RHOCA	NITROGENASE IRON-IRON PROTEIN ALPHA CHAIN (EC 1.18.6.1) (NITROGENASE COMPONENT 1) (DINITROGENASE	9.6

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					)	
732	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	7.00E-07	EFTU_CHLVI	ELONGATION FACTOR TU (EF-TU)	2.5
733	AB018335	Homo sapiens mRNA for KIAA0792 protein, complete cds	0	TRYM_RAT	MAST CELL TRYPTASE PRECURSOR (EC 3.4.21.59)	5.6
734	X98743	H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein)	0.04	<NONE>	<NONE>	<NONE>
735	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	2.00E-07	<NONE>	<NONE>	<NONE>
736	Z49314	S.cerevisiae chromosome X reading frame ORF YJL039c	3.2	<NONE>	<NONE>	<NONE>
737	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	0	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	2.00E-76
738	J04038	Human glyceraldehyde-3-phosphate dehydrogenase	2.00E-47	SDC1_HUMAN	SYNDECAN-1 PRECURSOR (SYND1) (CD138)	3.5
739	AF010238	Homo sapiens von Hippel-Lindau tumor suppressor	1.00E-09	LIN1_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.001
740	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	YQJX_BACSU	HYPOTHETICAL 13.2 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION	9.9

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
741	L21186	Human lysyl oxidase-like protein mRNA, complete cds.	e-145	OXRTL	<NONE>	1.00E-34
742	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-05	CC48_SOYBN	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP)	7.6
743	AF009203	Homo sapiens YAC clone 377A1 unknown mRNA, 3'untranslated region	3.3	<NONE>	<NONE>	<NONE>
744	Z74894	S.cerevisiae chromosome XV reading frame ORF YOL152w	0.12	CD14_RABIT	Q28680 oryctolagus cuniculus (rabbit). monocyte differentiation antigen cd14 precursor. 11/98	1.9
745	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	9.00E-10	KIN3_YEAST	SERINE/THREONINE-PROTEIN KINASE KIN3 (EC 2.7.1.-)	2.5
746	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-05	YA53_SCHPO	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I	7.00E-17
747	S61044	ALDH3=aldehyde dehydrogenase isozyme 3 [human, stomach, mRNA Partial, 1362 nt]	0	DHAP_HUMAN	ALDEHYDE DEHYDROGENASE, DIMERIC NADP-PREFERRING (EC 1.2.1.5) (CLASS 3)	2.00E-71
748	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	2.00E-08	CA1E_CHICK	COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN)	0.36
749	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
750	L14815	Entamoeba histolytica HM-1:IMSS galactose-specific adhesin 170kD subunit (hgl3) gene, complete cds.	0.12	<NONE>	<NONE>	<NONE>
751	X63785	T.thermophila gene for snRNA U2-2	1.1	<NONE>	<NONE>	<NONE>
752	M83756	Mytilus edulis mitochondrial NADH dehydrogenase subunit 5 (ND5) gene, 3' end; NADH dehydrogenase subunit 6 (ND6) gene, complete cds; and cytochrome b (cyt b), 5' end.	0.042	DSC1_HUMAN	DESMOCOLLIN 1A/1B PRECURSOR (DESMOSOMAL GLYCOPROTEIN 2/3) (DG2 / DG3)	2.6
753	AB001066	Brown trout microsatellite DNA sequence	0.38	IMB3_HUMAN	IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT)	1.2
754	AF064787	Lotus japonicus rac GTPase activating protein 1 mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
755	U20608	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds	0.043	<NONE>	<NONE>	<NONE>
756	M77812	Rabbit myosin heavy chain mRNA, complete cds.	1.2	RBL1_HUMAN	RETINOBLASTOM A-LIKE PROTEIN 1 (107 KD RETINOBLASTOM A-ASSOCIATED PROTEIN) (PRB1) (P107)	4.9

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
757	X63789	T.thermophila genes for snRNA U5-1, snRNA U5-2	0.058	<NONE>	<NONE>	<NONE>
758	D50646	Mouse mRNA for SDF2, complete cds	2.00E-27	PMT3_YEAST	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 3 (EC 2.4.1.109)	0.002
759	L81583	Homo sapiens (subclone 3_g2 from P1 H11) DNA sequence	3.00E-19	ALU5_HUMAN	!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!	0.86
760	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	SYFA_YEAST	PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN CYTOPLASMIC	5.7
761	AF000370	Homo sapiens polymorphic CA dinucleotide repeat flanking region	6.00E-89	APP1_MOUSE	AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP)	5.7
762	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.002	<NONE>	<NONE>	<NONE>
763	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	7.00E-06	PSF_HUMAN	PTB-ASSOCIATED SPLICING FACTOR (PSF)	0.72
764	AB018288	Homo sapiens mRNA for KIAA0745 protein, partial cds	0	TC2A_CAEBR	TRANSPOSABLE ELEMENT TCB2 TRANSPOSASE	1.5
765	AF020282	Dictyostelium discoideum DG2033 gene, partial cds	0.38	PMT2_YEAST	DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC 2.4.1.109)	0.18

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
766	AF017357	Oryza sativa low molecular early light-inducible protein mRNA, complete cds	0.38	RGS3_HUMAN	REGULATOR OF G-PROTEIN SIGNALLING 3 (RGS3) (RGP3)	0.23
767	U67599	Methanococcus jannaschii section 141 of 150 of the complete genome	0.13	<NONE>	<NONE>	<NONE>
768	X74178	B.taurus microsatellite DNA INRA153	0.13	FAG1_SYNY3	P73574 synechocystis sp. (strain pcc 6803). 3-oxoacyl-[acyl-carrier protein] reductase 1 (ec 1.1.1.100) (3-ketoacyl- acyl carrier protein reductase 1). 11/98	5.00E-16
769	AF041858	Mus musculus synaptojanin 2 isoform delta mRNA, partial cds	0.043	CA44_HUMAN	COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR	0.24
770	J01404	Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A6l, 2 and 3.	0.021	NU1M_CITLA	NADH-UBIQUINONE OXIDOREDUCTAS E CHAIN 1 (EC 1.6.5.3)	7.2
771	AL022317	Human DNA sequence from clone 140L1 on chromosome 22q13.1-13.31, complete sequence [Homo sapiens]	3.00E-41	ALU7_HUMAN	!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	4.00E-08
772	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.00E-09	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
773	AF095927	Rattus norvegicus protein phosphatase 2C mRNA, complete cds	0	P2C_PARTE	PROTEIN PHOSPHATASE 2C (EC 3.1.3.16) (PP2C)	1.00E-16
774	X87212	H.sapiens mRNA for cathepsin C	0	CATC_HUMAN	DIPEPTIDYL-PEPTIDASE I PRECURSOR (EC 3.4.14.1)	2.00E-46
775	X05283	Drosophila melanogaster PKCG7 gene exons 7-14 for protein kinase C	4.5	<NONE>	<NONE>	<NONE>
776	X03558	Human mRNA for elongation factor 1 alpha subunit	0	EF11_HUMAN	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	1.00E-83
777	X06960	Aspergillus nidulans mitochondrial DNA for cytochrome oxidase subunit 3, tRNA-Tyr	0.23	<NONE>	<NONE>	<NONE>
778	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	3.00E-09	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	5.00E-07
779	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-07	NAT1_YEAST	N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88)	5.00E-23
780	U59706	Gallus gallus alternatively spliced AMPA glutamate receptor, isoform GluR2 flop, (GluR2) mRNA, partial cds.	0.014	PPOL_SARPE	POLY (ADP-RIBOSE) POLYMERASE (EC 2.4.2.30) (PARP)	0.021
781	U57391	Rattus norvegicus FceRI gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds	1.00E-84	<NONE>	<NONE>	<NONE>

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
782	AB014591	Homo sapiens mRNA for KIAA0691 protein, complete cds	7.00E-57	SSGP_VOLCA	SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	5.3
783	AJ008065	Chrysolina bankii 16S rRNA gene, mitotype B2	0.043	<NONE>	<NONE>	<NONE>
784	AF067212	Caenorhabditis elegans cosmid F37F2	0.005	MEK1_RAT	MAPK/ERK KINASE KINASE 1 (EC 2.7.1.-) (MEK KINASE 1)	4.5
785	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.042	<NONE>	<NONE>	<NONE>
786	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	9.00E-09	<NONE>	<NONE>	<NONE>
787	Y13401	Homo sapiens CD3 delta gene, enhancer sequence	8.00E-08	<NONE>	<NONE>	<NONE>
788	AE001038	Archaeoglobus fulgidus section 69 of 172 of the complete genome	0.13	<NONE>	<NONE>	<NONE>
789	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	2.00E-06	<NONE>	<NONE>	<NONE>
790	AF041463	Manihot esculenta elongation factor 1-alpha	1.4	<NONE>	<NONE>	<NONE>
791	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.002	HXA3_HAEIN	HEME:HEMOPEXIN-BINDING PROTEIN PRECURSOR	2.7
792	Z12112	pWE15A cosmid vector DNA	3.00E-29	PKWA_THECU	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-)	2.00E-04



Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
793	U85193	Human nuclear factor I-B2 (NFIB2) mRNA, complete cds	4.00E-44	<NONE>	<NONE>	<NONE>
794	U89331	Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds	7.00E-06	NRL_HUMAN	NEURAL RETINA-SPECIFIC LEUCINE ZIPPER PROTEIN (NRL)	6.3
795	AF055666	Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds	0.52	PSPD_BOVIN	PULMONARY SURFACTANT-ASSOCIATED PROTEIN D PRECURSOR	0.33
796	L13321	Homo sapiens iduronate-2-sulfatase (IDS) gene, exon 1, incomplete 5' end.	0.14	YRP2_YEAST	HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION	0.27
797	AL010270	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-96, complete sequence	0.37	YTH3_CAEEL	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II	2
798	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.015	IMB3_HUMAN	IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT)	0.063
799	U70139	Mus musculus putative CCR4 protein mRNA, partial cds	0	CCR4_YEAST	GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (CARBON CATABOLITE REPRESSOR PROTEIN 4)	5.00E-11
800	L26507	Mouse myocyte nuclear factor (MNF) mRNA, complete cds.	3.00E-41	MNF_MOUSE	MYOCYTE NUCLEAR FACTOR (MNF)	4.00E-18

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
801	U20527	Mus musculus chemokine KC gene, 5' region.	0	GRO_MOUSE	GROWTH REGULATED PROTEIN PRECURSOR (PLATELET-DERIVED GROWTH FACTOR-INDUCIBLE PROTEIN KC) (SECRETORY PROTEIN N51)	1.00E-28
802	AF065482	Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds	0	MYSA_DROME	MYOSIN HEAVY CHAIN, MUSCLE	0.089
803	U05823	Mus musculus pericentrin mRNA, complete cds.	1.00E-94	M84D_DROME	MALE SPECIFIC SPERM PROTEIN MST84DD	0.099
804	U67468	Methanococcus jannaschii section 10 of 150 of the complete genome	0.4	<NONE>	<NONE>	<NONE>
805	U14178	Human type II IL-1 receptor gene, exon 1B	1.00E-19	AMPH_HUMAN	AMPHIPHYSIN	2.9
806	L40411	Homo sapiens thyroid receptor interactor	0	TRI8_HUMAN	THYROID RECEPTOR INTERACTING PROTEIN 8 (TRIP8)	4.00E-86
807	D17218	Human HepG2 3' region Mbol cDNA, clone hmd3g02m3	e-136	CA1A_HUMAN	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR	3.00E-04
808	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rt1a.	e-102	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-24
809	D14678	Human mRNA for kinesin-related protein, partial cds	0	NCD_DROME	CLARET SEGREGATIONAL PROTEIN	1.00E-70

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
810	X56317	Xiphophorus maculatus Xmrk(proto-oncogene) gene for receptor tyrosine kinase.	0.49	WN1B_MOUSE	WNT-10B PROTEIN PRECURSOR (WNT-12)	7.2
811	M36200	Human synaptobrevin 1 (SYB1) gene, exon 5.	0.2	VE2_HPV14	REGULATORY PROTEIN E2	3.1
812	M18157	Human glandular kallikrein gene, complete cds.	1.5	EKLF_MOUSE	ERYTHROID KRUEPPEL-LIKE TRANSCRIPTION FACTOR (EKLF)	1.1
813	D25215	Human mRNA for KIAA0032 gene, complete cds	1.9	YXIS_SACER	HYPOTHETICAL 28.9 KD PROTEIN IN XIS 5'REGION (ORF1)	1.3
814	M96628	Human gene sequence, 5' end.	2.00E-06	AGRI_DISOM	AGRIN (FRAGMENT)	9.5
815	Z57610	H.sapiens CpG DNA, clone 187a10, reverse read cpg187a10.rtl1a.	e-102	HN3B_MOUSE	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)	1.00E-19
816	X14168	Human pLC46 with DNA replication origin	5.00E-16	ZN44_HUMAN	ZINC FINGER PROTEIN 44 (ZINC FINGER PROTEIN KOX7)	1.6
817	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.28	LMA_DROME	LAMININ ALPHA CHAIN PRECURSOR	4.7
818	AF058055	Mus musculus monocarboxylate transporter 1	0.2	<NONE>	<NONE>	<NONE>
819	AB014570	Homo sapiens mRNA for KIAA0670 protein, partial cds	0.16	YGR1_YEAST	HYPOTHETICAL 34.8 KD PROTEIN IN SUT1-RCK1 INTERGENIC REGION	4.00E-06
820	M19262	Rat clathrin light chain (LCB3) mRNA, complete cds.	0.27	LMA_DROME	LAMININ ALPHA CHAIN PRECURSOR	4.5

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
821	Z54367	H.sapiens gene for plectin	0.29	YO93_CAEEL	HYPOTHETICAL 58.5 KD PROTEIN T20B12.3 IN CHROMOSOME III	1.00E-14
822	AB017026	Mus musculus mRNA for oxysterol-binding protein, complete cds	0	OXYB_HUMAN	OXYSTEROL-BINDING PROTEIN	2.00E-49
823	X58170	M.musculus mRNA for t-Complex Tcp-10a gene	1.00E-20	UL52_HSV11	DNA HELICASE/PRIMASE COMPLEX PROTEIN (DNA REPLICATION PROTEIN UL52)	5.3
824	X58430	Human Hox1.8 gene	0	HXAA_HUMAN	HOMEODOMAIN PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL)	1.00E-44
825	X53754	Porcine sarcoplasmic/endoplasmic-reticulum Ca(2+) pump gene 2 3'-end region	1.3	<NONE>	<NONE>	<NONE>
826	AB005786	Arabidopsis thaliana tRNA-Glu gene	0.46	<NONE>	<NONE>	<NONE>
827	AB012130	Homo sapiens SBC2 mRNA for sodium bicarbonate cotransporter2, complete cds	1.9	<NONE>	<NONE>	<NONE>
828	AB017430	Homo sapiens mRNA for kinesin-like DNA binding protein, complete cds	0	YBAV_ECOLI	HYPOTHETICAL 12.7 KD PROTEIN IN HUPB-COF INTERGENIC REGION	0.063
829	AB007886	Homo sapiens KIAA0426 mRNA, complete cds	0.042	YDF3_SCHPO	PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03	0.52
830	AB018335	Homo sapiens mRNA for KIAA0792 protein, complete cds	e-172	UROT_BOVIN	TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (EC 3.4.21.68)	0.86

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
831	D12646	Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds	0	KIF4_MOUSE	KINESIN-LIKE PROTEIN KIF4	9.00E-96
832	U38376	Rattus norvegicus cytosolic phospholipase A2 mRNA, complete cds	0.048	<NONE>	<NONE>	<NONE>
833	L40411	Homo sapiens thyroid receptor interactor	0	TRI8_HUMAN	THYROID RECEPTOR INTERACTING PROTEIN 8 (TRIP8)	4.00E-86
834	U08110	Mus musculus RNA1 homolog (Fug1) mRNA, complete cds.	8.00E-04	YNW7_YEAST	HYPOTHETICAL 68.8 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION	0.02
835	D50646	Mouse mRNA for SDF2, complete cds	1.00E-40	YB64_YEAST	HYPOTHETICAL 57.2 KD PROTEIN IN MET8-HPC2 INTERGENIC REGION	4.9
836	D50646	Mouse mRNA for SDF2, complete cds	1.00E-40	YB64_YEAST	HYPOTHETICAL 57.2 KD PROTEIN IN MET8-HPC2 INTERGENIC REGION	4.9
837	U67459	Methanococcus jannaschii section 1 of 150 of the complete genome	5.00E-05	GCS1_HUMAN	MANNOSYL-OLIGOSACCHARIDE GLUCOSIDASE (EC 3.2.1.106)	9.2
838	U18657	Haemophilus influenzae LeuA (leuA) gene, partial cds, DprA (dprA+), orf272 and orf193 genes, complete cds, and PfkA (pfkA) gene, partial cds.	0.01	STE6_YEAST	MATING FACTOR A SECRETION PROTEIN STE6 (MULTIPLE DRUG RESISTANCE PROTEIN HOMOLOG) (P-GLYCOPROTEIN)	7

Table 2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
839	U12523	Rattus norvegicus ultraviolet B radiation-activated UV98 mRNA, partial sequence.	1.00E-10	YMT8_YEAST	HYPOTHETICAL 36.4 KD PROTEIN IN NUP116-FAR3 INTERGENIC REGION	2.00E-06
840	D78255	Mouse mRNA for PAP-1, complete cds	e-175	<NONE>	<NONE>	<NONE>
841	D17263	Human HepG2 3' region MboI cDNA, clone hmd5f07m3	1.00E-58	<NONE>	<NONE>	<NONE>
842	AF006751	Homo sapiens ES/130 mRNA, complete cds	0.061	YRP2_YEAST	HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3'REGION	2.00E-07
843	U67459	Methanococcus jannaschii section 1 of 150 of the complete genome	6.00E-05	YC14_METJA	HYPOTHETICAL PROTEIN MJ1214	8.1
844	D88689	Mus musculus mRNA for flt-1, complete cds	0.084	ICP0_HSV2H	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (VMW118 PROTEIN)	0.014

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001340B:A06	17062	3	0	0	0	0	0
M00001340D:F10	11589	2	2	1	3	3	8
M00001341A:E12	4443	10	6	2	6	3	11
M00001342B:E06	39805	2	0	0	0	1	0
M00001343C:F10	2790	7	15	13	14	6	0
M00001343D:H07	23255	3	0	1	1	0	0
M00001345A:E01	6420	8	0	2	0	1	0
M00001346A:F09	5007	4	8	3	6	2	6
M00001346D:E03	6806	5	2	1	2	0	3
M00001346D:G06	5779	5	4	3	4	0	0
M00001346D:G06	5779	5	4	3	4	0	0
M00001347A:B10	13576	5	0	0	0	12	11
M00001348B:B04	16927	4	0	0	2	0	0
M00001348B:G06	16985	4	0	0	0	0	0
M00001349B:B08	3584	5	11	5	0	0	2
M00001350A:H01	7187	5	3	1	0	1	0
M00001351B:A08	3162	10	14	1	6	6	5
M00001351B:A08	3162	10	14	1	6	6	5
M00001352A:E02	16245	4	0	0	0	0	0
M00001353A:G12	8078	4	3	1	0	1	0
M00001353D:D10	14929	4	0	0	1	23	16
M00001355B:G10	14391	3	1	0	0	0	0
M00001357D:D11	4059	8	6	8	16	0	1
M00001361A:A05	4141	5	2	10	16	4	27
M00001361D:F08	2379	26	13	4	2	2	3
M00001362B:D10	5622	7	4	2	13	1	2
M00001362C:H11	945	9	21	2	1	0	0
M00001365C:C10	40132	2	0	0	0	3	0
M00001370A:C09	6867	7	3	0	0	0	0
M00001371C:E09	7172	3	5	1	2	0	1
M00001376B:G06	17732	1	3	5	0	1	4
M00001378B:B02	39833	2	0	0	0	0	0
M00001379A:A05	1334	27	38	35	28	3	0
M00001380D:B09	39886	2	0	0	0	0	0
M00001382C:A02	22979	2	1	0	0	0	0
M00001383A:C03	39648	2	0	0	0	0	0
M00001383A:C03	39648	2	0	0	0	0	0
M00001386C:B12	5178	5	5	4	2	5	2
M00001387A:C05	2464	5	19	25	16	1	0
M00001387B:G03	7587	6	2	1	0	0	0
M00001388D:G05	5832	10	3	0	1	5	0
M00001389A:C08	16269	3	0	0	0	1	1
M00001394A:F01	6583	2	7	3	2	0	0
M00001395A:C03	4016	5	14	0	6	0	0
M00001396A:C03	4009	6	4	13	5	4	10
M00001402A:E08	39563	2	0	0	0	0	0

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001407B:D11	5556	8	1	5	0	2	0
M00001409C:D12	9577	5	2	0	1	11	12
M00001410A:D07	7005	8	2	0	0	0	0
M00001412B:B10	8551	4	4	0	3	0	0
M00001415A:H06	13538	5	0	0	0	9	1
M00001416A:H01	7674	5	2	0	5	0	0
M00001416B:H11	8847	4	1	3	0	6	1
M00001417A:E02	36393	2	0	0	1	0	0
M00001418B:F03	9952	4	2	1	1	0	0
M00001418D:B06	8526	3	2	1	5	1	0
M00001421C:F01	9577	5	2	0	1	11	12
M00001423B:E07	15066	4	0	0	0	0	0
M00001424B:G09	10470	5	1	0	2	0	1
M00001425B:H08	22195	3	0	0	0	0	0
M00001426D:C08	4261	4	9	7	9	12	15
M00001428A:H10	84182	1	0	0	0	0	0
M00001429A:H04	2797	15	11	18	16	1	14
M00001429B:A11	4635	7	9	2	0	0	0
M00001429D:D07	40392	2	0	1	8	12	16
M00001439C:F08	40054	1	0	0	0	0	0
M00001442C:D07	16731	3	1	0	0	0	0
M00001445A:F05	13532	3	2	1	0	1	2
M00001446A:F05	7801	5	2	4	6	1	0
M00001447A:G03	10717	7	2	0	5	8	0
M00001448D:C09	8	1850	2127	1703	3133	1355	122
M00001448D:H01	36313	2	0	0	0	1	30
M00001449A:A12	5857	6	2	3	4	0	0
M00001449A:B12	41633	1	1	0	0	0	0
M00001449A:D12	3681	12	5	10	1	2	5
M00001449A:G10	36535	2	0	0	0	0	0
M00001449C:D06	86110	1	0	0	0	0	0
M00001450A:A02	39304	2	0	0	0	0	0
M00001450A:A11	32663	1	1	0	0	0	0
M00001450A:B12	82498	1	0	0	0	0	0
M00001450A:D08	27250	2	0	0	0	0	0
M00001452A:B04	84328	1	0	0	0	0	0
M00001452A:B12	86859	1	0	0	0	0	0
M00001452A:D08	1120	44	41	5	11	5	0
M00001452A:F05	85064	1	0	0	0	0	0
M00001452C:B06	16970	4	0	0	0	3	4
M00001453A:E11	16130	3	1	0	0	0	1
M00001453C:F06	16653	3	1	0	0	0	0
M00001454A:A09	83103	1	0	0	0	0	0
M00001454B:C12	7005	8	2	0	0	0	0
M00001454D:G03	689	58	95	17	36	66	95
M00001455A:E09	13238	4	1	0	0	0	0
M00001455B:E12	13072	4	1	0	0	0	0
M00001455D:F09	9283	4	1	0	1	0	1



Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001455D:F09	9283	4	1	0	1	0	1
M00001460A:F06	2448	23	22	2	3	3	1
M00001460A:F12	39498	2	0	0	0	0	0
M00001461A:D06	1531	20	23	32	17	14	14
M00001463C:B11	19	1415	1203	1364	525	479	774
M00001465A:B11	10145	2	0	2	0	0	0
M00001466A:E07	4275	11	2	5	0	4	2
M00001467A:B07	38759	2	0	0	0	1	1
M00001467A:D04	39508	2	0	0	0	0	0
M00001467A:D08	16283	3	0	0	0	0	0
M00001467A:D08	16283	3	0	0	0	0	0
M00001467A:E10	39442	2	0	0	0	0	0
M00001468A:F05	7589	6	2	1	1	1	0
M00001469A:C10	12081	4	0	0	0	0	0
M00001469A:H12	19105	2	0	2	0	1	0
M00001470A:B10	1037	53	48	4	22	0	0
M00001470A:C04	39425	2	0	0	0	0	0
M00001471A:B01	39478	2	0	0	0	0	0
M00001481D:A05	7985	3	1	4	0	1	0
M00001490B:C04	18699	2	1	0	0	0	3
M00001494D:F06	7206	4	3	3	1	2	0
M00001497A:G02	2623	12	4	31	4	6	1
M00001499B:A11	10539	2	1	1	0	1	0
M00001500A:C05	5336	9	2	4	8	3	15
M00001500A:E11	2623	12	4	31	4	6	1
M00001500C:E04	9443	4	2	1	1	0	0
M00001501D:C02	9685	3	2	0	7	2	3
M00001504C:A07	10185	5	1	0	0	2	4
M00001504C:H06	6974	7	3	0	1	0	0
M00001504D:G06	6420	8	0	2	0	1	0
M00001507A:H05	39168	2	0	0	0	0	0
M00001511A:H06	39412	2	0	0	0	0	0
M00001512A:A09	39186	2	0	0	0	0	0
M00001512D:G09	3956	9	9	5	2	0	0
M00001513A:B06	4568	10	4	0	9	2	0
M00001513C:E08	14364	1	0	0	0	0	0
M00001514C:D11	40044	2	0	0	0	0	0
M00001517A:B07	4313	13	6	1	0	1	0
M00001518C:B11	8952	3	4	0	4	2	0
M00001528A:C04	7337	4	4	3	16	12	21
M00001528A:F09	18957	3	0	0	0	0	0
M00001528B:H04	8358	3	3	2	0	0	0
M00001531A:D01	38085	2	0	0	0	0	0
M00001532B:A06	3990	6	12	4	1	3	1
M00001533A:C11	2428	14	14	13	9	2	19
M00001534A:C04	16921	4	0	0	1	2	1
M00001534A:D09	5097	6	5	1	1	3	2
M00001534A:F09	5321	11	7	1	5	10	26

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001534C:A01	4119	9	4	2	2	5	3
M00001535A:B01	7665	3	1	5	0	0	0
M00001535A:C06	20212	2	0	1	1	0	0
M00001535A:F10	39423	2	0	0	0	0	0
M00001536A:B07	2696	23	11	9	18	10	21
M00001536A:C08	39392	2	0	0	0	0	0
M00001537A:F12	39420	2	0	0	0	0	0
M00001537B:G07	3389	4	11	13	2	0	0
M00001540A:D06	8286	6	1	0	3	4	0
M00001541A:D02	3765	19	6	0	0	0	0
M00001541A:F07	22085	3	0	0	0	0	1
M00001541A:H03	39174	2	0	0	0	0	0
M00001542A:A09	22113	3	0	0	0	0	0
M00001542A:E06	39453	2	0	0	0	0	0
M00001544A:E03	12170	2	1	2	0	0	0
M00001544A:G02	19829	2	0	1	0	0	0
M00001544B:B07	6974	7	3	0	1	0	0
M00001545A:C03	19255	2	0	0	0	0	0
M00001545A:D08	13864	3	0	2	1	2	4
M00001546A:G11	1267	43	55	5	0	0	0
M00001548A:E10	5892	5	1	4	4	1	3
M00001548A:H09	1058	40	44	37	47	39	59
M00001549A:B02	4015	10	5	8	15	2	0
M00001549A:D08	10944	3	0	3	1	0	7
M00001549B:F06	4193	12	7	2	2	0	1
M00001549C:E06	16347	4	0	0	0	0	0
M00001550A:A03	7239	5	2	1	0	2	0
M00001550A:G01	5175	8	1	3	2	0	0
M00001551A:B10	6268	6	4	3	18	5	0
M00001551A:F05	39180	2	0	0	0	0	0
M00001551A:G06	22390	2	1	0	0	0	1
M00001551C:G09	3266	12	14	0	1	0	6
M00001552A:B12	307	73	60	196	75	79	27
M00001552A:D11	39458	2	0	0	0	0	0
M00001552B:D04	5708	5	4	4	3	1	4
M00001553A:H06	8298	4	3	1	3	0	0
M00001553B:F12	4573	5	7	2	5	0	1
M00001553D:D10	22814	3	0	0	0	0	0
M00001555A:B02	39539	2	0	0	0	1	0
M00001555A:C01	39195	2	0	0	0	0	0
M00001555D:G10	4561	8	4	4	8	0	0
M00001556A:C09	9244	2	0	3	2	10	17
M00001556A:F11	1577	12	40	25	3	4	0
M00001556A:H01	15855	2	1	1	2	12	213
M00001556B:C08	4386	7	8	3	1	3	21
M00001556B:G02	11294	4	0	2	0	0	1
M00001557A:D02	7065	5	3	2	1	0	0
M00001557A:D02	7065	5	3	2	1	0	0

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001557A:F01	9635	3	0	2	1	0	0
M00001557A:F03	39490	2	0	0	0	1	0
M00001557B:H10	5192	8	5	0	5	0	0
M00001557D:D09	8761	3	4	0	1	0	1
M00001558B:H11	7514	5	3	0	0	0	0
M00001560D:F10	6558	4	3	4	0	0	5
M00001561A:C05	39486	2	0	0	0	0	0
M00001563B:F06	102	289	233	278	116	123	184
M00001564A:B12	5053	11	4	2	2	1	1
M00001571C:H06	5749	4	1	9	0	0	0
M00001578B:E04	23001	2	1	0	2	0	0
M00001579D:C03	6539	8	3	0	0	0	1
M00001583D:A10	6293	3	5	2	6	0	0
M00001586C:C05	4623	3	4	12	2	1	1
M00001587A:B11	39380	2	0	0	0	0	0
M00001594B:H04	260	189	188	27	2	15	0
M00001597C:H02	4837	6	2	10	0	3	1
M00001597D:C05	10470	5	1	0	2	0	1
M00001598A:G03	16999	4	0	0	0	0	0
M00001601A:D08	22794	2	0	0	0	0	0
M00001604A:B10	1399	49	27	19	7	10	23
M00001604A:F05	39391	2	0	0	0	0	0
M00001607A:E11	11465	5	0	0	0	0	0
M00001608A:B03	7802	5	4	0	1	0	0
M00001608B:E03	22155	3	0	0	0	0	0
M00001614C:F10	13157	4	1	0	3	1	0
M00001617C:E02	17004	4	0	1	0	1	0
M00001619C:F12	40314	2	0	0	0	1	0
M00001621C:C08	40044	2	0	0	0	0	0
M00001623D:F10	13913	2	1	2	0	0	1
M00001624A:B06	3277	10	11	8	3	5	1
M00001624C:F01	4309	4	13	3	10	0	0
M00001630B:H09	5214	10	2	2	2	4	3
M00001644C:B07	39171	2	0	0	0	0	0
M00001645A:C12	19267	2	0	0	0	0	1
M00001648C:A01	4665	5	9	0	0	0	0
M00001657D:C03	23201	3	0	0	0	3	0
M00001657D:F08	76760	1	0	2	2	0	5
M00001662C:A09	23218	3	0	0	0	0	0
M00001663A:E04	35702	2	0	0	0	0	0
M00001669B:F02	6468	4	3	3	8	1	0
M00001670C:H02	14367	3	0	0	0	0	0
M00001673C:H02	7015	6	3	1	2	1	1
M00001675A:C09	8773	4	1	4	4	4	6
M00001676B:F05	11460	4	2	0	0	0	0
M00001677C:E10	14627	1	2	1	0	1	0
M00001677D:A07	7570	5	3	0	0	0	0
M00001678D:F12	4416	9	5	2	6	1	3

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00001679A:A06	6660	7	0	4	2	1	0
M00001679A:F10	26875	1	0	0	0	1	0
M00001679B:F01	6298	2	4	5	3	1	0
M00001679C:F01	78091	1	0	0	0	0	0
M00001679D:D03	10751	3	2	0	1	0	1
M00001679D:D03	10751	3	2	0	1	0	1
M00001680D:F08	10539	2	1	1	0	1	0
M00001682C:B12	17055	4	0	0	0	0	0
M00001686A:E06	4622	7	6	4	2	3	0
M00001688C:F09	5382	6	2	6	2	0	3
M00001693C:G01	4393	10	6	2	4	1	1
M00001716D:H05	67252	1	0	0	1	0	0
M00003741D:C09	40108	2	0	0	0	0	0
M00003747D:C05	11476	6	0	0	0	0	0
M00003759B:B09	697	76	52	30	72	21	30
M00003762C:B08	17076	4	0	0	0	0	0
M00003763A:F06	3108	14	11	7	5	0	1
M00003774C:A03	67907	1	0	0	0	0	0
M00003796C:D05	5619	3	5	3	3	0	4
M00003826B:A06	11350	3	3	0	0	1	0
M00003833A:E05	21877	2	1	0	0	0	1
M00003837D:A01	7899	5	4	0	2	1	0
M00003839A:D08	7798	5	2	2	0	0	1
M00003844C:B11	6539	8	3	0	0	0	1
M00003846B:D06	6874	6	3	0	0	0	0
M00003851B:D10	13595	4	0	1	0	0	1
M00003853A:D04	5619	3	5	3	3	0	4
M00003853A:F12	10515	5	1	0	1	1	2
M00003856B:C02	4622	7	6	4	2	3	0
M00003857A:G10	3389	4	11	13	2	0	0
M00003857A:H03	4718	4	5	5	2	4	6
M00003871C:E02	4573	5	7	2	5	0	1
M00003875B:F04	12977	5	0	0	0	0	0
M00003875B:F04	12977	5	0	0	0	0	0
M00003875C:G07	8479	4	3	1	1	2	4
M00003876D:E12	7798	5	2	2	0	0	1
M00003879B:C11	5345	7	1	7	4	6	27
M00003879B:D10	31587	1	1	0	0	1	0
M00003879D:A02	14507	3	1	0	0	3	1
M00003885C:A02	13576	5	0	0	0	12	11
M00003885C:A02	13576	5	0	0	0	12	11
M00003906C:E10	9285	4	3	0	0	1	2
M00003907D:A09	39809	1	0	0	0	2	1
M00003907D:H04	16317	3	0	0	0	0	0
M00003909D:C03	8672	4	4	0	0	0	0
M00003912B:D01	12532	4	1	0	1	0	1
M00003914C:F05	3900	9	6	8	1	7	13
M00003922A:E06	23255	3	0	1	1	0	0

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00003958A:H02	18957	3	0	0	0	0	0
M00003958A:H02	18957	3	0	0	0	0	0
M00003958C:G10	40455	2	0	0	0	0	0
M00003958C:G10	40455	2	0	0	0	0	0
M00003968B:F06	24488	2	0	1	4	0	0
M00003970C:B09	40122	2	0	0	0	0	0
M00003974D:E07	23210	3	0	0	0	0	0
M00003974D:H02	23358	3	0	0	0	1	0
M00003975A:G11	12439	4	0	0	0	0	0
M00003978B:G05	5693	7	4	1	3	1	1
M00003981A:E10	3430	9	10	7	3	0	0
M00003982C:C02	2433	10	13	21	18	8	8
M00003983A:A05	9105	5	1	1	1	0	0
M00004028D:A06	6124	4	8	1	9	1	0
M00004028D:C05	40073	2	0	1	0	0	1
M00004031A:A12	9061	5	2	0	0	0	0
M00004031A:A12	9061	5	2	0	0	0	0
M00004035C:A07	37285	2	0	0	1	0	1
M00004035D:B06	17036	4	0	0	0	0	0
M00004059A:D06	5417	10	4	0	9	2	0
M00004068B:A01	3706	7	14	4	22	1	0
M00004072B:B05	17036	4	0	0	0	0	0
M00004081C:D10	15069	3	0	0	1	0	0
M00004081C:D12	14391	3	1	0	0	0	0
M00004086D:G06	9285	4	3	0	0	1	2
M00004087D:A01	6880	2	6	1	1	0	0
M00004093D:B12	5325	5	5	2	0	2	1
M00004093D:B12	5325	5	5	2	0	2	1
M00004105C:A04	7221	5	2	2	2	0	0
M00004108A:E06	4937	4	9	3	1	3	1
M00004111D:A08	6874	6	3	0	0	0	0
M00004114C:F11	13183	2	3	0	7	0	1
M00004138B:H02	13272	3	2	0	3	0	0
M00004146C:C11	5257	2	8	5	5	5	25
M00004151D:B08	16977	4	0	0	0	0	0
M00004157C:A09	6455	3	1	6	0	0	0
M00004169C:C12	5319	6	2	8	2	2	3
M00004171D:B03	4908	6	7	2	2	2	0
M00004172C:D08	11494	4	0	0	0	0	0
M00004183C:D07	16392	3	0	0	0	0	0
M00004185C:C03	11443	5	1	0	0	0	0
M00004197D:H01	8210	2	6	0	0	0	0
M00004203B:C12	14311	4	0	0	0	1	2
M00004212B:C07	2379	26	13	4	2	2	3
M00004214C:H05	11451	3	2	1	2	1	1
M00004223A:G10	16918	4	0	0	0	0	0
M00004223B:D09	7899	5	4	0	2	1	0
M00004223D:E04	12971	4	0	0	0	1	0

Table 5 All Differential Data for Libs 1-4 and 8-9

Clone Name	Cluster ID	Clones in Lib1	Clones in Lib2	Clones in Lib3	Clones in Lib4	Clones in Lib8	Clones in Lib9
M00004229B:F08	6455	3	1	6	0	0	0
M00004230B:C07	7212	3	5	2	1	3	0
M00004269D:D06	4905	7	6	3	1	3	1
M00004275C:C11	16914	3	0	0	1	0	0
M00004283B:A04	14286	3	1	0	1	1	1
M00004285B:E08	56020	1	0	0	0	0	0
M00004295D:F12	16921	4	0	0	1	2	1
M00004296C:H07	13046	4	1	0	1	0	0
M00004307C:A06	9457	2	0	5	0	3	0
M00004312A:G03	26295	2	0	0	0	0	0
M00004318C:D10	21847	2	1	0	0	0	0
M00004372A:A03	2030	13	10	32	4	0	0
M00004377C:F05	2102	12	20	23	21	6	5

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001340B:A06	17062	0	0	0	0	0	0
M00001340D:F10	11589	0	0	0	0	0	0
M00001341A:E12	4443	0	0	0	1	0	0
M00001342B:E06	39805	0	0	0	0	0	0
M00001343C:F10	2790	0	0	0	0	0	0
M00001343D:H07	23255	0	0	0	0	0	0
M00001345A:E01	6420	0	0	0	0	0	0
M00001346A:F09	5007	0	0	0	0	0	0
M00001346D:E03	6806	0	0	0	0	0	0
M00001346D:G06	5779	0	0	0	0	0	0
M00001346D:G06	5779	0	0	0	0	0	0
M00001347A:B10	13576	0	0	0	0	0	0
M00001348B:B04	16927	0	0	0	0	0	0
M00001348B:G06	16985	0	0	0	0	0	0
M00001349B:B08	3584	0	0	0	0	0	0
M00001350A:H01	7187	0	0	0	0	0	0
M00001351B:A08	3162	0	1	0	0	1	0
M00001351B:A08	3162	0	1	0	0	1	0
M00001352A:E02	16245	0	0	0	0	0	0
M00001353A:G12	8078	0	0	0	0	0	0
M00001353D:D10	14929	0	3	1	0	5	0
M00001355B:G10	14391	0	0	0	0	0	0
M00001357D:D11	4059	0	0	0	0	0	0
M00001361A:A05	4141	0	0	0	0	0	0
M00001361D:F08	2379	0	0	0	0	0	0
M00001362B:D10	5622	0	0	0	0	0	0
M00001362C:H11	945	0	0	0	0	0	1
M00001365C:C10	40132	0	0	0	0	0	0
M00001370A:C09	6867	0	0	0	0	0	0
M00001371C:E09	7172	0	0	0	0	0	0
M00001376B:G06	17732	0	0	0	0	0	1
M00001378B:B02	39833	0	0	0	0	0	0
M00001379A:A05	1334	0	0	0	0	0	1
M00001380D:B09	39886	0	0	0	0	0	0
M00001382C:A02	22979	0	0	0	0	0	0
M00001383A:C03	39648	0	0	0	0	0	0
M00001383A:C03	39648	0	0	0	0	0	0
M00001386C:B12	5178	0	0	0	0	0	0
M00001387A:C05	2464	0	0	0	0	0	0
M00001387B:G03	7587	0	0	0	0	0	0
M00001388D:G05	5832	0	0	0	0	0	0
M00001389A:C08	16269	0	1	0	0	0	0
M00001394A:F01	6583	1	4	1	0	0	0
M00001395A:C03	4016	0	0	0	0	0	0
M00001396A:C03	4009	0	0	0	0	0	0
M00001402A:E08	39563	0	0	0	0	0	0
M00001407B:D11	5556	0	0	0	0	0	0
M00001409C:D12	9577	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001410A:D07	7005	0	0	0	0	0	0
M00001412B:B10	8551	0	0	0	0	0	0
M00001415A:H06	13538	0	0	0	0	0	0
M00001416A:H01	7674	0	0	0	0	0	0
M00001416B:H11	8847	0	0	0	0	0	0
M00001417A:E02	36393	0	0	0	0	0	0
M00001418B:F03	9952	0	0	0	0	0	0
M00001418D:B06	8526	0	0	0	0	0	0
M00001421C:F01	9577	0	0	0	0	0	0
M00001423B:E07	15066	0	0	0	0	0	0
M00001424B:G09	10470	0	0	0	0	0	0
M00001425B:H08	22195	0	0	0	0	0	0
M00001426D:C08	4261	0	0	1	0	0	1
M00001428A:H10	84182	0	0	0	0	0	0
M00001429A:H04	2797	0	0	0	0	0	0
M00001429B:A11	4635	0	0	0	0	0	0
M00001429D:D07	40392	0	0	0	0	0	0
M00001439C:F08	40054	0	0	0	0	0	0
M00001442C:D07	16731	0	0	0	0	0	0
M00001445A:F05	13532	0	0	0	0	0	0
M00001446A:F05	7801	0	0	0	0	0	0
M00001447A:G03	10717	0	0	0	0	0	0
M00001448D:C09	8	1	6	6	1	14	1
M00001448D:H01	36313	0	3	0	0	3	0
M00001449A:A12	5857	0	0	0	0	0	0
M00001449A:B12	41633	0	0	0	0	0	0
M00001449A:D12	3681	0	0	0	0	0	0
M00001449A:G10	36535	0	0	0	0	0	0
M00001449C:D06	86110	0	0	0	0	0	0
M00001450A:A02	39304	0	0	0	0	0	0
M00001450A:A11	32663	0	0	0	0	0	0
M00001450A:B12	82498	0	0	0	0	0	0
M00001450A:D08	27250	0	0	0	0	0	0
M00001452A:B04	84328	0	0	0	0	0	0
M00001452A:B12	86859	0	0	0	0	0	0
M00001452A:D08	1120	0	0	0	0	0	0
M00001452A:F05	85064	0	0	0	0	0	0
M00001452C:B06	16970	0	0	2	0	1	0
M00001453A:E11	16130	0	0	0	0	0	0
M00001453C:F06	16653	0	0	0	0	0	0
M00001454A:A09	83103	0	0	0	0	0	0
M00001454B:C12	7005	0	0	0	0	0	0
M00001454D:G03	689	0	2	2	0	4	2
M00001455A:E09	13238	0	0	0	0	0	0
M00001455B:E12	13072	0	0	0	0	0	0
M00001455D:F09	9283	0	0	0	0	0	0
M00001455D:F09	9283	0	0	0	0	0	0
M00001460A:F06	2448	0	0	0	0	0	0
M00001460A:F12	39498	0	0	0	0	0	0



Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001461A:D06	1531	0	0	0	0	0	0
M00001463C:B11	19	2	13	13	0	69	10
M00001465A:B11	10145	0	0	0	0	0	0
M00001466A:E07	4275	0	0	0	0	0	0
M00001467A:B07	38759	0	0	0	0	0	0
M00001467A:D04	39508	0	0	0	0	0	0
M00001467A:D08	16283	0	0	0	0	0	0
M00001467A:D08	16283	0	0	0	0	0	0
M00001467A:E10	39442	0	0	0	0	0	0
M00001468A:F05	7589	0	0	0	0	0	0
M00001469A:C10	12081	0	0	0	0	0	0
M00001469A:H12	19105	0	0	0	0	0	0
M00001470A:B10	1037	0	0	0	0	0	0
M00001470A:C04	39425	0	0	0	0	0	0
M00001471A:B01	39478	0	0	0	0	0	0
M00001481D:A05	7985	0	0	0	0	0	0
M00001490B:C04	18699	0	0	0	0	0	0
M00001494D:F06	7206	0	0	0	0	0	0
M00001497A:G02	2623	0	0	0	0	0	0
M00001499B:A11	10539	0	0	0	0	0	0
M00001500A:C05	5336	0	0	0	0	0	0
M00001500A:E11	2623	0	0	0	0	0	0
M00001500C:E04	9443	0	0	0	0	0	0
M00001501D:C02	9685	0	0	0	0	0	0
M00001504C:A07	10185	0	0	0	0	0	0
M00001504C:H06	6974	0	0	0	0	0	0
M00001504D:G06	6420	0	0	0	0	0	0
M00001507A:H05	39168	0	0	0	0	0	0
M00001511A:H06	39412	0	0	0	0	0	0
M00001512A:A09	39186	0	0	0	0	0	0
M00001512D:G09	3956	0	0	1	0	0	0
M00001513A:B06	4568	0	0	0	0	0	0
M00001513C:E08	14364	0	0	0	0	0	0
M00001514C:D11	40044	0	1	0	0	0	0
M00001517A:B07	4313	0	0	0	0	0	0
M00001518C:B11	8952	0	0	0	0	0	0
M00001528A:C04	7337	0	0	0	0	0	0
M00001528A:F09	18957	0	0	0	0	0	0
M00001528B:H04	8358	0	0	0	0	0	0
M00001531A:D01	38085	0	0	0	0	0	0
M00001532B:A06	3990	1	1	0	0	0	0
M00001533A:C11	2428	0	0	1	0	0	0
M00001534A:C04	16921	0	0	0	0	0	0
M00001534A:D09	5097	0	0	0	0	0	0
M00001534A:F09	5321	0	1	0	0	2	0
M00001534C:A01	4119	0	0	0	0	0	0
M00001535A:B01	7665	0	0	0	0	0	0
M00001535A:C06	20212	0	0	0	0	0	0
M00001535A:F10	39423	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001536A:B07	2696	0	0	0	0	3	0
M00001536A:C08	39392	0	0	0	0	0	0
M00001537A:F12	39420	0	0	0	0	0	0
M00001537B:G07	3389	0	0	0	0	0	0
M00001540A:D06	8286	0	0	0	0	0	0
M00001541A:D02	3765	0	0	0	0	0	0
M00001541A:F07	22085	0	0	0	0	0	0
M00001541A:H03	39174	0	0	0	0	0	0
M00001542A:A09	22113	0	0	0	0	0	0
M00001542A:E06	39453	0	0	0	0	0	0
M00001544A:E03	12170	0	0	0	0	0	0
M00001544A:G02	19829	0	0	0	0	0	0
M00001544B:B07	6974	0	0	0	0	0	0
M00001545A:C03	19255	0	0	0	0	0	0
M00001545A:D08	13864	0	0	0	0	0	0
M00001546A:G11	1267	1	0	0	0	7	0
M00001548A:E10	5892	0	0	0	0	0	0
M00001548A:H09	1058	0	0	1	0	0	0
M00001549A:B02	4015	0	0	0	0	0	0
M00001549A:D08	10944	0	0	0	0	0	0
M00001549B:F06	4193	0	0	0	0	0	0
M00001549C:E06	16347	0	0	0	0	0	0
M00001550A:A03	7239	0	0	0	0	0	0
M00001550A:G01	5175	0	0	0	0	0	0
M00001551A:B10	6268	0	0	0	0	0	0
M00001551A:F05	39180	0	0	0	0	0	0
M00001551A:G06	22390	0	0	0	0	0	0
M00001551C:G09	3266	0	0	1	0	0	0
M00001552A:B12	307	0	0	0	0	3	0
M00001552A:D11	39458	0	0	0	0	0	0
M00001552B:D04	5708	0	1	0	0	0	0
M00001553A:H06	8298	0	0	0	0	0	0
M00001553B:F12	4573	0	0	0	0	0	0
M00001553D:D10	22814	0	0	0	0	0	0
M00001555A:B02	39539	0	0	0	0	0	0
M00001555A:C01	39195	0	0	0	0	0	0
M00001555D:G10	4561	0	0	0	0	0	0
M00001556A:C09	9244	0	0	0	0	0	0
M00001556A:F11	1577	0	0	0	0	0	0
M00001556A:H01	15855	3	5	5	0	3	1
M00001556B:C08	4386	1	2	0	0	0	0
M00001556B:G02	11294	0	0	0	0	0	0
M00001557A:D02	7065	0	0	0	0	0	0
M00001557A:D02	7065	0	0	0	0	0	0
M00001557A:F01	9635	0	0	0	0	0	0
M00001557A:F03	39490	0	0	0	0	0	0
M00001557B:H10	5192	0	0	0	0	0	0
M00001557D:D09	8761	0	0	0	0	0	0
M00001558B:H11	7514	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001560D:F10	6558	0	0	0	0	0	0
M00001561A:C05	39486	0	0	0	0	0	0
M00001563B:F06	102	22	38	65	7	43	10
M00001564A:B12	5053	0	0	1	0	0	0
M00001571C:H06	5749	0	0	0	0	0	0
M00001578B:E04	23001	0	0	0	0	0	0
M00001579D:C03	6539	0	0	0	0	0	0
M00001583D:A10	6293	0	0	0	0	0	0
M00001586C:C05	4623	0	0	0	0	1	0
M00001587A:B11	39380	0	0	0	0	0	0
M00001594B:H04	260	0	0	0	0	1	0
M00001597C:H02	4837	0	0	0	0	0	0
M00001597D:C05	10470	0	0	0	0	0	0
M00001598A:G03	16999	1	1	1	0	0	0
M00001601A:D08	22794	0	0	0	0	0	0
M00001604A:B10	1399	0	0	0	0	0	0
M00001604A:F05	39391	0	0	0	0	0	0
M00001607A:E11	11465	0	0	0	0	0	0
M00001608A:B03	7802	0	0	0	0	0	0
M00001608B:E03	22155	0	0	0	0	0	0
M00001614C:F10	13157	0	0	0	0	0	0
M00001617C:E02	17004	0	0	0	0	1	0
M00001619C:F12	40314	0	0	0	0	0	0
M00001621C:C08	40044	0	1	0	0	0	0
M00001623D:F10	13913	0	0	0	0	0	0
M00001624A:B06	3277	0	0	0	0	0	0
M00001624C:F01	4309	0	0	0	0	0	0
M00001630B:H09	5214	1	0	0	1	1	0
M00001644C:B07	39171	0	0	0	0	0	0
M00001645A:C12	19267	0	0	0	0	1	0
M00001648C:A01	4665	0	0	0	0	0	0
M00001657D:C03	23201	0	0	0	0	0	0
M00001657D:F08	76760	0	0	0	0	0	0
M00001662C:A09	23218	0	0	0	0	0	0
M00001663A:E04	35702	0	0	0	0	0	0
M00001669B:F02	6468	0	0	0	0	0	0
M00001670C:H02	14367	0	0	0	0	0	0
M00001673C:H02	7015	0	0	0	0	0	0
M00001675A:C09	8773	0	0	0	0	0	0
M00001676B:F05	11460	0	0	0	0	0	0
M00001677C:E10	14627	0	1	0	0	0	0
M00001677D:A07	7570	0	0	0	0	0	0
M00001678D:F12	4416	0	0	0	0	0	0
M00001679A:A06	6660	0	0	0	0	0	0
M00001679A:F10	26875	0	0	0	0	0	0
M00001679B:F01	6298	0	0	0	0	0	0
M00001679C:F01	78091	0	0	0	0	0	0
M00001679D:D03	10751	0	0	0	0	0	0
M00001679D:D03	10751	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00001680D:F08	10539	0	0	0	0	0	0
M00001682C:B12	17055	0	0	0	0	0	0
M00001686A:E06	4622	0	0	0	0	0	0
M00001688C:F09	5382	0	0	0	0	0	0
M00001693C:G01	4393	0	0	0	0	0	0
M00001716D:H05	67252	0	0	0	0	0	0
M00003741D:C09	40108	0	0	0	0	0	0
M00003747D:C05	11476	0	0	0	0	0	0
M00003759B:B09	697	0	0	0	0	1	0
M00003762C:B08	17076	0	0	0	0	0	0
M00003763A:F06	3108	0	0	0	0	0	0
M00003774C:A03	67907	0	0	0	0	0	0
M00003796C:D05	5619	0	0	0	0	0	0
M00003826B:A06	11350	0	0	0	0	0	0
M00003833A:E05	21877	0	0	0	0	0	0
M00003837D:A01	7899	0	0	0	0	0	0
M00003839A:D08	7798	0	0	0	0	0	0
M00003844C:B11	6539	0	0	0	0	0	0
M00003846B:D06	6874	0	0	1	0	0	0
M00003851B:D10	13595	0	0	0	0	0	0
M00003853A:D04	5619	0	0	0	0	0	0
M00003853A:F12	10515	0	0	0	0	0	0
M00003856B:C02	4622	0	0	0	0	0	0
M00003857A:G10	3389	0	0	0	0	0	0
M00003857A:H03	4718	0	0	0	0	0	0
M00003871C:E02	4573	0	0	0	0	0	0
M00003875B:F04	12977	0	0	0	0	0	0
M00003875B:F04	12977	0	0	0	0	0	0
M00003875C:G07	8479	0	0	0	0	0	1
M00003876D:E12	7798	0	0	0	0	0	0
M00003879B:C11	5345	0	0	0	2	0	1
M00003879B:D10	31587	0	0	0	0	0	0
M00003879D:A02	14507	0	0	0	0	0	0
M00003885C:A02	13576	0	0	0	0	0	0
M00003885C:A02	13576	0	0	0	0	0	0
M00003906C:E10	9285	0	0	0	0	0	0
M00003907D:A09	39809	0	0	0	0	0	0
M00003907D:H04	16317	0	0	0	0	0	0
M00003909D:C03	8672	0	0	0	0	0	0
M00003912B:D01	12532	0	0	0	0	0	0
M00003914C:F05	3900	0	0	0	0	1	0
M00003922A:E06	23255	0	0	0	0	0	0
M00003958A:H02	18957	0	0	0	0	0	0
M00003958A:H02	18957	0	0	0	0	0	0
M00003958C:G10	40455	0	0	0	0	0	0
M00003958C:G10	40455	0	0	0	0	0	0
M00003968B:F06	24488	0	0	0	0	0	0
M00003970C:B09	40122	0	0	0	0	0	0
M00003974D:E07	23210	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00003974D:H02	23358	0	0	0	0	0	0
M00003975A:G11	12439	0	0	0	0	0	0
M00003978B:G05	5693	0	0	0	0	0	0
M00003981A:E10	3430	0	0	0	0	1	0
M00003982C:C02	2433	0	0	0	0	0	0
M00003983A:A05	9105	0	0	0	0	0	0
M00004028D:A06	6124	0	0	0	0	0	0
M00004028D:C05	40073	0	0	0	0	0	0
M00004031A:A12	9061	0	0	0	0	0	0
M00004031A:A12	9061	0	0	0	0	0	0
M00004035C:A07	37285	0	0	0	0	0	0
M00004035D:B06	17036	0	0	0	0	0	0
M00004059A:D06	5417	0	0	0	0	0	0
M00004068B:A01	3706	0	0	0	0	0	0
M00004072B:B05	17036	0	0	0	0	0	0
M00004081C:D10	15069	0	0	0	0	0	0
M00004081C:D12	14391	0	0	0	0	0	0
M00004086D:G06	9285	0	0	0	0	0	0
M00004087D:A01	6880	0	0	0	0	0	0
M00004093D:B12	5325	1	1	0	1	0	1
M00004093D:B12	5325	1	1	0	1	0	1
M00004105C:A04	7221	0	0	0	0	0	0
M00004108A:E06	4937	0	0	0	0	0	0
M00004111D:A08	6874	0	0	1	0	0	0
M00004114C:F11	13183	0	0	0	0	0	0
M00004138B:H02	13272	0	0	0	0	0	0
M00004146C:C11	5257	0	1	0	0	0	0
M00004151D:B08	16977	0	0	0	0	0	0
M00004157C:A09	6455	0	0	0	0	0	0
M00004169C:C12	5319	0	0	0	0	0	0
M00004171D:B03	4908	0	0	0	0	0	0
M00004172C:D08	11494	0	0	0	0	0	0
M00004183C:D07	16392	0	0	0	0	0	0
M00004185C:C03	11443	0	0	0	0	0	0
M00004197D:H01	8210	0	0	0	0	0	0
M00004203B:C12	14311	0	0	0	0	0	0
M00004212B:C07	2379	0	0	0	0	0	0
M00004214C:H05	11451	0	0	0	0	0	0
M00004223A:G10	16918	0	0	0	0	0	0
M00004223B:D09	7899	0	0	0	0	0	0
M00004223D:E04	12971	0	0	0	0	0	0
M00004229B:F08	6455	0	0	0	0	0	0
M00004230B:C07	7212	0	0	0	0	0	0
M00004269D:D06	4905	0	0	0	0	0	0
M00004275C:C11	16914	0	0	0	0	0	0
M00004283B:A04	14286	0	0	0	0	0	0
M00004285B:E08	56020	0	0	0	0	0	0
M00004295D:F12	16921	0	0	0	0	0	0
M00004296C:H07	13046	0	0	0	0	0	0

Table 6 All Differential Data for Libs 15-20

Clone Name	Cluster ID	Clones in Lib15	Clones in Lib16b	Clones in Lib17	Clones in Lib18	Clones in Lib19	Clones in Lib20
M00004307C:A06	9457	0	0	0	0	0	0
M00004312A:G03	26295	0	0	0	0	0	0
M00004318C:D10	21847	0	0	0	0	0	0
M00004372A:A03	2030	0	0	0	0	0	0
M00004377C:F05	2102	0	0	0	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001340B:A06	17062	0	0	0
M00001340D:F10	11589	0	0	0
M00001341A:E12	4443	4	2	0
M00001342B:E06	39805	0	0	0
M00001343C:F10	2790	0	0	0
M00001343D:H07	23255	0	0	0
M00001345A:E01	6420	0	0	0
M00001346A:F09	5007	0	0	0
M00001346D:E03	6806	0	1	1
M00001346D:G06	5779	0	0	0
M00001346D:G06	5779	0	0	0
M00001347A:B10	13576	0	0	0
M00001348B:B04	16927	0	0	0
M00001348B:G06	16985	0	0	0
M00001349B:B08	3584	0	0	0
M00001350A:H01	7187	0	0	0
M00001351B:A08	3162	0	0	1
M00001351B:A08	3162	0	0	1
M00001352A:E02	16245	0	0	0
M00001353A:G12	8078	0	0	0
M00001353D:D10	14929	0	1	0
M00001355B:G10	14391	0	0	0
M00001357D:D11	4059	0	0	0
M00001361A:A05	4141	1	2	1
M00001361D:F08	2379	0	0	0
M00001362B:D10	5622	0	2	1
M00001362C:H11	945	0	0	0
M00001365C:C10	40132	0	0	0
M00001370A:C09	6867	0	0	0
M00001371C:E09	7172	0	0	1
M00001376B:G06	17732	2	0	0
M00001378B:B02	39833	0	0	0
M00001379A:A05	1334	0	0	0
M00001380D:B09	39886	0	0	0
M00001382C:A02	22979	1	0	0
M00001383A:C03	39648	0	0	0
M00001383A:C03	39648	0	0	0
M00001386C:B12	5178	0	0	0
M00001387A:C05	2464	0	0	0
M00001387B:G03	7587	0	0	0
M00001388D:G05	5832	0	0	0
M00001389A:C08	16269	2	0	0
M00001394A:F01	6583	0	0	0
M00001395A:C03	4016	0	0	0
M00001396A:C03	4009	2	0	0
M00001402A:E08	39563	0	0	0
M00001407B:D11	5556	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001409C:D12	9577	0	0	0
M00001410A:D07	7005	0	0	0
M00001412B:B10	8551	0	0	0
M00001415A:H06	13538	0	0	0
M00001416A:H01	7674	0	0	0
M00001416B:H11	8847	1	0	0
M00001417A:E02	36393	0	0	0
M00001418B:F03	9952	0	0	0
M00001418D:B06	8526	0	0	0
M00001421C:F01	9577	0	0	0
M00001423B:E07	15066	0	0	0
M00001424B:G09	10470	0	0	0
M00001425B:H08	22195	0	0	0
M00001426D:C08	4261	0	0	0
M00001428A:H10	84182	0	0	0
M00001429A:H04	2797	0	0	0
M00001429B:A11	4635	0	0	0
M00001429D:D07	40392	0	0	0
M00001439C:F08	40054	0	0	0
M00001442C:D07	16731	0	0	0
M00001445A:F05	13532	0	0	0
M00001446A:F05	7801	0	1	0
M00001447A:G03	10717	0	0	0
M00001448D:C09	8	7	6	9
M00001448D:H01	36313	1	0	0
M00001449A:A12	5857	0	0	0
M00001449A:B12	41633	0	0	0
M00001449A:D12	3681	1	0	0
M00001449A:G10	36535	0	0	0
M00001449C:D06	86110	0	0	0
M00001450A:A02	39304	0	1	0
M00001450A:A11	32663	0	0	0
M00001450A:B12	82498	0	0	0
M00001450A:D08	27250	0	0	0
M00001452A:B04	84328	0	0	0
M00001452A:B12	86859	0	0	0
M00001452A:D08	1120	0	0	0
M00001452A:F05	85064	0	0	0
M00001452C:B06	16970	1	0	0
M00001453A:E11	16130	0	0	0
M00001453C:F06	16653	0	0	0
M00001454A:A09	83103	0	0	0
M00001454B:C12	7005	0	0	0
M00001454D:G03	689	0	0	1
M00001455A:E09	13238	0	0	0
M00001455B:E12	13072	0	0	0
M00001455D:F09	9283	0	0	0
M00001455D:F09	9283	0	0	0



Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001460A:F06	2448	0	0	0
M00001460A:F12	39498	0	0	0
M00001461A:D06	1531	0	0	1
M00001463C:B11	19	17	32	31
M00001465A:B11	10145	0	0	0
M00001466A:E07	4275	0	0	0
M00001467A:B07	38759	0	0	0
M00001467A:D04	39508	0	0	0
M00001467A:D08	16283	0	0	0
M00001467A:D08	16283	0	0	0
M00001467A:E10	39442	0	0	0
M00001468A:F05	7589	0	0	0
M00001469A:C10	12081	0	0	0
M00001469A:H12	19105	0	0	0
M00001470A:B10	1037	0	0	0
M00001470A:C04	39425	0	0	0
M00001471A:B01	39478	0	0	0
M00001481D:A05	7985	0	0	0
M00001490B:C04	18699	0	0	0
M00001494D:F06	7206	0	0	0
M00001497A:G02	2623	1	0	0
M00001499B:A11	10539	0	1	0
M00001500A:C05	5336	0	0	0
M00001500A:E11	2623	1	0	0
M00001500C:E04	9443	0	0	0
M00001501D:C02	9685	0	0	0
M00001504C:A07	10185	0	0	0
M00001504C:H06	6974	0	0	0
M00001504D:G06	6420	0	0	0
M00001507A:H05	39168	0	0	0
M00001511A:H06	39412	0	0	0
M00001512A:A09	39186	0	0	0
M00001512D:G09	3956	0	0	0
M00001513A:B06	4568	0	0	0
M00001513C:E08	14364	0	0	0
M00001514C:D11	40044	0	0	0
M00001517A:B07	4313	0	0	0
M00001518C:B11	8952	0	0	0
M00001528A:C04	7337	1	2	2
M00001528A:F09	18957	0	0	0
M00001528B:H04	8358	0	0	0
M00001531A:D01	38085	0	0	0
M00001532B:A06	3990	0	0	0
M00001533A:C11	2428	0	0	0
M00001534A:C04	16921	0	0	0
M00001534A:D09	5097	0	0	0
M00001534A:F09	5321	4	7	6
M00001534C:A01	4119	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001535A:B01	7665	0	2	4
M00001535A:C06	20212	0	0	0
M00001535A:F10	39423	0	0	0
M00001536A:B07	2696	0	0	0
M00001536A:C08	39392	0	0	0
M00001537A:F12	39420	0	0	0
M00001537B:G07	3389	0	0	0
M00001540A:D06	8286	0	0	0
M00001541A:D02	3765	0	0	0
M00001541A:F07	22085	0	0	0
M00001541A:H03	39174	0	0	0
M00001542A:A09	22113	0	0	0
M00001542A:E06	39453	0	0	0
M00001544A:E03	12170	0	0	0
M00001544A:G02	19829	0	0	0
M00001544B:B07	6974	0	0	0
M00001545A:C03	19255	0	0	0
M00001545A:D08	13864	0	0	0
M00001546A:G11	1267	0	0	0
M00001548A:E10	5892	0	1	0
M00001548A:H09	1058	1	3	0
M00001549A:B02	4015	0	1	0
M00001549A:D08	10944	1	0	0
M00001549B:F06	4193	0	0	0
M00001549C:E06	16347	0	0	0
M00001550A:A03	7239	0	1	0
M00001550A:G01	5175	1	0	0
M00001551A:B10	6268	0	0	1
M00001551A:F05	39180	0	0	0
M00001551A:G06	22390	0	0	1
M00001551C:G09	3266	0	0	0
M00001552A:B12	307	6	11	4
M00001552A:D11	39458	0	0	0
M00001552B:D04	5708	0	0	0
M00001553A:H06	8298	0	0	0
M00001553B:F12	4573	0	0	0
M00001553D:D10	22814	0	0	0
M00001555A:B02	39539	0	0	0
M00001555A:C01	39195	0	0	0
M00001555D:G10	4561	0	0	0
M00001556A:C09	9244	0	1	0
M00001556A:F11	1577	0	0	2
M00001556A:H01	15855	1	1	0
M00001556B:C08	4386	3	0	1
M00001556B:G02	11294	0	0	0
M00001557A:D02	7065	0	0	0
M00001557A:D02	7065	0	0	0
M00001557A:F01	9635	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001557A:F03	39490	0	0	0
M00001557B:H10	5192	0	0	0
M00001557D:D09	8761	0	0	0
M00001558B:H11	7514	0	0	0
M00001560D:F10	6558	0	0	0
M00001561A:C05	39486	0	0	0
M00001563B:F06	102	2	1	2
M00001564A:B12	5053	0	0	0
M00001571C:H06	5749	0	0	0
M00001578B:E04	23001	0	0	0
M00001579D:C03	6539	0	0	0
M00001583D:A10	6293	0	0	0
M00001586C:C05	4623	0	0	0
M00001587A:B11	39380	0	0	0
M00001594B:H04	260	1	0	0
M00001597C:H02	4837	1	0	0
M00001597D:C05	10470	0	0	0
M00001598A:G03	16999	4	2	6
M00001601A:D08	22794	0	0	0
M00001604A:B10	1399	6	3	3
M00001604A:F05	39391	0	0	0
M00001607A:E11	11465	0	0	0
M00001608A:B03	7802	0	0	0
M00001608B:E03	22155	0	0	0
M00001614C:F10	13157	0	0	0
M00001617C:E02	17004	0	0	0
M00001619C:F12	40314	0	0	0
M00001621C:C08	40044	0	0	0
M00001623D:F10	13913	0	0	0
M00001624A:B06	3277	0	0	0
M00001624C:F01	4309	0	0	0
M00001630B:H09	5214	0	1	2
M00001644C:B07	39171	0	0	0
M00001645A:C12	19267	0	0	0
M00001648C:A01	4665	0	0	0
M00001657D:C03	23201	0	0	0
M00001657D:F08	76760	0	0	0
M00001662C:A09	23218	0	0	0
M00001663A:E04	35702	0	0	0
M00001669B:F02	6468	0	0	0
M00001670C:H02	14367	0	0	0
M00001673C:H02	7015	0	0	0
M00001675A:C09	8773	0	0	0
M00001676B:F05	11460	2	0	0
M00001677C:E10	14627	0	0	0
M00001677D:A07	7570	0	0	0
M00001678D:F12	4416	1	2	0
M00001679A:A06	6660	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00001679A:F10	26875	0	0	0
M00001679B:F01	6298	0	0	0
M00001679C:F01	78091	0	0	0
M00001679D:D03	10751	0	0	0
M00001679D:D03	10751	0	0	0
M00001680D:F08	10539	0	1	0
M00001682C:B12	17055	0	0	0
M00001686A:E06	4622	0	0	0
M00001688C:F09	5382	0	0	0
M00001693C:G01	4393	0	0	0
M00001716D:H05	67252	0	0	0
M00003741D:C09	40108	0	0	0
M00003747D:C05	11476	0	0	0
M00003759B:B09	697	0	0	0
M00003762C:B08	17076	0	0	0
M00003763A:F06	3108	0	0	0
M00003774C:A03	67907	0	0	0
M00003796C:D05	5619	0	1	0
M00003826B:A06	11350	0	0	0
M00003833A:E05	21877	0	0	0
M00003837D:A01	7899	0	0	0
M00003839A:D08	7798	0	0	0
M00003844C:B11	6539	0	0	0
M00003846B:D06	6874	0	0	0
M00003851B:D10	13595	0	0	0
M00003853A:D04	5619	0	1	0
M00003853A:F12	10515	0	0	1
M00003856B:C02	4622	0	0	0
M00003857A:G10	3389	0	0	0
M00003857A:H03	4718	0	0	0
M00003871C:E02	4573	0	0	0
M00003875B:F04	12977	0	0	0
M00003875B:F04	12977	0	0	0
M00003875C:G07	8479	1	0	0
M00003876D:E12	7798	0	0	0
M00003879B:C11	5345	4	8	3
M00003879B:D10	31587	0	0	0
M00003879D:A02	14507	0	0	0
M00003885C:A02	13576	0	0	0
M00003885C:A02	13576	0	0	0
M00003906C:E10	9285	0	0	0
M00003907D:A09	39809	0	0	0
M00003907D:H04	16317	0	0	0
M00003909D:C03	8672	0	0	0
M00003912B:D01	12532	0	0	0
M00003914C:F05	3900	0	1	0
M00003922A:E06	23255	0	0	0
M00003958A:H02	18957	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00003958A:H02	18957	0	0	0
M00003958C:G10	40455	0	0	0
M00003958C:G10	40455	0	0	0
M00003968B:F06	24488	0	0	0
M00003970C:B09	40122	0	0	0
M00003974D:E07	23210	0	0	0
M00003974D:H02	23358	0	0	0
M00003975A:G11	12439	0	0	0
M00003978B:G05	5693	0	0	0
M00003981A:E10	3430	0	0	0
M00003982C:C02	2433	2	4	0
M00003983A:A05	9105	0	0	0
M00004028D:A06	6124	0	0	0
M00004028D:C05	40073	0	1	0
M00004031A:A12	9061	0	0	0
M00004031A:A12	9061	0	0	0
M00004035C:A07	37285	0	0	0
M00004035D:B06	17036	0	0	0
M00004059A:D06	5417	0	0	0
M00004068B:A01	3706	0	0	0
M00004072B:B05	17036	0	0	0
M00004081C:D10	15069	0	0	0
M00004081C:D12	14391	0	0	0
M00004086D:G06	9285	0	0	0
M00004087D:A01	6880	0	0	0
M00004093D:B12	5325	0	0	0
M00004093D:B12	5325	0	0	0
M00004105C:A04	7221	0	0	0
M00004108A:E06	4937	0	0	0
M00004111D:A08	6874	0	0	0
M00004114C:F11	13183	0	0	0
M00004138B:H02	13272	0	0	0
M00004146C:C11	5257	0	0	1
M00004151D:B08	16977	0	0	0
M00004157C:A09	6455	0	0	0
M00004169C:C12	5319	0	0	0
M00004171D:B03	4908	0	0	0
M00004172C:D08	11494	0	0	0
M00004183C:D07	16392	0	0	0
M00004185C:C03	11443	2	0	0
M00004197D:H01	8210	0	0	0
M00004203B:C12	14311	0	0	0
M00004212B:C07	2379	0	0	0
M00004214C:H05	11451	0	0	0
M00004223A:G10	16918	0	0	0
M00004223B:D09	7899	0	0	0
M00004223D:E04	12971	0	0	0
M00004229B:F08	6455	0	0	0

Table 7 All Differential Data for Libs 12-14

Clone Name	Cluster ID	Clones in Lib12	Clones in Lib13	Clones in Lib14
M00004230B:C07	7212	0	0	1
M00004269D:D06	4905	0	0	0
M00004275C:C11	16914	0	0	0
M00004283B:A04	14286	0	0	0
M00004285B:E08	56020	0	0	0
M00004295D:F12	16921	0	0	0
M00004296C:H07	13046	0	0	0
M00004307C:A06	9457	1	0	0
M00004312A:G03	26295	0	0	0
M00004318C:D10	21847	0	0	0
M00004372A:A03	2030	0	0	0
M00004377C:F05	2102	0	0	0

We Claim:

1. A library of polynucleotides, the library comprising the sequence information of at least one of SEQ ID NOS:1-844.

5

2. The library of claim 1, wherein the library is provided on a nucleic acid array.

3. The library of claim 1, wherein the library is provided in a computer-readable format.

10

4. The library of claim 1, wherein the library comprises a differentially expressed polynucleotide comprising a sequence selected from the group consisting of SEQ ID NOS:9, 39, 42, 52, 62, 74, 119, 172, 317, and 379.

15

5. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human breast cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

20

6. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human colon cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

25

7. The library of claim 1, wherein the library comprises a polynucleotide differentially expressed in a human lung cancer cell, where the polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

30

8. An isolated polynucleotide comprising a nucleotide sequence having at least 90% sequence identity to an identifying sequence of SEQ ID NOS:1-844 or a degenerate variant thereof.

9. An isolated polynucleotide according to claim 8, wherein the polynucleotide comprises a sequence encoding a polypeptide of a protein family selected from the group consisting of: 4 transmembrane segments integral membrane proteins, 7 transmembrane  
5 receptors, ATPases associated with various cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of transcription factors, G-protein alpha subunit, phorbol esters/diacylglycerol binding proteins, protein kinase, protein phosphatase 2C, protein tyrosine phosphatase, trypsin, wnt family of developmental signaling proteins, and WW/rsp5/WWP domain containing proteins.

10. The polynucleotide of claim 9, wherein the polynucleotide comprises a sequence of one of SEQ ID NOS: 24, 41, 101, 157, 291, 305, 315, 341, 63, 116, 134, 136, 151, 384, 404, 308, 213, 367, 188, 251, 202, 315, 367, 397, 256, 382, 169, 23, 291, 324, 330, 341, 353, 188, 379, and 395.

11. The polynucleotide of claim 8, wherein the polynucleotide comprises a sequence encoding a polypeptide having a functional domain selected from the group consisting of: Ank repeat, basic region plus leucine zipper transcription factors, bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger (C2H2 type),  
20 zinc finger (CCHC class), and zinc-binding metalloprotease domain.

12. The polynucleotide of claim 11, wherein the polynucleotide comprises a sequence of one of SEQ ID NOS: 116, 251, 374, 97, 136, 242, 379, 306, 386, 18, 335, 61, 306, 386, 322, 306, and 395.

13. A recombinant host cell containing the polynucleotide of claim 8.

14. An isolated polypeptide encoded by the polynucleotide of claim 8.

15. An antibody that specifically binds a polypeptide of claim 14.

16. A vector comprising the polynucleotide of claim 8.



17. A polynucleotide comprising the nucleotide sequence of an insert contained in a clone deposited as ATCC accession number xx, xx, xx, xx, xx, xx, xx, xx, or xx.

18. A method of detecting differentially expressed genes correlated with a cancerous  
5 state of a mammalian cell, the method comprising the step of:

detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where the gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS:4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338,  
10 379, 384, 386, 388, 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, 374, 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400;

wherein detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.

19. The method of claim 18, wherein said detecting step is by hybridization of the  
15 test sample to a reference array, wherein the reference array comprises an identifying sequence of at least one of SEQ ID NOS:1-844.

20. The method of claim 18, wherein the cell is a breast tissue derived cell, and the  
20 differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 4, 9, 39, 42, 52, 62, 65, 66, 68, 74, 81, 114, 123, 144, 130, 157, 162, 172, 178, 183, 202, 214, 219, 223, 258, 298, 317, 338, 379, 384, 386, and 388.

21. The method of claim 18, wherein the cell is a colon tissue derived cell, and the  
25 differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 1, 39, 52, 97, 119, 134, 172, 176, 241, 288, 317, 357, 362, and 374.

22. The method of claim 18, wherein the cell is a lung tissue derived cell, and the  
30 differentially expressed gene product is encoded by a gene corresponding to a sequence of at least one of SEQ ID NOS: 9, 34, 42, 62, 74, 106, 119, 135, 154, 160, 260, 308, 323, 349, 361, 369, 371, 379, 395, 381, and 400.

## SEQUENCE LISTING

<110> Lewis T. Williams  
Jaime Escobedo  
Michael A. Innis  
Pablo Dominiguez Garcia  
Julie Sudduth-Klinger  
Christoph Reinhard  
Klause Giese  
Filippo Randazzo  
Giulia C. Kennedy  
David Pot  
Altaf Kassan  
George Lamson  
Radoje Drmanac  
Radomir Crkvenjakov  
Mark Dickson  
Snezana Drmanac  
Ivan Labat  
Dena Leshkowitz  
David Kita  
Veronica Garcia  
William Lee Jones  
Birjit Stache-Crain

<120> Novel Human Genes and Gene Expression  
Products I

<130> 2300-1480P

<140> 09/  
<141> 1998-12-21

<150> 60/068,755  
<151> 1997-12-23

<150> 60/080,664  
<151> 1998-04-03

<150> 60/105,234  
<151> 1998-10-21

<160> 844

<170> FastSEQ for Windows Version 3.0

<210> 1  
<211> 300  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 1

tctccccga gctgcaggcc tgcatacca gtaggtctac tggacatctg tactggttgt	60
tgngggaggaa cctctggctt gtcattaag tcctactgat ttctactatc ccctgaattt	120
ccccacttat ttttgtcttt cactatcgca ggccttagaa gaggtctacc tgcctccagt	180
cttacctagt ccagtctacc ccctggagtt agaattggcca tcctgaagtg aaaagtaatg	240
tcacattact cccttcagtg atttcttgta gaagtgccaa tccctgaatg ccaccaagat	300

&lt;210&gt; 2

&lt;211&gt; 299

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

cccagctgct caggaggctg aggcaggaga attgcttgaa cccaagaggc ggaggttgtg	60
gtgagccgag attgcacctt tgtactccag cctgggcaac gagcaaaaaa ctctgtctca	120
aacaaaaaga agaaaaaaa aaaaaaann nnnnnnnnnn nnnnnnnnnn nnnntnttct	180
ggcgncnagt cccaaantcn taccttgtaa gacctttann tnnctgngg tntttntnna	240
cncttanata nnnntntttn ctatcaanta tagggagant tttcntttng gggcaactt	299

&lt;210&gt; 3

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

atagattcg aacnnggaca agacgagtat ggaataatat cccactnnnt ttacaatact	60
ganattatgc nngatagng cttgttccat tcnaccagcg aatnatgcat tnacncnaca	120
cnngagttac tatccaaaca cacgttttca cgntacctga ngctggtnga naattatgcy	180
accatgagge tttccangat ntttctannt ancagacngn gnacaatgnt gaanaagcng	240
tacacaccgc nctngncnnc cnnactgan cangtnacnn ngctcactgn ngcctcttct	300

&lt;210&gt; 4

&lt;211&gt; 287

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

aaancngcac gangccagct ncgnnnngnt nntactnnnc natngccnnc tcantggcng	60
ncagctagac gcctaacagc cgangancca nccntnntgt ganccngtcn tgacngnnag	120
cntgccggtc ttgctcnttt tgtctaccnn gagganannn ntntgggaca tcccagactg	180
agtgaggaga tctgcngctg cnnctgtact tggttacanc ncacacgang actntncctt	240
ggactanana cactagccta anattcngca ctacctantc ctctggc	287

&lt;210&gt; 5

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

gtccttttga accaccccaa agaactcaac atggcaaagc aatgggtaaa agcttcccga	60
ctgttctact ttgggtccgc gcgaagccca ctcacgtgtg atctgtgttg ccctgggag	120

gccccggggcg accggaaaaag ggctctctca agttctgaaa agagaatctg ccaccagatc 180  
 gaatttcgac ccctgagctt gttcggacgt atgggccaaa ttcagattaa ggtgggtcacc 240  
 caacccgaga tgtcaggaaa ggccttctgc agagaaaatg tccccccacc cgccatctgc 300

<210> 6  
 <211> 284  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 tntcccccttt gacgccttan tgccctnncg ctacnngtcc nttaggcctt atccccatcgn 60  
 ccntcgtttn gcattctgccc nnagantgac tttncnatca tgcntnatnn gtnnttacna 120  
 ggggctnngg tgaattntta caccctgcn ntccatanca cantgccntg cnagctncac 180  
 cctcntgaat aaatgcaata aantttcngt tgatcttata caccttatgc nccntantta 240  
 atcagccctn tnttacnana tcnanttatg cnggtattaa aaca 284

<210> 7  
 <211> 277  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 gtgctgcaga caacacacct tcctgatgga ggtgtccggc tgatggagaa gtctgtgggc 60  
 ttgtaaatca tctttgatgt taaccaggcc gacgctgtgg ccacattccg aaagattaac 120  
 cctgtcaaac cctannnnnn nnnnnnnnnn nnggatttg atnagcctgt nccanacctc 180  
 tgcagcctcn ancggtnngtn ntaccatagt ggggatgacc ctctgatact ttgncctggg 240  
 ngancatgnt gacanntgct tctacagctt nngggac 277

<210> 8  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<400> 8  
 cttgggaggc tgagtcagga gaattgcttg agcccaggag atggagggtg cagtgaacca 60  
 agatcatgcc actgcactcc agactgggca acagaggag actccgtctc aaaaactaaa 120  
 aaaaaaata catttagtat agcggggggg gggcgggaga aataatgtta tttcctatgc 180  
 aaatgacggn nnnnnnnnnn cccatggtaa atgtnaatat actgcgtctn ttttgggana 240  
 gccttttant aaangagtct tanatgaatc tctanntnat gantttaact tg 292

<210> 9  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 9  
 ccagggttagc tgctgaatca aagcttcaaa cagaagttaa agaaggaaaa gaaacttcaa 60  
 gcaaattgga aaaagaaact tgtaagaaat cacaccctat tctatatgtg tcttctaaat 120  
 ctactccaga gaccagtgcc cctcaacagt aaagactttt ctttaataag agtacgggtgc 180  
 cacttgccctc aaaagtact atggtgctta agattgtctt gatctgacat atatcacctt 240  
 ctgggttatt tactcattgt gccaggacct ggcattttca tgtgcctttg accaagtgtt 300

<210> 10  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 10  
 aggaggcgga gcttgcaagt agctgagatc gcgccactgc actccagcct gggcaacaga 60  
 gtgagactct gtctcaaaaa aaaaaaaaaa nnnnnnnnnn nnnnnnnnaa nctcgtnttn 120  
 gnaagggaan ggggnaangg accggtntta tncctatgtn gtntttgcag gcaaangaaa 180  
 nggaccntt tttgtaaaaa aaagtctttt gnncaantaa acgggggtntg ngggtnccagg 240  
 ccctggnggg gcncncantt gcctggnggc ttntgnnaaa tcggnaaagg gaggaaggc 300

<210> 11  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 cgtctgtaat ccagctgct tgggaggctg aggcaggaga atcacttgaa ccctggagggt 60  
 ggcggtttca gtgagcacag atcatgccac tgcactccag cctgggcaac aaaacgagac 120  
 ttcgtctcaa aaaaaaaaaa nnnnnnnnnn nnnnnnnnnn nncgggttct cccaaattnt 180  
 ttnnaggggn ccatggncaa ctgnttnacn tttgtttngg naacccttg cccnaagncc 240  
 cananaggct gtnnttncc ttgttnccaa ggntgaggan caaaaagtac cctntgtttt 300

<210> 12  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 12  
 caaagatggt cgtattacta aaggatgaata accagcgcgg ggggcacgtg gagtcaactgg 60  
 aacatttgtg caatgctggt gggaatgtca acccgtgcgg ccctctggaa taagcctggc 120  
 agtcctcca agagttaccg tgtgaccacg caattccact cctagctcca cccacaggaa 180  
 ttgaaagcaa agacgcaaac agatgcctgt gcaccaaagt tcacggcagc atccttcgcc 240  
 atagtggcag catcgtcgt cacagcggca tcatecttca tcatagcggc agcatccgtc 300

<210> 13  
 <211> 278  
 <212> DNA  
 <213> Homo sapiens

<400> 13  
 cctgcagcca ctaatgcatt gtgtatgata acaaaaactc tggatgaca ctttttctgt 60  
 gatcattgtt aattagtac atagtaacat ctgtagcagc tggtagtaa acctcatgtg 120  
 ggggaggtgt gggaggtttt nncggnannn nnnngcnnnn annccccggn nngnnngaag 180  
 ctgnnnttn naannngcnn nnnannatga naannncenn ngactggnnn nangaggcct 240  
 anccctgtnt ttananaaac nnnncnncagn ntctctca 278

<210> 14  
 <211> 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 14

gtgtcttcat	cttaccagct	ggaacctaa	aaattaaatt	ctccagaaga	aactgctttt	60
cagacaccaa	aatctagcca	gatgcctcgg	ccttcagtgc	caccattagt	taaaacatca	120
ctgttttctt	caaaattatc	tacacctgat	gttgtagagc	catttgaggc	cccatttggc	180
tctagtgtaa	tgaatcggat	ggctggaatt	tttgatgtaa	acacctgcta	tgggtcaccg	240
caaagtcctc	agctaataag	aagggggcca	agattgtgga	catcagcttc	tgatcagcaa	300

&lt;210&gt; 15

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

gttatattaa	attattcttt	gtttttcttt	ttcttttaat	aaagcctgca	agttactaaa	60
ttgtagtttc	ataaattctg	tagtaaagta	tcatcttggc	agtgtgccaa	aggtgaaaat	120
gatgctttct	ctaacagaga	aattcttagt	gactccagtc	gtagaaaaac	gtcttttaca	180
cctgaataag	attgaagaat	tgtgaacata	ccatggccta	ttggatgaat	catttgccgt	240
aggctaaatc	agactgtagg	gtttgcatg	gatttatgga	gtatgtgggt	atagaaatca	300

&lt;210&gt; 16

&lt;211&gt; 276

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

gtttcattta	agaagaatga	gctagataaa	tgtgctcttc	tggttacccc	accctgacag	60
agtgcatttt	tacacggcta	gcaggggttg	agactgcagc	ctggcctnnn	nnnnnnnnnn	120
ngnnnnnnngc	nnacttnact	tcccngaanc	actataattg	gnanacnttn	ctaannggtn	180
atctngccga	cctgnnagat	anactcnnga	taaaanccnn	tgcagaaagc	gcccttccat	240
gtcangcncn	tnaganacnn	ncntaccncc	tangna			276

&lt;210&gt; 17

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 17

ggtgcccata	accacaccca	gctaactttt	gtatttttag	tagagacggg	gtttcaccat	60
gttggccagg	ctggtcttga	actcctgacc	togtgatecg	cccgcttgg	ccccgcaaag	120
tgctgggatt	acaagcatga	gcccagcgcc	tggctgtatc	tttcatttta	cccaagtcac	180
tttaccceaag	taagtaatta	ggggaaagcc	tgagtcttgt	accacctgtt	catttgggga	240
actgtgggaa	acggagccaa	cggacctaa	tgcccttga	cagtgagttt	cataccattt	300

&lt;210&gt; 18

&lt;211&gt; 273

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 18

ctcagctgag gcaattaaac tggaaaagaa atagattgaa aagatactac agaagaagca	60
gtacagaagt tgggggactg aaggagaggg agccactgca ggtgctagct gcttaagggg	120
ataccagtcc ttttacagat ataatagata cagcttctga ggtggagggg gataggagtg	180
tgtagagaaa ttgcagttca gaactggagc atgcagttag gcaagaggca tcccatgtga	240
agatgtcaag caagtactgg aaaatgctga act	273

&lt;210&gt; 19

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

gggtcctggt gggagttcca tccagcagtg agtgcatttt ttccccagag cagttaaggg	60
tcttattaaa agccaccact ttgctgaggc ctgtacaggc cttgggggtt tggggaagag	120
aaataaggca ggcacttgct ccttcaggga gggacttgct cctcactggg aggtttgggg	180
ttgaccttgg ctccagcaga gatacccagc ctggcgtgga aggggcagggt ctgagcttac	240
gcttgactgc agggcaagct gcaggcctct tctgccttcc cctgcattca ccaaggacag	300

&lt;210&gt; 20

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

atggcatgca ctgacctctt cttggagccc agaactttat agagttgcct accagggtta	60
ctgtaatgga atttatgac ttaagaaatt actagttgta ttatttatcc tatgattcat	120
tcattcaata agcttttact gcataaactt tacatccagc actgtagtta agtaccctaaa	180
attgaataga aataatggct ttgaaaatc gcacaaagca ggccaggcac ggtggctcac	240
gcctgtaatc ccagcatttt gggaggccga ggcaggcgga tcacgagggtc aagagatcca	300

&lt;210&gt; 21

&lt;211&gt; 293

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 21

cgtctgtaat ccagctgct tgggaggctg aggcaggaga atcacttgaa ccctggaggt	60
ggcgggttga gtgagcacag atcatgccac tgcactccag cctgggcaac aaaacgagac	120
ttcgtctcaa aaaaaaaaaa nnnnnnnnnn nnnnccttng gncgggttnt cccaaattnt	180
tttgaggngn ccatggncaa ctgcttnanc tttgttttgg caaccccntg ccnaagtcg	240
catataggct gtncttcacc ttgtttccaa ggctgnggaa canaaagtaa cct	293

&lt;210&gt; 22

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 22

ctggtctcga acacctgacc tcagggtgac cattcgtctt ggctctcga agtgctggga	60
ttccaggcgt gagccactgc ggccagcaca ttccacttt tagatcctac tccataccac	120

```

aggttttcatt taagaagaaa gagctagata aatgtgctct tctgggtacc ccaccctgac      180
agagtgcatt tttacacggc tagcaggggt tgagactgca gcctggcctg ccagccattg      240
gaggtgttta aggaagggca gataatgtga ctctttgcgg ggtgccatct gcttaccat      300

```

```

<210> 23
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 23
gaaccaaaga cgtgtatgga gtgttctctt gtccttatcg acttgctctg ctcccagctt      60
tccaagcgac cggatctgag tgatgcttct agaacatttg ggtgttgggg gggtcccaat      120
agtagaaagg gtccccattc ctgctcagca ccgcacctct ctaccccccc acagacacac      180
atgcagacac acacatgcag acaacacgca gacacacaca tgcaggcact cacatgcagg      240
cccatgcaca cacacgtgca cacacatgca gagacatgca gacacgcagg cacacatgca      300

```

```

<210> 24
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 24
cctcccacaa cacgtgggaa ttcaagatga gatttggttg gggacacagc caacccatat      60
caccatgcc tggatgccct tctcatgctt gggttctgtc atctgcacca ggccttctgc      120
tgccgtctg tcttaccac caggactctg actctccacg ctggggccacc tctcttctcc      180
aacactgcta tggattgaat gtttatgtta tccccaaatt tgcattgtgc aatcccaatc      240
tccaatgcca tagtattagg aggtgggggc ctttgggagg tgatttggtc atgaagggtg      300

```

```

<210> 25
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 25
ggaaaatgaa atctgactat ctgctagttg ccaaaaccca gaaacattcc tgtgtaatgg      60
ttagttggga aagaaggcag cacttgaaaa aatttaccag gtccctcact gggagatgtg      120
ggaaggggcg tgggacgcac gcggtcactc cctctcagcc cccacattt ctagaacaca      180
ctgtagctgt gcctctacag actcccgtg cctggcctcc acagatcctg ctgagattca      240
ccagtaggca aagcttggcc ctattagctt tttctctcca tggctctgtg ggaatgtgcg      300

```

```

<210> 26
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 26
ctgcagtgag attctctgca atgactggcc tcagcaaggg ggcagcttag gaccctgaca      60
tcccaggtca ctaagccaca taggataagt aatgggtgga cagaagcggg aaaggagaag      120
ggcagggcac atgtttaaaa cttgaacttt ctgaggctaa gactggaaaa ggaatggttt      180
cagctgatat atttggatac cagttgacta tttttaggaa aaaaacacaa atggctttta      240

```



aacatcacag tgtgatacag tctaactcag aattagagac aggcaaaaca gaactccatc 300

<210> 27

<211> 300

<212> DNA

<213> Homo sapiens

<400> 27

gtactgcttc tgtggctctt cacagacctc acggatgtga ccggagatga gtgccgatga	60
ccacgtttta aaggagaaag agagctcctg gtggggccct cgggggtggc tcaggtccca	120
tttgcaagtct gcaacagtga cgcgcagccc ggtccggagc gtggtagagct ttgtttgcct	180
tctgggtcag ctttcgctgt gtctcctgtg tgtgttagaa tccagagccc agaggaagtg	240
caagcgggtc ctccgccaac ggggagagcc tcttcgcggc gctgttggeg acagcacgct	300

<210> 28

<211> 298

<212> DNA

<213> Homo sapiens

<400> 28

aangnaannn ngggnggtg antcnacctn ngaaccgtgt anaaacccat ggaaacagct	60
antaganntt gggcagganc agagngaggc caagntacgg gggaggcnag gagcngagan	120
tggggnnnnn nnangnnaan tnnngaaggg gngngannga gggggggana naagggggga	180
ngagggcgaa ngncaggann nagaaaannn ggggacgana nggngaacag ggnnnaaacg	240
gaannnnnga gnnnnnanag atgncgggca gngncngngn agnganann ngagacgg	298

<210> 29

<211> 300

<212> DNA

<213> Homo sapiens

<400> 29

cctcagcccc acaccagctc tatttcaggg gtgagagtca gagagcactg caatatgtgc	60
ttcatgggat ttcgattcga agatcctaga ccaggagagc actgtgagcc agggatacaa	120
caaaatacta ggtaagtcac tgcagaccga cctccctgca gtttgggaaa gaagctgggt	180
ttgtggagaa tcagagcatc ttgacatgac tgetgaccta aagatccctg gcattggcca	240
gggatcctgt ggaacctctt ctagttcagg ggtgtgagca ttagactgcc agttgtctag	300

<210> 30

<211> 300

<212> DNA

<213> Homo sapiens

<400> 30

gtttgtttcc ccgagatgtg aacttgctga aggaaaacag tgtaaagagg aaggccatac	60
agagaactgt cagctcttca ggatgtgaag gcaagaggaa tgaagacaag gaagcagtga	120
gcatgttggt taactgccct gcctactaca gtgtgtctgc tcccaaggct gagctactga	180
acaaaatcaa agagatgccca nnnnnnnnnn nntgaggaag aggaacaggc anatgtcaat	240
gaaaagaagg ctgatctcat tggaagtctc acccacaagc tggagaccct ccaggaggcg	300

<210> 31

<211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 ttttaaactga gctccaaatg acgttcaaac acccctctcg ggtagagttt tcatggtgga 60  
 acggttgctg ccaccaaaaca gaagcttatg tttttggcac agaaggcctg ggccattttc 120  
 atggacacct ggctggacct cggtggaagt gaactccgta ggttggtgctg ttactgacag 180  
 cacctcacat gataccgtcc cctctcatgg aacggagcct ccccatgca gccccactc 240  
 aatggagtt ttaaaggctg ggttcagggt acgggggctg ttctcacctg ctgaatgcgg 300

<210> 32  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 gtgaaacaga aagtggagat gctttccttg acctgaagaa gcctcctgcc tccaaatgcc 60  
 cccatcgcta taaaaaagaa gaactcttgg atataaaaga actccccat tccaaacaga 120  
 ggccttcctg cttttctgaa aaatatgaca gtgatggtgt ctgggacctg gagaagtggc 180  
 atgcctctct ctaccagct tcagggcgga gtcaccagt ggaaagtctg aagaaagagt 240  
 tggatacaga ccggccttcc ctggtgcgca ggatagtaga tccacgagag cgtgtgaaag 300

<210> 33  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 33  
 gtctgattga agctgttcag gtttatcatg caaatcctcg cctctggcta eggctggctg 60  
 aatgctgcat tgctgccaat aaggggactt ctgaacaaga aactaaaggc cttcccagca 120  
 aaaaaggaat tgtacagtct attgttggtc aaggctatca tcgtaaaata gttttggcat 180  
 cacagtctat acagaatact gtttataatg atgggcagtc ttcggccatt cctgtagcca 240  
 gtatggagtt tgcagccata tgtctcagaa atgccttggt gctgctacct gaagaacagc 300

<210> 34  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 34  
 tgacagagct gttcagcgta caccagatcg atgagctggc caagtgcaca tcagacactg 60  
 tgttctctgga gaagaccagt aagatctcgg accttatcag cagcatcacg caggactacc 120  
 acctggatga gcaggatgct gagggccgcc tggtagcgg catcattcgc attattaccc 180  
 gaaagagccg tgctcgccca cagacctcgg agggtcgttc aactcgggct gctgccccaa 240  
 ccgctgctgc ccctgacagt ggccatgaga ccatggtggg ctcagggtctc agccaggatg 300

<210> 35  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 35

cttttttaag	caaagcagtt	tctagttaat	gtagcatctt	ggactttggg	gcgtcattct	60
taagcttggt	gtgcccggta	accatgggtc	tcttgctctg	attaaccctt	ccttcaatgg	120
gcttcttcac	ccagacacca	aggtatgaga	tggccctgcc	aagtgtcggc	ctctcctggt	180
aaacaaaaac	attctaaagc	cattgttctt	gcttcatgga	caagaggcag	ccggagagag	240
tgccaggggtg	ccctgggtctg	agctggcatc	cccattgtctt	ctgtgtccga	gggcagcatg	300

&lt;210&gt; 36

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

gctggccaaa	gccaaatctc	ctaagtccac	cgcccaggag	ggaacctga	agcctgaagg	60
agttacggag	gccaaacatc	cagctgcagt	tcgcctccaa	gaaggggtcc	atggccctag	120
tcgagtccat	gtgggtctctg	gggaccatga	ctattgtgtc	cggagcagga	ccccccaaa	180
aaagatgcct	gccctagtca	ttccagaggt	gggctcccga	tggaatgtca	agcgccatca	240
ggacatcacc	atcaaacctg	tcttgtcctt	gggcccagct	gcccttcgcc	ccatgcatag	300

&lt;210&gt; 37

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 37

gtccaaggac	aacttcgaga	cattttctttt	tgccaccgta	tctaacaggg	agcaggaaga	60
tctctgccga	ggaattgtcc	agctctgctt	caatgagcaa	agccaacagc	tgctagcaga	120
ggtccagccc	tctgactctt	tcctcatggt	agagacaact	gcatactttg	aggcctacag	180
gcacgtcctg	gaaggactcc	aggaggtcca	ggaggaagat	gttcccttcc	agaggaatat	240
cgtggagtgt	aactctcatg	tgaaggagcc	aagggtacttg	ctaattggggg	gcagatatga	300

&lt;210&gt; 38

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

catccaggga	gaacctcggg	gctgggacac	ctcctggccc	tcacctggg	tcattgtttac	60
agtccctcagt	gccccacacc	ggtggccccc	tgaggacacc	tccacctga	ccttgatttt	120
cccaaacgct	gcctcttggt	gacagactca	gccccaaaacc	ccttccctct	gtctctggag	180
acccttgagc	ttggggaaat	atggaggggt	gtgtgtctgc	aatcaaggcc	tctgcagctc	240
acggctggcc	cgggtgggctg	ggacttccgt	atgaattnta	aatacttagg	gttcattttt	300

&lt;210&gt; 39

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

gggaaggagc	ggcgtgagg	ccagctgagg	catggtgacc	cctgggaagg	agcgggcgtg	60
aggccagctg	aggcatggcg	acccctggga	aggagcgggc	gtgaggccag	ctgaggcatg	120

gtgacccctg ggaaggagcg ggcgtgaggg cagctgaggg atggtgaccc ctgggtacgg	180
gggacttggg ggcgcacct tggtttgccc agggcccctc ctgcaccacg ggccacatgc	240
ggaggacggc gtgggatagg ctccctgggt ccacagcttc tgcccgtgta tggggaaccc	300

<210> 40  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 40	
ccaaaagctt gtggcaaatt tgaaatttct gccattaggg accttacaac tggctatgat	60
gatagccaac ctgataaaaa agctgttctt cccactagta aaagcagcca aatgatcacc	120
ttcacctttg ctaatggagg cgtggccacc atgcgcacca gtgggacaga gcccacaaatc	180
aagtaactatg cagagctgtg tgccccacct gggaacagtg atcctgagca gctgaagaag	240
gaactgaatg aactggtcag tgctattgaa gaacattttt tccagccaca gaagtacaat	300

<210> 41  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 41	
aaaaggctcc ccttctggga aagaccgagt gaagaaaggt ggatcctaca tgtgccatag	60
gtcttattgt tacaggtatc gctgtgctgc tcggagccag aacacacctg atagctctgc	120
ttcgaatctg ggattccgct gtgcagccga ccgcctgccc actatggact gacaaccaag	180
gaaagtcttc cccagtccaa ggagcagtcg tgtctgacct acattgggct tttctcagaa	240
ctttgaacga tcccatgcaa agaattccca ccctgagggt gggtacatac ctgcccacatg	300

<210> 42  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 42	
ttctaagtca ggagtacagt acaaaggaca tgtggagatc cccaatttgt ctgatgaaaa	60
cagcgtggat gaagtggaga ttagtgtgag ccttgccaaa gatgagcctg acacaaatct	120
cgtggcctta atgaaggaag aaggggtgaa acttctaaga gaagcaatgg gaatttacat	180
cagcaccctc aaaacagagt tcacccaggg catgatctta cctacaatga atggagagtc	240
agtagacca gtggggcagc cagcactgaa aactgaggag cgcaaggcta agcctgctcc	300

<210> 43  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 43	
gccaccgaag cttcaggatg acatcttaga ctctcttggg caggggatca atgagttaaa	60
gactgcagaa caaatcaacg agcatgtttc agggcccttt gtgcagttct ttgtcaagat	120
tgtgggcat tatgtttcct atatcaagcg ggaagcaaat gggcaaggcc acttccaaga	180
aagatccttc tgtaaggctc tgacctccaa gaccaaccgc cgatttgtga agaagtttgt	240
gaagacacag ctcttctcac ttttcatcca ggaagccgag aagagcaaga atcctcctgc	300

<210> 44  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 44  
 ggcttataca acatagtggg gaacgcatgg gaatggactt cagactgggtg gactgttcat 60  
 cattctgttg aagaaacgct taacccaaaaa ggtccccctt ctgggaaaga ccgagtgaag 120  
 aaagggtgat cctacatgtg ccataggtct tattgttaca ggtatcgctg tgctgctcgg 180  
 agccagaaca cacctgatag ctctgcttcg aatctgggat tccgctgtgc agccgaccgg 240  
 ctgcccacta tggactgaca accaaggaaa gtcttcccca gtccaaggag cagccgtgtc 300

<210> 45  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 45  
 gtggaagaaa attttttgct gcttctgggtt cccagaaaag ggagccattt taacagacac 60  
 atctgtcaaa agaaatgact tgtcgattat ttctggctaa tttttcttta tagcagagtt 120  
 tctcacacct ggcgagctgt ggcattgcttt taaacagagt tcatttccag taccctccat 180  
 cagtgcaccc tgctttaaga aaatgaactt atgcaaatac acatccacag cgtcggtaaa 240  
 ttaaggggtg atcaccaagt ttcataatat tttcccttta taaaaggatt tgttggccag 300

<210> 46  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 46  
 gtggaagaaa attttttgct gcttctgggtt cccagaaaag ggagccattt tangngacac 60  
 atctgtcaaa agaaatgact tgtcgattat ttctggctaa tttttcttta tagcagagtt 120  
 tctcacacct ggcgagctgt ggcattgcttt taaacagagt tcatttccag taccctccat 180  
 cagtgcaccc tgctttaaga aaatgaactt atgcaaatac acatccacag cgtcggtaaa 240  
 ttaaggggtg atcaccaagt ttcataatat tttcccttta taaaaggatt tgttggccag 300

<210> 47  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 acacagataa ttttaataca atgtgaaaaa gtgtatgggt gtgtagaaga ggggttctta 60  
 gagtttctgg agagaatgat tctgagctcg gttttgacaa aagaggagct gctgaggcta 120  
 aaagtggatg aaaagggcct tataattaaa agaaacaaga caggactcag aggtgtgaaa 180  
 caaatattat gcatggtgaa ttacaatgag ttgggggtat tctgtagccc taaagtacaa 240  
 ggtataaaga gacagaaaat gatcctggaa tatagacaga ggataacttca tctctcatga 300

<210> 48  
 <211> 300  
 <212> DNA

<213> Homo sapiens

<400> 48

gatggaacat	gagtggaa	gttggcag	ttttcttt	tattcagctga	gtgaatgaag	60
atntagaggg	cagcagagtc	atgacatgga	tgacgttggg	tctctggatg	gctaaatgga	120
agacccgccc	cccaacgcca	ctctaccccc	ctgctttgaa	ctatgctttg	agaaatgagc	180
ttatgagacc	actgagactt	gggggctgtt	tgttcagcag	ttcacctaca	cttattagga	240
aaggttgact	tcttgtaact	acgcctttcc	ttaaatacatc	ttttgtataa	ttctcagaag	300

<210> 49

<211> 300

<212> DNA

<213> Homo sapiens

<400> 49

ccctccccgg	cttccccgg	agtgggtcac	cacactgttt	tttatcatca	tggaatcat	60
ttcattgact	gtcacatgtg	gtttgctggt	ggcttccac	tggcgaagag	aagctacaaa	120
atatgctoga	tggatagcat	tactggaac	cactatgaga	agattatagg	aaaaacacca	180
agactagagg	actctgggtt	ccttttatgc	aaagtcaact	cttctgggtc	acagttaccc	240
agcaacaaaa	ataaagagag	gaccaggacg	atgccagcac	cccgtttatc	ctgagtgaac	300

<210> 50

<211> 300

<212> DNA

<213> Homo sapiens

<400> 50

ctcctgtctc	agcctcctgg	gtagctggga	ctacagggtgc	atgccaccat	gcctgggctaa	60
cttttgtatt	tttagtacag	acagggtttc	accacattgg	tcaggctggt	ctcgaactcc	120
taacctcagg	tgatccacct	gccttggcct	cccaaagtgc	tgagattaca	ggcgtgagcc	180
accgcgcctg	gcctgattgg	ttttttaaca	tgatttttct	ctaagcttaa	ataccacaag	240
gccaaagaga	aatggtcata	atttaaacca	ttattatatt	ggtgagggtat	ccctagctat	300

<210> 51

<211> 300

<212> DNA

<213> Homo sapiens

<400> 51

ggaggctaga	ctcaagctgt	ctggagagtg	tgaacaaaa	gtgtgtgaag	agttgtaact	60
gtgtgactga	gcttgatggc	caagttgaaa	atcttcattt	ggatctgtgc	tgccttgctg	120
gtaaccagga	agaccttagt	aaggactctc	taggtcctac	caaatcaagc	aaaattgaag	180
gagctggtac	cagtatctca	gagcctccgt	ctcctatcag	tccgtatgct	tcagaaagct	240
gtggaacgct	acctcttctc	ttgagacctt	gtggagaagg	gtctgaaatg	gtaggcaaag	300

<210> 52

<211> 300

<212> DNA

<213> Homo sapiens

&lt;400&gt; 52

atatgggtata gttggaaata ggttattgtg agttatttgt agtcatgtct ttaatggccc	60
ttgcatgggtg tctaacttct gcaataaatg atctgccagt cctagtgtct ggctttatgc	120
aatttgtttt cctttgtgga tgaagtggga gtaagacttg ttgctgtgag gattagatga	180
agtggctagg atatggacac actttacttg aattggaaaa caagccatgt atccctaadc	240
tgcaaatgt ggcatgtcac acgtgtaatc tctgaggttt agtttttgct caagattgca	300

&lt;210&gt; 53

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 53

aagaagctct gcttgggtact actattatga acaacattgt tatttggaaat ttaaaaactg	60
gtcaactcct gaaaaagatg cacattgatg attcttacca agcttcagtc tgtcacaaaag	120
cctattctga aatggggctt ctctttattg tcctgagtca tcctgtgcc aaagagagtg	180
agtcgttgcg aagccctgtg tttcagctca ttgtgattaa ccctaagacg actctcagcg	240
tgggtgtgat gctgtactgt ctctctccag ggcaggctgg caggttcctg gaaggtgacg	300

&lt;210&gt; 54

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 54

ccaagatgcc aatttccatg aagtcctgat ttatatatat gtacacatgt tatgcacata	60
catgtttgtt ttctaacagt tattttttaa gcttttgaga taattttaga cttacagaag	120
agttgtaaaa gtagtagagt tcttgatata tctgcaccca ccttgccctt atgttaacat	180
cttacgtaac aatagaacat ttgtcaaat taagaaatta accttgatat aataactaact	240
aaagtagaaa gtttaaaaag tagagatttt agtcttttca ctaatgtcct tttactgttc	300

&lt;210&gt; 55

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 55

gggagggacc cttgggggca ggttgtgggt agccagttgc agtctgtggc ctccctcaga	60
ggtttgaggt cgggcgtggc atgctgctgt tggcctcttt ccgagggagt gccatccact	120
ccctgtccca ccgctgtccg cgggtaggac agtgagggca gtgctacgtg gtggggaggt	180
gtgtgagaag ccacggaagg gcttcacagg gcagatgcca aggccagtgg gccccggaca	240
gagtcaggct ccctgggcgg ccttgtgtct tgggtggcct gatcatcctg ccaatgcaaa	300

&lt;210&gt; 56

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 56

ctttgtctc tccattccaa gttgttctct gttctagaaa gcagatgtag tagacatcta	60
ctgtttttgc ctaaacagaa tccctttttc ctttttttgt taaaagtact catccctaact	120

attacattgt tctggaagga ctgaaaataa cagaactcag caccatgatc ggaccgggac	180
aatcagatta ttccattcct cagcaaacgg agatcgatcc gaaaagtgga aatatgagct	240
cttcttttgggt gttggcatat ggaccctgag agaaagaact ttaatttttt ctcttggact	300

<210> 57  
 <211> 276  
 <212> DNA  
 <213> Homo sapiens

<400> 57	
cctccctgga tgtgcagaca tggaggagga cagaaggccc agctcagtgg cccccgctcc	60
ccacccccca cggccgaaca gcaggggcag agccagnnnn nnntcgaagt gtgtccnngt	120
tgtcttttga nccttgtnnt ggngccttgc ctanatgtat ntntntnnn tntntnatt	180
tnnnnntnn ntntntnct nttntaaat tgnttnnaan ttntntann ttntnnatt	240
nnnnnnnnn ntantgtntt gnattgntat nnatca	276

<210> 58  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 58	
ctgtaagtct ctttcttgcc catcaccaca tccctagtagc tgggtatcag tctggccact	60
tggtcttctg gtttgcccca atgtggtcta ttcttgatgc agctaccaa gtaatgtttt	120
aaaaccatta taccaagtta ctatccttgc caaaaccccc agtaactgcc aatctcactt	180
agaataaaat cggactcct gtgaagcaca gcataaactg gccactgcct atgcagcaac	240
ctcatcttta cggtttctg ccttgctcac tcccttcag cgccgttatt ctctctgatg	300

<210> 59  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 59	
gaccaggtta gaccagctca agagttcatg ttctttgtca tccnngtgag agctctctgt	60
aagtctcttt cttgcccac accacatccc tagtactggg tatcagtctg gccacttggc	120
tttctgggtt gcccaatgt ggtctattct tgatgcagct accaaagtaa tgtttataaa	180
ccattatacc aagttactat ccttgtcaaa acccccagta actgccaatc tcaactagaa	240
taaaatccgg actcctgtga agcacagcat aaactggcca ctgcctatgc agcaacctca	300

<210> 60  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 60	
gggtcctgggt gggagttcca tccagcagtg agtgcatttt ttcccagag cagggttaagg	60
gtcttattaa aagccaccac tttgctgagg cctgtacagg ccttgggggt ttggggaaga	120
gaaataaggc aggcacttgt cccttcaggg agggacttgt ccctcactgg gaggtttggg	180
gttgaccttg gctccagcag agatacccag cctggcgtgg aaggggcagg tctgagctta	240
cgcttgactg cagggaagc tgcaggcctc ttctgccttc cctgcattc accaaggaca	300



<210> 61  
 <211> 292  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
 caaggcccga ggtgccatcc cctctgggaa gcagaagcct ggnggcaccc agagtgggta 60  
 ctgtngnggt aaagngntca cctctcaca gcaccaccag cggcgagaca gacccacca 120  
 ccatcttccc ctgcaaggag tngggcaaag tcttcttcaa gatcaaaagc cgaaatgcac 180  
 acatgaaaac tcacaggcag caggaggaac aacagaggcn aaaggctcag aaggcggtt 240  
 tngcagctga gatggcagcc acgattgaga ggactacggg gcccggtggg gc 292

<210> 62  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 62  
 agcaaataca gatcttcagg tacagttgga ccaggcactc cagcaagcct tggatcccaa 60  
 tagtaaaggc aactctttgt ttgcagaggt ggaagatcga agggcagcaa tggaaactca 120  
 gcttatcagt atgaaagtca agtatcagtc actaaagaag caaaatgtat ttaacagaga 180  
 acagatgcac agaataagt tacaatttgc cacgttgcta cagatgaaag ggtctcaaac 240  
 tgaatttgag cagcaggaac ggttgcttgc catgttggag cataataatg gtgaaataaa 300

<210> 63  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 caggcctgga cttcgcccc aggcctagga ccgcggaggg tggaaacctg ctactgcccc 60  
 aacagggaact ccaatcaatc ggagttctcc ccttgccgga gctgcccttc acctttgggg 120  
 cccgagacag tcataaggga tggacttagt tttcttgca ggaataagggt ggacagccgt 180  
 gtttcttaag gatgctgagg gcatggggcc aggaccaggg gagaggcaca gctccttctt 240  
 gagcagcctc tcaccactgc cacaaggctc cctaattgctg gtctctgctc cactccccgg 300

<210> 64  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<400> 64  
 gctgcatctg caatgaggat gccaccctac gctgcgctgg ctgcgatggg gacctcttct 60  
 gtgcccgtctg cttccggtgg gtgcaggtgg aatgttctgt gcgagagctc aagggtgcc 120  
 tggatccctg acttgatatc ctttgttcca cagagagggc catgatgcct ttgagcttaa 180  
 agagcaccag acatctgcct actctctcc acgtgcaggc caagagcact gaagacaccc 240  
 tggctctccc ggaaggcag tcccacaggc agcggcacc atttctgggc cccg 294

<210> 65  
 <211> 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 65

aattgatgag	ccttattaac	tatcttttca	ttatgagaca	aaggttctga	ttatgcctac	60
tggttgaaat	tttttaattct	agtcaagaag	gaaaatttga	tgaggaagga	aggaatggat	120
atcttcagaa	gggcttcgcc	taagctggaa	catggataga	ttccattcta	acataaagat	180
ctttaagttc	aaatatagat	gagttgactg	gtagatttgg	tggtagtgtc	tttctcggga	240
tataagaagc	aaaatcaact	gctacaagta	aagaggggat	ggggaagggtg	ttgcacattt	300

&lt;210&gt; 66

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 66

agcagatttg	tgataaactt	gctgtagaag	aaaccaaagg	ggaacttctg	ttgcaactat	60
gtcgttttga	agatgctgca	gatgtttata	gaggattgca	agagagaaat	cctgaaaact	120
gggcctatta	caaaggcttg	gaaaaagcac	tcaagccagc	taatattgta	gaacggctaa	180
aaatttatga	ggaagcctgg	actaaatatc	ccaggggact	ggtgcccaaga	aggctgccgt	240
taaaactttt	atctggtgag	aagttttaaag	aatgtttgga	taagttccta	aggatgaatt	300

&lt;210&gt; 67

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 67

tgttcttgta	gtgtttgttg	ctattgttag	aaagattatt	agtgatattg	ggggtgtctt	60
anctaaacaa	cagacacatg	taagaaaaca	ccagtttgat	catggagagc	tggtttacca	120
tgcattgcaa	ttgttagcat	atacagccct	tggtatttta	attatgagac	taaaactctt	180
cttgacacca	cacatgtgtg	ttatggcatc	actgatctgc	tcaagacagc	tatttggtatg	240
gctcttttgc	aaagtacatc	ctggtgctat	tgagtttgct	atattagcag	caatgtcaat	300

&lt;210&gt; 68

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

agacaaagaa	aagggtggcaa	tcatagaaga	gttagtagta	ggttatgaaa	cctctctaaa	60
aagctgccgg	ttatttaacc	ccaatgatga	tggaaaggag	gaaccaccaa	ccacattact	120
ttgggtccag	tactacttgg	cacaacatta	tgacaaaatt	ggtcagccat	ctattgcttt	180
ggagtacata	aatactgcta	ttgaaagtac	acctacatta	atagaactct	ttctcgtgaa	240
agctaaaatc	tataagcatg	ctggaaatat	taaagaagct	gcaagggtgga	tggtatgaggc	300

&lt;210&gt; 69

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 69

aattcnacac	gaggtggccc	ataagtttta	ccttttaaac	atccggctgc	ctgtgaatga	60
gaagaataaa	atcaatgtgg	gaattgggga	gataaaggat	atccggttgg	tggggatcca	120
ccacaatgga	ggcttcacca	aggcgtgggt	tgccatgaag	acctttctta	cgcccagcat	180
cttcatcatt	atggtgtggt	attggaggag	gatcaccatg	atgtcccgac	ccccagtgt	240
tctggaaaaa	gtcatctttg	cccttgggat	ttccatgacc	tttatcaata	tcccagtagg	300

&lt;210&gt; 70

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

cccaaggcaa	gctgttaaca	aatcaacct	gggccaatca	tcaaaggggt	ggacctaaag	60
ttgctatact	caatagaaca	agcattttta	ataaatttct	cgtaagttgt	tgctttcttt	120
atgtggtggg	tgtggcttta	aagagcacia	aaccacaaca	aatcaaagag	tagctcgggc	180
ttgtcttttg	ctttatggct	gagggtttga	aggatgattc	atggacttgt	gaatgccagc	240
cccagtcceg	gcttaggtct	atctgccaat	accaccaggg	ccaacaaatt	cacgcaacaa	300

&lt;210&gt; 71

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 71

ggaaatgcaa	gtcaaaacag	ctttgtaggt	ctcagagttt	gcttttaaga	agtagtacia	60
gaaggaatag	ttatatcaat	acaccagtgg	ctgaaattat	catgaaacca	aatgttggac	120
aaggcagcac	aagtgtgcaa	acagctatgg	aaagtgaact	cggagagtct	agtgccacia	180
tcaataaaaag	actctgcaaa	agtacaatag	aactttcaga	aaattcttta	cttcagctt	240
cttctatgtt	gactggcaca	caaagcttgc	tgcaacctca	tttagagagg	gttgccatcg	300

&lt;210&gt; 72

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

ggattctttc	actgagcaca	aagagttgtt	ggggcttttag	catctgactg	attttgttac	60
ggggttgatt	ctgaccatag	gaagtatgca	atgtgaatca	ctatttacag	agaaacctac	120
aacagatgct	tgatgttgta	gaaactggga	catatagata	ccaagcaaaa	ttataagaaa	180
cctataaggt	gttcaatacg	cttgtgtttc	caaaattcac	tgtacatgat	cagtttgggtg	240
ttcttgtagc	acagttttta	actgaaggaa	ccagtgttaa	cagtctcaat	tttaactaaa	300

&lt;210&gt; 73

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

ataacacaca	tcacagtatg	ctctcagaaa	tttcttttatt	tgaaccttat	accaatatct	60
gttgatcaat	gaccattttt	gctcagcatg	gagaaacagt	gccctgcatg	aagggtagtg	120

agaataaaaa	ggatcttacc	acctttatca	tgagggtggc	tttgctctct	ccattccaag	180
ttgttctctg	ttctagaaag	cagatgtagt	agacatctac	tgtttttgcc	taaacagaat	240
ccctttttcc	tttttttggt	aaaagtactc	atccctaata	ttacattggt	ctggaaggac	300

<210> 74  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 74						
cagagtcaac	atggagcatc	tcactgtgaa	atgatccatg	gattgaagga	tatggtaaaa	60
tgtttatagg	ttactttgaa	agtaaaatat	actatgtctt	ggttttgagg	atattggata	120
caaaactctc	ttccttttagg	gctactgaga	cttgattcct	gatcatcaga	aatttcacca	180
gaaacaactt	gcttccaata	taccaaatcc	tatatgaaga	attcatggag	agtgtactgg	240
cactgnnnnn	nnnnnnngan	ncntgctgct	ncgaanntnt	nntattnact	gannttgaat	300

<210> 75  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 75						
caagagagag	tgatagaatt	ggcagtgaaa	tatacgaacc	accctcctgc	cctctgggtt	60
cacaatacgt	gtacacttga	ctgtgaagtg	gctgtgagag	tgggtggaga	gttcttcttt	120
gacctcagc	ctgcggatgc	ctctagaaac	ctcgtgttga	ttgcaggagg	agtcggaatt	180
aacctctctc	tttccatcct	gcggcacgca	gcagatctcc	tcagagagca	ggcaaacaaa	240
agaaatggat	atgagatagg	aacaataaaa	ctattctaca	gtgcaaaaaa	taccagcgaa	300

<210> 76  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 76						
gctagacgaa	gtggtgaagc	ccaaggactt	atttttgagc	tcgctgtaag	actgagaaat	60
cacgtactcc	ttcctgaaac	cactaagagg	aaaaatgtct	gtgacactgc	atacagatgt	120
aggtgatatt	aaaattgaag	tcttctgtga	gaggacaccc	agaacatgtg	agatggagtc	180
tcgctgtgtc	ccccaggctg	gagtacaatg	gcgcgatctc	ggctcactgc	aacctccgcc	240
tactgggttc	aagcaagtct	tctgcctcag	cctcccgaga	actgcaagag	gaggcaactg	300

<210> 77  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 77						
agagactttt	gtttgtgttt	aattagggct	atgagagatt	tcagggtgaga	agttaaacct	60
gagacagaga	gcaagtaagc	tgccctttt	aactgttttt	ctttggtctt	tagtcaccca	120
gttgacact	ggcattttct	tgctgcaagc	ttttttaaat	ttctgaactc	aaggcagtgg	180
cagaagatgt	cagtcacctc	tgataactgg	aaaaatgggt	ctcttgggcc	ctggcactgg	240

ttctccatgg cctcagccac aggggtcccct tggaccccct ctcttccttc cagatcccag 300

<210> 78

<211> 300

<212> DNA

<213> Homo sapiens

<400> 78

caggagcaat caattcctgt cgaagtgaat accatgcagc ttttaacagt atgatgatgg 60  
aacgcatgac cacagatata aatgcactga agcggcagta ctctcgaatt aaaaagaagc 120  
aacagcagca ggttcacatcag gtgtacatca gggcagacaa agggccagtg accagcattc 180  
tcccgtctca ggtaaacagt tctccagtta taaaccacct tcttttagga aagaagatga 240  
aaatgactaa cagagctgcc aagaatgctg tcatccacat ccctgggtcac acaggaggga 300

<210> 79

<211> 278

<212> DNA

<213> Homo sapiens

<400> 79

gtgctgcaga ggaagacagc ctgtcaggat actgacgagg aggaggaaga ggaagatgat 60  
gatcaggctg aatacagcgc catgttgctg gagcacgctg gagaggccat ccctgccctg 120  
gcagccgcgg ctgggggaga ctcccttgcc ccattctttg ccggtttcct gccattattg 180  
gtgtgcaaga caaaacaggg ctgcacagtg gcagagaagt cctttgcagt ggggaccttg 240  
gcagagacta ttcagggcct ggggtgctgct cagcccag 278

<210> 80

<211> 300

<212> DNA

<213> Homo sapiens

<400> 80

ggaacttctg agtaattggt atcatttctc agtgactcgg ctcttgact ccaatccac 60  
agtaaaaccc attgatctgc actactatgc ccagtccagc ctggacctgt ttctgggagg 120  
tgagagcagc ccagaacccc tggacaacat cttgttggca gcctttgagt ttgacatcca 180  
tcaagtaata aaagagtgca gcatcgccct gagcaactgg tggtttgtgg cccacctgac 240  
agacctgctg gacctctgca agctcctcca gtcacacaac ctctatttcg gttccaacat 300

<210> 81

<211> 300

<212> DNA

<213> Homo sapiens

<400> 81

acctgtaccg cctggccact ggctgtcacc ggcgtgatga gctgccggtg ttngaacgca 60  
acctatgctg gactctcccg gcagactgcc tggatatggt cgccatgcag gaagccgccc 120  
agcactcctc cggcacacac gacttcagcg ccttcagtc cgctggcagc ccggtgccga 180  
gccccgtgcg aacgtgctgc cgggtctccg tttcccagg ccaagccagc cccttggtca 240  
cccccgagga gagcaggaag ctgcggttct ggaacctgga gtttgagagc cagtctttcc 300

<210> 82

<211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 82  
 cccagctgga cctggtggcc ctttcctagt gcctctgctg ggggaggaga acctgggtcc 60  
 acgtggaggc taggaggtct cagggtgctgc cctggcagca ccagagtgtg ggccggggccc 120  
 gagtgtctgc ccctcgggcc tcagggtggg gcacttagca ccagaaggga accaaaagca 180  
 gggcatggcg gtgcagagga gtttgggagg tgtaaacagc cccatgcacg tggaggagga 240  
 gctggccttc agcccagac cccacgctag cactttccac gctgcttgcc cgctgttgat 300

<210> 83  
 <211> 272  
 <212> DNA  
 <213> Homo sapiens

<400> 83  
 tctagatatt gcccaatgc tgcccacagt gcacatacct ttccaccagt cacatgtgag 60  
 agggcagatt ttccaaatgc tcatcaccac ttggcactgt gtggactata attttggcca 120  
 gttaggaaat ggcattctcat tgttttcac ttaatttgcg tcagcctgat tactcattga 180  
 aacttgtgag gttgagaaac ttttcttaag cttattggcc attcaagttt cctcctttat 240  
 gaaatggttg ttcattgtcat ttgctcattt tt 272

<210> 84  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 84  
 cccactgccc ccggtcaaca aacccacttt tatgacagtt ttcttccgca gcttggtctt 60  
 taaattttac tggcaggtgt atggttggtg gagggttcct agtgagttgg gggacctggc 120  
 aatagagctg cttggttgga ggaagtgaag ctggcttagt accagcagct gatctcttcc 180  
 acgtgctgct gctttttttg ccactctgat actaaaccag agaaagctgc aggtggataa 240  
 agaagctgtg gctgtttttt gcttttgggt ggcaatgaga aagagtcaca gtgtgggtta 300

<210> 85  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
 ctggggagcca ccaacatagc agattaccat gtgaagttgc cactgctgca tctcctgaaa 60  
 cctggctgat gggagaggtc tcattttgtg tctgagaatg tccaggttgt ctgcagacca 120  
 cagcactgat ttcccattag cagttattat ttccctggcca tttcttctctg aagggtttgt 180  
 ggttaaaactc cctgtcctca atattttatc agcagtaggg ctgtcattct tctggttatc 240  
 aacctctaca ttatgaagta aggttcaacc cttctgcttt tctcaggccc ccaaaacggt 300

<210> 86  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 86

agaacattgg	tgtgtgagtg	ttttttgatg	gtgcaggacc	cggaggtgct	ttccttgcca	60
agaatagaaa	catccagaat	gtcctcctcc	atcccccaat	cccagacagc	aattatgtca	120
gccctgtaag	gcattgcctg	ctcttgaccc	tttgggccat	ctttttatct	ttaaaaaatt	180
cccatgtcac	agatgccctg	tctatgcaga	gggtggcgtg	ggatgggtga	ccactaagtt	240
taggctggtg	aagggtggtg	gcccttctga	ggcctgata	gaactttcca	ggagttcatg	300

&lt;210&gt; 87

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 87

ctccaaggaa	aatccacctc	gcagcttgta	aatctacagc	ctgattacat	caaccccaga	60
gccgtgcagc	tgggtccctt	tctcgtccgc	ggcctcacca	ctctgggttt	agtcaacagc	120
gcatgtggct	tcccctggaa	gacgagtgat	ttcatgccct	ggaatgtatt	tgacgggaag	180
ctttttcatc	agaagtactt	gcaatctgaa	aagggttatg	ctgtggaggt	tcttttagaa	240
caaaatagat	ctcggctcac	caaattccac	aacctgaagg	cagtcgtctg	caaggcctgc	300

&lt;210&gt; 88

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 88

ctgaaacaaa	agatgtatct	caattaaaag	acttggagaa	gattgctccc	aaagagaaa	60
gcattactgc	tatgtcagta	aaagaagtc	ttcaaagctt	agttgatgat	ggtatgggtg	120
actgtgagag	gatcggaact	tctaattatt	attgggcttt	tccaagtaaa	gctcttcatg	180
caaggaaaca	taagttggag	gttctggaat	ctcagttgtc	tgagggaagt	caaaagcatg	240
caagcctaca	gaaaagcatt	gagaaagcta	aaattggccg	atgtgaaacg	gaagagcgaa	300

&lt;210&gt; 89

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 89

ggggacatgt	gtccctcagc	tcagcagagg	ctgtggtaca	acatggctct	tggtgaagac	60
ctgcacccct	ggaacctccc	accatcgtca	caactgtagt	ctcatttgca	gtggagaaaa	120
gaacccgatg	tcccacagcc	agatatacac	ccagctccat	gccagccctt	catgtttacc	180
ttttgctttg	ttaattacat	gtcagaactc	tagagggcct	ccagactaat	aggaagcatt	240
tctgtaacca	acctgccacc	cactgattca	gaaatggaaa	tcacattcca	caatctatgg	300

&lt;210&gt; 90

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 90

ctcatcacaga	aagtcagatc	aacaaagagt	ccaagaaaaa	tgcgaccag	ctagaccatt	60
-------------	------------	------------	------------	-----------	------------	----

```

tgatcccagg cttagcacac gattgcatgg catccccctt agccacttca accactgcag 120
acatccagga agctggactc tctcctcagt ccctccagac ttctggccac cacagaatga 180
aaacccatt ttcaactgag ctatctttgc tccagcctga tactccagac tgtgctggag 240
atagtcatac cccactggct ttttccttca ccgaggactt ggaaagtctt tgtttgctag 300

```

```

<210> 91
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 91
aatgcaaagg gctgcagttc tcattcaggc tactttcagg atgcacagaa catatattac 60
atttcagact tggaaacatg cttcaattct aattcagcaa cattatcgaa catatagagc 120
tgcaaaattg caaagagaaa attatatcag acaatggcat tctgctgtgg ttattcaggc 180
tgcataataa ggaatgaaag caagacaact tttaagggaa aaacacaaag cttctattgt 240
aatacaaggc acctacagaa tgtataggca gtattgtttc taccaaaagc ttcagtgggc 300

```

```

<210> 92
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 92
aagatatgca gagatattcc aggatctttt agctttgggt cggctctctg gagacagtgt 60
tattcgccaa cagtgtgttg aatatgtcac atccattttg cagtctctct gtgacagga 120
cattgcactt atcttaccaa gctcttctga aggttctatt tctgaactgg agcagctctc 180
caattctcta ccaaataaag aattgatgac ctcaatctgt gactgtctgt tggctacgct 240
agctaactct gagagcagtt acaactgttt actgacatgt gtcagaacaa tgatgtttct 300

```

```

<210> 93
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 93
cgattcgcca gttctccatt ctgagagtca atcacgttcc tgatagggtg tcattgattt 60
ttttctctgt tggttttaac cttctaaaca tctccaggcc actttcttag ctttttcta 120
ggtactaaaa agaggtccta cccacacctg cctcacactt ctcctttcca aggctgcctg 180
agtttgaggg ggcttgggtg tgtgtgaaca agggccctgc attgtctagg cctgcagttc 240
ccaggcttgg gttcactttc accatgcatt ggcaaaacta gaaaagtaag cttgtgacaa 300

```

```

<210> 94
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 94
tttgtgcctg agcaccacaa atttcaggat ttagactgtg tggcacctca gctttcctct 60
ggatgtaacc actccttggg gagagagggg actcctcacc aatcccattt gacaaaggct 120
aggcaatctt cattctgctt ggctttagtc attcttgtca ttgggctgca gaagaaaaac 180
aactttgctg ggtgatccca ctgccttgat ttcacctcgg agcgaggctg ggccatgtcc 240

```



aagtcttatg aggtcaccct gactagaaaa aattgaactc acctacaaat agtctgaaag 300

<210> 95  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 95  
 gtgagtcgga gcatcagtgg cttctggagc agaccagcca cgtggaagag aagccttaca 60  
 gagatgggtc ggcagagccc tgctgatggc tgggccttgt gggcagccac tctgtgtgag 120  
 cagggtgttg ggcccatata cttcaaagac cagagccctg cactgggaga gtgctcctgg 180  
 cccaggcttg gaatcacctt tcgaggccct tcagactctg gcggggcttg ctgtggcctc 240  
 cctccagcta gtggtgtggc tgagcagact ccagggccag ggccagttcc cttctccctc 300

<210> 96  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 96  
 acaactccag acataattaa agactggccc aggaggaaga gggcggtggg ctgtggcgcc 60  
 ggctcctctt ccgggagggg cgaggtcggg gcagaccttc ctgggagcct gtcactgctt 120  
 gagacagagg gcaaggacca cggccttgaa ctcagcatcc acaggacgcc catcttgagg 180  
 gattttgagc tcgagggagt gtgccagctc ccagaccagt cgctcccag gaacagcatg 240  
 cctaaggccg aggaagcctc ttcttgggga cagtttgggt tgagttccag gaagagagtc 300

<210> 97  
 <211> 286  
 <212> DNA  
 <213> Homo sapiens

<400> 97  
 gtccagggcc cangttttta tttnttttta aaaagcttta ggtcttgccg ggacggtggg 60  
 tcacncnnnn nnnnnnnnnn nnnnnnnagg cctaggcggg tggatcacia ggtcagcagt 120  
 tcaagaccag cctgaccagc atggtgagac cctgtctcta ctggaaatac aaaaaaattg 180  
 gctgggagag gtggcaggca cctgtggtcc cagctacctg ggaggctgag gcgggagagt 240  
 ctcttgaaac tggaaggcag aggttgccgt gagccgagat tgcgcc 286

<210> 98  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 98  
 caccatTTTT attttgatgc ttactcat ttattctgtt tttgtaaaac agtttcggga 60  
 atttaaaaat ccttccagtt aatagagctt ttgttattat attataattt tgtaaaccca 120  
 ctttgttttt ccacttttaa agccacaggg tcgactcatg gatgatacct ctattgctgc 180  
 tgcatgatgt tcaagaccgg cccttggttg ttgttacaga gatgttgggc agagctatgc 240  
 aggtgtttca ttgtgaactc tagctttgat catggtaaaa agttaaccct ttctattttt 300

<210> 99

<211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 99  
 agcctcgctt gggccggcct gtggctccca ttttcctttc agcgggacaa aggggacttg 60  
 ttaccaggcc attttctgga tggcctgtga gatctctgcc cctccaagac cctccaagtc 120  
 tgagcctgac ccacagctgg gacactgaat tcagccctgg gaaccatggg ggcttctatc 180  
 tggcaccagg ctgcagcctc cccaatccca gccactttg ctgtgtctct ggcgggctgt 240  
 cctccttggg gggagctgtc ctgcacactg taggatgctt aaaggatatcc ctggcctcca 300

<210> 100  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 100  
 tccaaccttg gcgatgtcac cagcatgggtg gctcagggtta gagctctctg aggacctcagc 60  
 atagagcact ggtgccaggg accaaactga gacccaccca ccgtcatcaa cacttacata 120  
 ccataaaggc cttcagagtg ccttggccct agacctccct tcattctttg tagagatgga 180  
 atctaagaat gaaacatctc cactcagtc tgcaaatatg gaagttcttg agataccttt 240  
 ttttggtaga tacttgtgtc ggtattctga gagtcacttt actctgatgg ttgcaagat 300

<210> 101  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
 gtgtttcttc tacctcccct gcacaacatt gtttatatgc ccctaaaat gtaacttctt 60  
 tagattctgt tggtacgtgc aacactgtat atctctccat agcacttaat cagagtttgt 120  
 aattaggcat ctttttgtgt gattatttgg taaatgtcca tatccctac tagcctataa 180  
 gctccatgac ttctaggtac cctgtctgac tacgtgtatc actggttcta ccgcctaaca 240  
 ttgcctagca cattcattgc ttcacaggca tctgaatatg gggtttataaa atacattgct 300

<210> 102  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens

<400> 102  
 cctggccctg ctgccctcc tgaatctcgt atgatgggtca cagtccgggtg gccgtggggg 60  
 tgctctgcct tccctggtec ccactgcca tatctgtgga ctgcccttc caaagacccc 120  
 tggaggaggt gtnnnnnnnn nnnttnntgn nccactacc ntgcactgaa ctggcctgt 180  
 tacancaann actgnnccn nttgttatna caccttnnac aaacacctgc tgctgtacat 240  
 gncnctactt taaggactnn anacctgtgc 270

<210> 103  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

gctggagcac gctggagagg ccateccctgc cctggcagcc ggggctgggg gagactcctt	60
tgccccattc tttgccggtt tcttgccatt attggtgtgc aagacaaaac agggctgcac	120
agtggcagag aagtcctttg cagtggggac cttggcagag actattcagg gcctgggtgc	180
tgctcagcc cagtttgtgt ctgggtgct ccctgtgctg ttgagcaccg cccaagaggc	240
agaccccgag gtgcgaagca atgccatctt cgggatgggc gtgctggcag agcatggggg	300

&lt;210&gt; 104

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

ctcgctctc ttcactgcac attgcaatgc atttgcgatt cccatttctc tgctaggagc	60
cagcctgggt ggcgtgctc ccagagccgt ggggccaga ccttgcttc cttttgttcc	120
tgtccgttta tcaggacacg ggccccacct gtcacgtgcc cgaggccacc caagcccagc	180
ctgcggggcg ttccactgc ctggatgccg gcttgagttc tgcgcacgca ggattcagtg	240
tggggacggc ccctgccgga taggcctagc cctggcccag gtggtgagcg gtttgcaagt	300

&lt;210&gt; 105

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 105

gggcactgtg gggctctccc cgcctctcct gccttgtttg cccctcagcg tgccaggcag	60
actgggggca ggacagccgg aagctgagac caaggctcct cacagaaggg cccaggaagt	120
ccccgccctt gggacagcct cctccgtagc ccctgcacgg caccagttcc ccgaggagcg	180
cagcagggcg cctcccgcag cggccgtggg tctgcacagc ccagcccagc ccaaggcccc	240
caggagctgg gactctgcta caccagtgta aatgctgtgt cccttctccc ccgtgccct	300

&lt;210&gt; 106

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

gctcaacgcc tatgtgacct atctccatgc cgaatacaat cgacagaagg acatctacct	60
agcacatcgt gtggcccaag cttgggaatt ggcccagttc atccaccaca catccaagaa	120
ggcagacgtg gttctgttgt gtggagacct caacatgcac ccagaagacc tgggtgctg	180
cctgctgaag gaggggacag ggcttcatga tgcctatctt gaaactcggg acttcaaggg	240
ctctgaggaa ggcaacacaa tggtagccaa gaactgctac gtcagccagc aggagctgaa	300

&lt;210&gt; 107

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

tgtgagtttc ctatctgttc cagactagta tcgccaatct ctcccagctc tcttttttcc	60
tcctggcct ttgtcctgca ggaggtagca tcacctcttg gcatttttga catgctttta	120

aacaattgga	ggagctgccc	aggcagtttt	atggcctcct	ggttgtgtgc	cttcacaccc	180
gcctacagcc	ccacctcacc	atcaagcgct	gagccaatgc	gggtgtggct	ggccctgagt	240
tcctgagtca	gtccttgcc	agggccagag	ctggtaacag	cggggcagca	gggtgggtag	300

&lt;210&gt; 108

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

aggttgctca	cctgaaggag	cacaggaggg	ttttccaggc	catgtggctc	aggttcctca	60
agcacaagct	gccctcagc	ctctacaaga	aggtgctgct	gattgtgcat	gacgccatcc	120
tgcgcagct	ggcgcagccc	acgctcatga	tgcacttcct	caccgcgccc	tgcgacctcg	180
ggggggccct	cagcctcttg	gccttgaacg	ggctgttcat	cttgattcac	aaacacaacc	240
tggagtaccc	tgacttctac	cggaagctct	acggcctctt	ggacccctct	gtctttcacg	300

&lt;210&gt; 109

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

cacaaggaga	agaaagttaa	ttaacattga	aagatgagaa	gacatcttgg	aagaacttga	60
attgggcctt	ggaagaagaa	cagccattca	aatagataga	attgtggtag	caaaggcata	120
gaggtaggaa	agtatagatc	tccagggaca	gtagtcatgg	ggttggggca	ctgttggaat	180
ttaaggttgg	aaggatatat	tggagccccct	tgaatacggg	aacaaggcac	accttgggca	240
gtggagagtt	atcagagtgt	ttgaaaagga	gggttattga	gtaaataaat	agactggtac	300

&lt;210&gt; 110

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 110

gacaccccag	atgcagccac	caccagcaga	agcgatcagc	tgaccccaca	agggcacgtg	60
gctgtggccg	tgggctcagg	tggcagctat	ggagccgagg	atgagggtgga	ggaggagagt	120
gacaaggccg	cgctcctgca	ggagcagcag	cagcagcagc	agccgggatt	ctggaccttc	180
agctactatc	agagcttctt	tgacgtggac	acctcacagg	tcctggaccg	gatcaaaggc	240
tcactgctgc	ccgggcctgg	ccacaacttt	gtgcggcacc	atctgcggaa	tcggccggat	300

&lt;210&gt; 111

&lt;211&gt; 271

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 111

cctggccctg	ctgccctcc	tgaatctcgt	atgatgggtca	cagtccgggtg	gccgtggggg	60
tgctctgcct	tccctgggtc	ccactgccca	tatctgtgga	ctgccccttc	caaagacccc	120
tggggggggg	ggggnnntcc	ttctannccn	ntacnctatg	tgtttaatnn	ncntantnct	180
ttantantat	ttncantgn	tnntnatatn	nttnnanana	nnctnctta	nnnacattat	240
tttanntang	ngatnntacc	ttnttgnaan	g			271

<210> 112  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 112  
 gttccctcac cttattcctc caagttcccc cttgggaacc tctgagatta acttgataag 60  
 ctccctgggc aagctcttta tcctaagatt cctcagtgag ccttatagag ttgctgag 120  
 aattacattt gttcatgatg tcaagtgtct ggtatgtagc taatgcttat tgaacacata 180  
 gtaatttatt gaataattgt catgatcact ggatgagata tagccactgt ggaggtaggc 240  
 acaccagggt ttttagaggct tgggatcttg caacaggatt ttctctctgc ctctccaaac 300

<210> 113  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 113  
 cccacatgta ccagggttgag tttgaagatg gatcccagat agcaatgaag agagaggaca 60  
 tctacacttt agatgaagag ttaccaaga gagtgaagc tcgattttcc acagcctctg 120  
 acatgcgatt tgaagacacg ttttatggag cagacattat ccaaggggag agaaagagac 180  
 aaagagtgtc gagctccagg tttaagaatg aatatgtggc cgaccctgta taccgcactt 240  
 ttttgaagag ctctttccag aagaagtgcc agaagagaca gtagtctgca tacatcgctg 300

<210> 114  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 114  
 acagtttagtg taaaggatct gaatggcata gacttaactc ctgtgcaaga tactcctgtg 60  
 gcttcaagaa aagaagatac atatgtacat tttaatgtgg acattgagct ccagaagcat 120  
 gttgaaaaat taaccaaagg tgcagctatc ttctttgaat tcaaacta caagcctaaa 180  
 aaaaggttta ccagcaccaa gtgttttgct ttcatggaga tggatgaaat taaacctggg 240  
 ccaattgtaa tagaactata cacgaaacc actgacttta aaagaaagaa attgcaatta 300

<210> 115  
 <211> 288  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
 gtgatctgcc tgccttggtc tcccaaagtg ctgggaatac aggcattgagc caccgcactc 60  
 ggccaggagc tagttttatc agcatcctgc tccactgcct tcctctagtg cagcctggaa 120  
 gacatggcag cgggtagctc ctggggctga gccagaagca tcaactgcagt gaaagtctct 180  
 gcttacctgt ctggctcagc ttgggcaagg gctgggcat atgtgctcag ggacgtgctt 240  
 ctcttgtaag gcaggaggat anaanaggac cannaanggn gggagctg 288

<210> 116  
 <211> 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 116

tcaattagta	acatctgaaa	aaacagcttt	gtcctgggtg	aaaaaggatg	ccaaaattgc	60
ctggaaaaga	gcagtgaag	gagtcggga	gatgtgtgat	gcatgtgaag	caacattgtt	120
taacattcac	tgggtctgcc	aaaaatgtgg	atttgtggtc	tgcttagatt	gttacaaggc	180
aaaggaaagg	aagagttcta	gagataaaga	actatatgct	tggatgaagt	gtgtgaaggg	240
acagcctcat	gatcacaac	atttaatgcc	aacccaaatt	atacctggtt	ctgttttgac	300

&lt;210&gt; 117

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 117

gcactttcca	gaattctctc	atatttgtgg	gctgggatca	agcctgcagc	ttgaggaaag	60
cacaaggaaa	ggaaagaaga	tctgggtgaa	agctcagggtg	gcagcggact	ctgactccac	120
tgaggaaactg	cctcagaagc	tgcgatcaca	actttggctg	aagcccctgc	ctcactctag	180
ggcacctgac	ctggcctctt	gcctaaacca	caaggctaag	ggctatagac	aatggtttcc	240
ttaggaacag	taaaccagtt	tttctaggga	tggcccttgg	ctgggggatg	acagtgtggg	300

&lt;210&gt; 118

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 118

agaacgttct	caggttgacc	agctgctgaa	tatttcttta	agggaggaag	aacttagtaa	60
gtcattgcag	tgcatggata	acaatcttct	gcaagccgt	gcagcccttc	agacagctta	120
tgtggaagtt	cagaggctac	ttatgctcaa	gcagcagata	actatggaga	tgagtgcact	180
gaggacccat	agaatacaga	ttctacaggg	attacaagaa	acatatgaac	cttctgagca	240
cccaggtttg	gcatagaaat	ggtaccctt	gttcaaaatg	aacaagaagc	cttagatttg	300

&lt;210&gt; 119

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 119

gaacaaagaa	ggaatgtctt	cctcatgttt	gggtctatag	aagacgttaa	agaaaacttc	60
cagaaagtgg	gtttgaggca	tgagccacca	cgctggcca	aaggatttaa	tgaattaatg	120
gatgtacagt	gctggggctg	gtattctagg	gcctgcattg	agactcacat	tttgccatca	180
aaagcctttt	aagaggtgga	ggttgcggtg	agctgacatg	gtgccactgc	actccggcct	240
gagtgcacaga	gtgagactct	gtctcacaaa	aaaaataatg	ccctttaaat	aatgaataat	300

&lt;210&gt; 120

&lt;211&gt; 273

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 120

cctcagcctt	ctaaaaagct	ggggctacac	ccagctgaag	aaattgtaac	taaagataga	60
ttgtttaaag	caaagcaaga	aacttctgaa	gaaatggaac	aaagtggaga	agcctcagga	120
aagcccaaca	gagagtgtgc	accccagatt	ccttgtagta	ctcctattgc	tactgaaagg	180
acagttgcac	atttgaacac	tctgaaggac	cgtcaccacag	gtgatttgtg	ggcccgcacg	240
cacatctcat	cccttggaat	atgctgcagg	aga			273

&lt;210&gt; 121

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 121

agaacgttct	caggttgacc	agctgctgaa	tatttcttta	agggaggaag	aacttagtaa	60
gtcattgcag	tgcatggata	acaatcttct	gcaagcccgt	gcagcccttc	agacagctta	120
tgtggaagtt	cagaggctac	ttatgctcaa	gcagcgata	actatggaga	tgagtgcact	180
gaggacccat	agaatacaga	ttctacaggg	attacaagaa	acatatgaac	cttctgagca	240
cccaggtttg	gcatagaaat	ggtacccctt	gttcaaaatg	aacaagaagc	cttagatttg	300

&lt;210&gt; 122

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 122

gttgcaagca	gccttggaat	agtaactctt	ctcatttgtt	tgggatctgg	ccaccaagtt	60
ccagaatgat	acacggatca	gtgcagaagt	tcacagggt	ctcggacctt	agggctgttg	120
gagaaggctt	cagcagcaga	actgatggtg	aaggctcgtg	ttctccatcc	tcaactttct	180
ttgcttcgat	catacacaag	aatacatttg	gaaggggcaaa	aaaatgaaca	ctgtcgttca	240
ttgcagccgt	gttttgtgac	acagatgcac	agtctgctgt	gaagaccttc	tctcaagtgg	300

&lt;210&gt; 123

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 123

gtgatttcag	cttcocaaact	ggtatacatt	ccaaactgat	agtacattgc	catctccagg	60
aagacttgac	ggctttggga	ttttgtttta	acttttataa	taaggatcct	aagactgttg	120
ccttttaaata	gcaaagcagc	ctacctggag	gctaagtctg	ggcagtgggc	tggccctgg	180
tgtgagcatt	agaccagcca	cagtgcctga	ttggtatagc	cttatgtgct	ttcctacaaa	240
atggaattgg	aggccgggcg	cagtggctca	cgctgtgaat	cccagcactt	tgggaggcca	300

&lt;210&gt; 124

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 124

catgctggcc	agcatccctg	cctgtgcaag	ctctggatga	gctgtgagcc	cctgccaccc	60
acacccccac	tccctgccag	cctggcctca	gggcctctga	tccatgtgca	ctggagagga	120

```

gatgactgac agggccactg gggcatttcc acgttaacag cagctgccac tggcaaaaga      180
agtgactcgc caatggaggc atctcagatg tgggccagg agtctgggga gctactttga      240
acagggttat ccattcattg tcccaccaa ggctatggag cccacccacc atgtgctgga      300

```

```

<210> 125
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 125
ggtaaatgg ttgaattatt gtattgaagc ttgagctgta gctaaaagta atttaggttt      60
cccctaagat gttattatgt tagggacata acacttttgg gaggttggtg tgggagatgg      120
ttgatttagg ttttcaaaag ctagaaataa aattttacatg ccttagattt cataaaattc      180
tgctctaatt ggttgggaagg tgctgtatct aacttgtggt cctcctaagg ttatgtccta      240
ataactattc ttttaggagt atacttctac tttatagaag gttgcttttc tttttaattt      300

```

```

<210> 126
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 126
tgaagaggag atcgggtgacc tgggctcctt atgtgcctga aagagtttga gtttcctggt      60
aactccaaat caacagtatt ttcaacaaga aatgtgcaat tgaaatcaag tgctgtttaa      120
gtgcagctag gatttccaca ggaagacact tgcagtgaac agagttatgg agcagcaaaa      180
acacagatct atttggaaaa agagaaaaca tatgcgttgt attttgcttc aattataaaa      240
taccatcttc tcaaagggtg ttctaaatta caaaggactt tgatttctag gtagattctg      300

```

```

<210> 127
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 127
ggtgattccc atgctgaaca gtttgatctc ctgccagagt gtcgggccac aaactgggca      60
gcacatcagg atcacctggg ggccttcaaa aatcaaaaat ccacccccag gccatgccct      120
ggacccactg caccaggaca agaaatccac cccaggcctc tccccagacc cactgcacca      180
ggacaagaaa tccaccccca ggccacgccc cagaccact gccctaggat gtgggggtgg      240
gaaccagggt gtgctttgta aagacgtgca ggtggtaacc ccaggccccc acgctcggaa      300

```

```

<210> 128
<211> 300
<212> DNA
<213> Homo sapiens

```

```

<400> 128
tgagctggga gaaggggaga aagtttgtga agaggagatc ggtgacctgg gtcctttatg      60
tgectgaaag agtttgagtt tcctgttaac tccaaatcaa cagtattttc aacaagaaat      120
gtgcaattga aatcaagtgc tgtttaagtg cagctaggat ttccacagga agacacttgc      180
agtgaacaga gttatggagc agcaaaaaca cagatctatt tggaaaaaga gaaaacatat      240
gcgttgtatt ttgcttcaat tataaaatac catcctctca aaggtggttc taaattacaa      300

```



<210> 129  
 <211> 285  
 <212> DNA  
 <213> Homo sapiens

<400> 129  
 ggaaagcaca aggaaaggaa agaagatctg gtggaaagct cagggtggcag cggactctga 60  
 ctccactgag gaactgcctc agaagctgcg atcacaaactt tggctgaagc ccctgcctca 120  
 ctctagggca cctgacctgg cctcttgctt aaaccacaag gctaagggct atagacaatg 180  
 gtttccttag gaacagtaaa ccagtttttc tagggatggc ccttggtctg gggatnnnnn 240  
 nnnnnnnnnn nnnnnnnnnn nnaggaagat accatttctt gacgg 285

<210> 130  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 130  
 ccggacgcag gccctcgggc aggagcatct ggcagagtgg gggcggtggc aggcaccctc 60  
 ctttgcaggg cgaggtgggg cctctgcagc catcctggac aggcgggggt ggcggcagct 120  
 ttgcccacgt ggaagcgggg tgggtctcac ttgctgtgtg gcccctggcc ccatcttgcc 180  
 tgctgcggcc tggggagcag gcgctgggtg gtggttctgc ctgcttgctg ctggttcccc 240  
 gggcatgcgt gggcagcggg gggcatgcgt gggcagcagg gggccgtggg cagcgggggc 300

<210> 131  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
 gatctctata ctagtgaaca gtgccagttc cacacttttg acttagaact gttctctagt 60  
 tattgtaaca cagaatactg tcaatcccta atttacttaa tggtacttat tggaagtggg 120  
 gctgatgaaa tacgcacagg agggaaatct actgtgttta ggcacaggca gcccagtggt 180  
 ataaggagat catattccaa aagggtgtca gttggttggg tgcaacctgg aatgtatttt 240  
 ccttttagaga ccaggttatc catggtgggt aggccctag agcagctgga aaagatgac 300

<210> 132  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 132  
 ctcccatgga ggtggtggga atggcaccga gaagtttgat gacagttatc taatggacta 60  
 gaggttggca aactttctgt aaatggccag gtagtaaata gttctgcttt tgaaggcata 120  
 tgggtctctg cacctactcg aggtgaaag cagctataga caatacataa atgaatgagc 180  
 gtgagtgtgt tccaataaga aaaaaacatg gctgtttgct tcggccccag ggttgtagct 240  
 taccagtcct gtaacagatc acagtttgct cttttgggtc caaatacttg aaccctccc 300

<210> 133  
 <211> 269  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 133

atgctatgcc aaagcctgct gccagctcca tagcctggac ctacagcact gcatgggtgga	60
gtccacagct gtggtgagct tcttgaggga ggcagggtcc cgaatgcgca agttgtggct	120
gacctacagc tcccagacga cagccatcct gggcgactg ctgggcagct gctgccccca	180
gctccaggct ctggagggtga gcaccggcat caaccgtaat agcattcccc ttcagctgcc	240
tgtccaggct ntgcaaaaag gctgccctc	269

&lt;210&gt; 134

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 134

gatggatgag actgttgctg agttcatcaa gaggaccatc ttgaaaatcc ccatgaatga	60
actgacaaca atcctgaagg cctgggattt tttgtctgaa aatcaactgc agactgtaaa	120
tttccgacag agaaaggaat ctgtagttca gcacttgatc catctgtgtg aggaaaagcg	180
tgcaagtatc agtgatgctg cctgtttaga catcatttat atgcaatttc atcagcacca	240
gaaagtttgg gatgtttttc agatgagtaa aggaccaggt gaagatgttg acctttttga	300

&lt;210&gt; 135

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 135

ggcgagcggg aacagctctt gaggagttag actgcaggag atgtgggccc tgccaaagag	60
atggatgaga ctgttgctga gttcatcaag aggaccatct tgaaaatccc catgaatgaa	120
ctgacaacaa tctgaaggc ctgggatttt ttgtctgaaa atcaactgca gactgtaaat	180
ttccgacaga gaaaggaatc ttagttagc cacttgatcc atctgtgtga ggaaaagcgt	240
gcaagtatca gtgatgctgc cctgttagac atcatattata tgcaatttca tcagaccag	300

&lt;210&gt; 136

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 136

gacttctaaa tatatcttgg atataatagg tgataagttc tgtcaattag taacatctga	60
aaaaacagct ttgtcctggg tgaaaaagga tgccaaaatt gcctggaaaa gagcagttag	120
aggagtccgg gagatgtgtg atgcatgtga agcaacattg tttaacattc actgggtctg	180
ccaaaaatgt ggatttgtgg tctgcttaga ttgttacaag gcaaaggaaa ggaagagttc	240
tagagataaa gaactatatg cttggatgaa gtgtgtgaag ggacagcctc atgatcacia	300

&lt;210&gt; 137

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 137

ttgacaaatt gctggaacac acttattgtg gtttaccggt ttttaattat gtcagagatt	60
gcatcatcct tatgcttggt tacatctata atcttctatg aaatgggtgt accaaggggc	120
gccaacagc ttttatcccc attcttagag catattcttt attataatga ttatccaaca	180
tattttcttta attttaatac aaaaaatata tcatttaatt tttgttacat atgaacattc	240
atttttaaat gctcagcctc aagtgcaggc atttttgagt ggcttgatta catattcctc	300

&lt;210&gt; 138

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

ggaaggggag ggttggtgag tcccagacct taaaaatata aggttaagag ggaccccaaa	60
gcaaaaaatt ccaacccttt tcctcccagt cattgaaaca ccaaaactat tataccggag	120
ggtgtaatag ttttgctgcc cagttgtggt aggccagtag tggcctccca agatgcccat	180
gtcctaatac caggaacctg tcaaaattac cttgtatggc caaaggggct ttgcagatgt	240
aatgaagtta aggatctttc gccaggaaga ttatcccage ttgttcagga gggcttgatg	300

&lt;210&gt; 139

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 139

gacatcattt tcttattcta gtaagagaaa gtacacagat tcaacttttag agaggacttt	60
tttttttctg gagctaaatc aaggaaggat tatcacgtgg cctcccttga atataatttt	120
gaagctgtga acagtaccat cagtaacatt ttatggacag ctctgatggt ttttatacca	180
cggcactctt cttacctttg ggggaagcta tctggagtta tgactgatgt gtaaagtggg	240
ttactgttag aatcctggtg tgctaggatt ctgggagagt cactttcagg aagttacctg	300

&lt;210&gt; 140

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

gctgcccagg cagttttatg gcctcctggt tgtgtgcctt cacaccgccc tacagcccca	60
cctcaccatc aagcgctgag ccaatgcggg tgtggctggc cctgagttcc tgagtcagct	120
ccttgccagg gccagagctg gtaacagcgg gccagcaggg tgggtagcct ctaccagcca	180
gggcagtccc tgaggggcca gcaggggggc tgactgccta gtggctcaac ctctgaacc	240
caccactccc cagcgatgct acccagaacc ccaacggcat gaatcctgca cagtgcggg	300

&lt;210&gt; 141

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

cccaaaactta tcgggggtgc cagaggcaga gtagacaagc cttagtggcc gccatttgtt	60
gaatatctac tgtgcgcca gacgtgcgtc acaactttat gaagtaggta ttattatcat	120
ccccatttta caggtgaaga aactgagtct ctgagagacc aacttttcca aggtcacaca	180

gaggtgggat ccagcccact tccgtctgac cccaagcccc tgctgttaac ccctgcccc 240  
 ttgtggggag gttccggccc actctggagt tctctgggtc gcgtcagtc tcaggagaag 300

<210> 142  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 142  
 gaaaggtggc gcgcttctca cggctgagtt gctgcgcctg cagacggaag ctccccacag 60  
 gcagagctgc ttggatgtgt gagtcatgaa gccagagaag ccccgctcca tgagcagtga 120  
 ctccccaggc cctgtgacct ccctcctgtc ttgcagctcc tcctggcacc agtccccagg 180  
 gctctcctgt tggtagttcc tgcttttctt cttggaaatt cctcgtggac ctcgagatct 240  
 ttaccctaaa atagtctgt tgaatttcac cctggcaatg taaattgata gcttatcttc 300

<210> 143  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
 cttggccttg cttctctgag aaaactttgg tcacacctcc agagccaggg tgggtgcctc 60  
 cctggaggag ggggctttcc tggttggtgg cacagcagga gtccaggctt tgtaccgtgg 120  
 acaccatggg ctatggcaac accttctca ccctcctcc atgaggacct cgggagagag 180  
 tggacatgaa accctttgtg ctctgaagca ttcaacagaa gctttctggt tctgtgccta 240  
 tttctttggc acttgagcgt gtttgaggt tcattacaca catgatgaa gctctggccc 300

<210> 144  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 144  
 cctgactgag tgcctgacgg tggaccccct cagtgccagc gtctgaaggc agctgtaccc 60  
 taagcacctg tcacagtcca gccttctgt ggagcacttg ctcagctcct gggagcagat 120  
 tcccaagaag gtacagaagt ctttgcaaga aaccattcag tcctcaagc ttaccaacca 180  
 ggagctgctg aggaagggtg gcagtaacaa ccaggatgtc gtcacctgtg acatggcctg 240  
 caagggcctg ttgcagcagg ttcagggtcc tcggctgccc tggacgcggc tcctcctggt 300

<210> 145  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
 gccagagcct agaggagaga tcaaagaccc tggccgaagt gaagcccatt ctgcaagcaa 60  
 ctgggttccc atggcatgtg gtggccttag aggaggtgtt cagcctgcca ccgtcgtgac 120  
 tttggtgctc tgcccaggag ctggtgggat ccgagggggc ctacaaggcg gccgtggaca 180  
 gcttctccca gcagcagcat gtgctggggg ccgggggtgg tcctggnccg actcaagggg 240  
 annnnnnnnn nnnncnaacc cccgctggac cccngaanc tggcaagacc ngctgcccct 300

<210> 146  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 146  
 tgacttttcta cctggtccaa gctgttgggg aattgctgct gttgaccag gcaggagtct 60  
 gactagagaa caaactaagg ttgctgcaac aaacaaggac ctcttccaag aagggtccc 120  
 aggcctggcg cagtactca tgcctgtgat ccagcactt gggaggccga ggcgggtgga 180  
 tcatttgagg ccaggagttc gagaccagct tggccaacat gatgagacc cgtctctatt 240  
 aaaaatacaa aaattagcca ggcgtggtgg cgctgtagt ccagctact caggaggttg 300

<210> 147  
 <211> 295  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 ggnaangcna nngnaggaga nagagaagna ncagtnnagn ccangaaac ccnntgaaac 60  
 ccttagaagn cagaggagng aaaggangaa aaananggng ggangagaac nnannnnngn 120  
 caaannaagg angannnta ggngngaaaa anaanaacaa anggggaaaa ngggaaaaaa 180  
 ggcganaaag gnaanannag nanaaggngg aananannnn annagaaagg ncaanaaaag 240  
 aagnacaaag aaaaangana anaagnaann annanangga cagagacaag aagga 295

<210> 148  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 148  
 cgctgtgctt gagaccaacc tgacgggtac cttctacatg tgcaaagcag tttacagctc 60  
 ctggatgaaa gagcatggag gatctatcgt caatatcatt gtccctacta aagctggatt 120  
 tccattagct gtgcattctg gagctgcaag agcaggtgtt tacaacctca ccaaactctt 180  
 agctttggaa tgggcctgca gtggaatacg gatcaattgt gttgccctg gagttattta 240  
 ttcccagact gctgtggaga actatggttc ctggggacaa agcttctttg aagggtcttt 300

<210> 149  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 149  
 agtgtcagtt ttcctaactc cagtccaggt aggaattaag aaatatctca agtgttgatg 60  
 ctatccaagc atgttggggt ggaagggaat tgggtcccag aaaatgggac tggagtggag 120  
 aatatctttt cttttgagag taccctcagt ttattttctac tgtgctttat tgctactgtt 180  
 ctttattgtg aatgttgtaa cattttaaaa atgttttgcc atagcttttt aggacttggt 240  
 gttaaaggag ccagtgtgtc ctctgggtgg gtactataat gagttattgt gaccacagc 300

<210> 150  
 <211> 300  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 150

tgtagacttt atgtcagttc tgtgtagact ttatgtcagt ttttgtcatt atttgaaaat	60
ctattctgac aactttttaaa ttcccttgat cttataagtt aaagctgtaa caactgaaat	120
tgcattggatc aagtaagcat agttttatcc agggagaaaa ataaaaggaa gccatagaat	180
tgctctggtc aaaaccaagc acaccatagc cttaactgaa tatttaggaa atctgcctaa	240
tctgcttata tttgggtgtt gttttttgac tggtgggctt tgggaagatg ttatttatga	300

&lt;210&gt; 151

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 151

gcgggcccgg ccagcggag cccctgcgcc cgcgccatgt caaagaaaaa aggactgagt	60
gcagaagaaa agagaactcg catgatggaa atattttctg aaacaaaaga tgtatttcaa	120
ttaaaagact tggagaagat tgctccaaa gagaaaggca ttactgctat gtcagtaaaa	180
gaagtccttc aaagcttagt tgatgatggg atgggtgact gtgagaggat cggaacttct	240
aattattatt gggcttttcc aagtaaagct cttcatgcaa ggaaacataa gttggagggt	300

&lt;210&gt; 152

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 152

gatattcaca cagtatgtat tatattaacc atatcacact taagttatta aattcagact	60
atttgttaact tattgttata gggcctgccg tatggcttag gatatttgag taatcatata	120
tttaaagtaa aaactttggg ctgggcacag tggctcacac ctgtaatccc agcacttggg	180
gaagctgagg tgggcagatc agttgaggtc aggagttcta gaccagcctg gtcaacatgg	240
cgaaccccca tctctactaa aaatacaaaa attagctggg cgtggtggca cacacctgta	300

&lt;210&gt; 153

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 153

cagagaccag ctttctccag aggctgtcac tgcaggagcc gtgggcctgg gaagacttgg	60
aagcggcctc tctcaactgg tttctgtctc cgtggagctg gaactgcctg cacttgctt	120
cagagggagg cacagtccac ccagatccac ctttccagca agacccccag tggctgccc	180
gcctgggagc acctctttgc tttcacacc aaacaaaac tggcgagagc ccctcctagc	240
caccagtgat cccaagcat ccagtacaga accaggcatc gagctagctc cctgcacggc	300

&lt;210&gt; 154

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 154  
 cttgacctct gtacttttaa gaaatcacta accaaatttt caaagtttcc ttttaaattgc 60  
 gtttagctag aaatctatgt atttatccct ttcttatttt gcattcttct ccactattt 120  
 ttaaaaactc atttacagta gaaaccattc ttctttctcc caacagtatc ctttgccaag 180  
 accatgagaa cagtatggga gcatgttggt ggtcaggggt tcagaatacg cgtgatgtca 240  
 ctgagaatgt ttgctcacag tcaataattg tctttgtgga tgtgataatt ttggagatac 300

<210> 155  
 <211> 81  
 <212> DNA  
 <213> Homo sapiens

<400> 155  
 gatcattggt aattagtgac atagtaacat ctgtagcagc tggtagtaa acctcatgtg 60  
 ggggaggtgt gggaggtttt a 81

<210> 156  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
 ggcagcacia gtgtgcaaac agctatggaa agtgaactcg gagagtctag tgccacaatc 60  
 aataaaagac tctgcaaaag tacaatagaa ctttcagaaa attctttact tccagcttct 120  
 tctatgttga ctggcacaca aagcttgctg caacctcatt tagagagggg tgccatcgat 180  
 gctctacagt tatgttgttt gttacttccc ccaccaaate gtagaaagct tcaactttta 240  
 atgcgtatga tttcccgaat gagtcaaaat gttgatatgc ccaaacttca tgatgcaatg 300

<210> 157  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 ctggtaggga gtctttgcga gagcgaggag cagcggttac tggaacagggt gcatggcgaa 60  
 gaggagcggg cccaccagag catcctgaca cagcggtgac actgggccga ggcgctgcag 120  
 aaacttgaca ccattccgac tggcctgggt ggcattgcta ctcacctgga tgacctccag 180  
 ctgattcaga aggagcaaga gattttcgag aggaccgaag aagcagaggg cattttggat 240  
 cccaggaggt cggaaatggt aaactttaat gagaagtgca ctcgagagccc actactgacc 300

<210> 158  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 158  
 cgacagctct ccaataactca ggttaatgct gaaaaatcat ccaagacagt tattgcaaga 60  
 gtttaatttt tgaaaactgg ctactgctct gtgtttacag acgtgtgcag ttgtaggcat 120  
 gtatgtacag gacattttta agggcccagg atcggttttt cccagggcaa gcagaagaga 180  
 aaatgttgta tatgtctttt acccggcaca ttccccttgc ctaaaataca gggctggagt 240  
 ctgcacggga cctattagag tattttccac aatgatgatg atttcagcag ggtgacgtc 300

<210> 159  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
 agtaccacaga gttgagagga gttttttaac tgatttagcc aggtggcaat catgagtga 60  
 tggatgaaga aaggccctt agaatggcaa gattacattt acaaagaggt cagagtgaca 120  
 gccagtgaaga agaatgagta taaaggatgg gttttaacta cagaccagat ctctgccaat 180  
 attgtccttg tgaacttcct tgaagatggc agcatgtctg tgaccggaat tatgggacat 240  
 gctgtgcaga ctgttgaaac tatgaatgaa ggggaccata gagtgaggga gaagctgatg 300

<210> 160  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<400> 160  
 ctttgagcta ggataaaaat tgggttaaagg acatttgctt acctgcaaat gaatcactgt 60  
 ggaaatgtga tcttcccata tcatcaagaa acttgttttc tggatgaata ctgggagaat 120  
 aaaatgagaa ctctggagtg agctaaattg atcccaatta agtttttctg cttagcagac 180  
 agaaggtata attttttgac accctttccc acctggtgcc tatgctaggc ttgtntctgat 240  
 aacatccctc actnactnga tnntcacatn gnncttnenc tgangtccca tttt 294

<210> 161  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 ctctctcaaa gcatggttgc tgagtaccca gagttgagag gagtttttta actgatttag 60  
 ccagggtgga atcatgagtg aatggatgaa gaaaggcccc ttagaatggc aagattacat 120  
 ttacaaaagag gtccgagtga cagccagtga gaagaatgag tataaaggat gggttttaac 180  
 tacagaccca gtctctgcca atattgtcct tgtgaacttc cttgaagatg gcagcatgtc 240  
 tgtgaccgga attatgggac atgctgtgca gactgttgaa actatgaatg aaggggacca 300

<210> 162  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 162  
 gccccgtgtg gggagacgga cagcaccctc ctcatctggc aggtgccctt gatgctatag 60  
 cgcctccctt ctccctcag agggcacagc tgcaggcctg accaaggcca cggccggctc 120  
 tcgtgtctta ggacctgcac gggacttgtg gatgggcctg gactctccag aaactacttg 180  
 ggccagagca aaggaaaacc tcttgtttta aaaaaatttt ttccagagtg ttttggggag 240  
 gagtttttagg gcttggggag agggaggaca catctggagg aaatggcctt ctttttaaaa 300

<210> 163  
 <211> 300  
 <212> DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 163

gaccggctgg	gcctacaaaa	agatcgagct	ggaggatctc	aggtttcctc	tggctctgtgg	60
ggagggcaaa	aaggctcggg	tgatggccac	cattgggggtg	accgaggct	tgaggagacca	120
cagccttaag	gtctgcagtt	ccaccctgcc	catcaagccc	tttctctcct	gcttccctga	180
ggtacgagtg	tatgacctga	cacaatatga	gcactgcccc	gatgatgtgc	tagtccctggg	240
aacagatggc	ctgtgggatg	tcactactga	ctgtgaggta	tctgccactg	tggaacagggt	300

&lt;210&gt; 164

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

aaaatttata	ngtaatgaca	aatgacttat	cagtgttcat	catctgaaag	ctaagtgggt	60
cgttcaatca	ctttttcaaa	gttgatagta	gattgcatgg	tttcatgttt	cctcatattg	120
gtttattaat	tctatttaat	caaggaaaat	aacttcagat	tccataaagt	ttcagtttat	180
ttttagttta	ctactaggtg	agatagcaca	ttacatactt	ttactatcaa	atattatttt	240
agcagcttcc	catagtacca	aatgatttga	ttccctactc	tcatttttta	aagcatataa	300

&lt;210&gt; 165

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 165

ctggactctg	agtcgtcttg	gtcccaggag	ccagtagtga	aggcaacagt	ctgcccacct	60
gtggacacca	gacccctgga	gctcctgggt	agcaagttag	atctctggga	tgtcagttag	120
gctgggtgaa	gaccagaggt	aaactgcaga	ggtcaccacc	cccaccatgt	cccagggtgat	180
gtccagccca	ctgctggcag	gaggccatgc	tgtcagcttg	gogccttggtg	atgagcccag	240
gaggaccctg	caccagcac	ccagccccag	cctgccaccc	cagtgttctt	actacaccac	300

&lt;210&gt; 166

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 166

cttctgttga	ttggtttgtt	taaagtacct	aagtactacc	ctttgactcc	ctacaaaaag	60
ttcttttgtt	ttttaaacia	cttttatttg	tgacttactt	tcttgagaag	tggtcttaat	120
gaattgcata	aaatagtggg	agcagcttat	ttcttaagta	ctttattatt	tgtgctttac	180
catttcaggt	tcttatcttt	aacccttatt	tactcagttt	tccatctgaa	tgatcctatc	240
tctaaattaa	ggatttaata	aatgctgcaa	attgtccact	ttgcaaattg	tccaaaagct	300

&lt;210&gt; 167

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 167

gcgagatgaa gctacactgt gaggtggagg tgatcagccg gcacttgccc gccttggggc	60
ttaggaaccg gggcaagggc gtccgagccg tgttgagcct ctgtcagcag acttccagga	120
gtcagccgcc ggtccgagcc ttctgtctca tctccaccct gaaggacaag cgcgggaccc	180
gctatgagct aagggaagac attgagcaat tcttcaccaa atttgtagat gaggggaaag	240
ccactgttcg gttaaaggag cctcctgtgg atatctgtct aagtaaggat tccatatggc	300

&lt;210&gt; 168

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 168

gtctgggag cctacgcttt ccggataaaa atggcagaat gaaagaatta tgagtggaaac	60
tagagaatag gaaagacatg aaccaacgcc caaaatgaga aagaaggaca tataaagaaa	120
aagacaaata caagtgaaaa aaatatacta atggattaac gtccctgtcg agtgacattt	180
tctgactatg gaaatgatat tagacaaaaa gcaacttcaa gtgggtttct tatttgagtt	240
caaaatgggt cataacgcag catagataac ttgaaacatg aacagcgcat ttggcccagg	300

&lt;210&gt; 169

&lt;211&gt; 296

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

gagatctctg ggatgtcagt gaggttggtt gaagaccaga ggtaaactgc ggaggtcacc	60
accctcacca tgtcccaggt gatgtccagc ccactgctgg caggaggcca tgctgtcagc	120
ttggcgctt gtgatgagcc caggaggacc ctgcaccag caccagccc cagcctgcca	180
cccagtggt cttactacac cacggaaggc tggggagccc aagccctgat ggcccgtgc	240
cctncattgg gncctctggc tanttcanen agnccncag gtngagncca aagcca	296

&lt;210&gt; 170

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 170

gggtgttga gcagattgta gttgatccac agcaaagagc atcaccaaag ccattccagg	60
aggaactaga tccaccactt cctctgctgg gcatgctcca aaaatggttg tggcttcag	120
agaggactcc aaaagaaagc aaaaaacta gacagtggga gggcataccc aaaagccctg	180
agtttctgaa aaaatattga aagtttctat ggtgaaatag gaagttaatg tgcttaggaa	240
gaaaaaagtg gtaatgattc aaggaaacat aatcacacac ggtttttagtt ttaatggaca	300

&lt;210&gt; 171

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 171

atggaggcac cagcaggtag tggcccctgt aagcagggcc agagtcggga caaagagcag	60
gagtgaagca gccaaagagc agaggaccag gctggagcca gtgggcacgc aggagcctgc	120
ctgggaaaag ccggggggca aggctggcat gggaaatgaac acctgctggt gacacctctc	180

tgagcttcag ttcctttaac tagaaaaata gaacaggccc ggtgcggtgg ctcatacctg 240  
 taatcccagc actttgggag gctgaggcgg gtggatcatg aggtcaggag atcaagacca 300

<210> 172  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 172  
 ggcgaggag cagaagctca agctggagcg gctcatgaag aacccggaca aagcagttcc 60  
 aattccagag aaaatgagtg aatgggcacc tcgacctccc ccagaatttg tccgagatgt 120  
 catgggttca agtgctgggg ccggcagtgg agagtccac gtgtacagac atctgcgccg 180  
 gagagaatat cagcgacagg actacatgga tgccatggct gagaagcaaa aattggatgc 240  
 agagtttcag aaaagactgg aaaagaataa aattgctgca gaggagcaga ccgcaaagcg 300

<210> 173  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 173  
 gtctttccca ttcacttctc tagaaagctg ccaagacaga ggcagaaaga aatggatgat 60  
 agttctgtca agcacacttc tgttctctta gaacttagaa gtgtttctaa gagaacagaa 120  
 gtaataagag aaacagttac gtgtggaatt caacatcttt ggttggaaac cattggcttt 180  
 tttttcttg ttttgataga aatggaatta agcaaaagta gtttttgtct tttctgttgt 240  
 cttcaaattt caggccatct atttttaatt taatcccgtt caagtacttg attgttatac 300

<210> 174  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 174  
 attatttcca aagcagccta cagtagaaaa tagtcattat ggcagcagct tctgatgttt 60  
 ttgtttggta ggttttctga tttcaatata tagaatcata ttcataagat atcttctttt 120  
 aacgaattgc acaaagtacc catttaaaat ttacatgcac agttcattgc cacctttctt 180  
 aggcctatgc atagttaata aggttataat ctactcaaca tggaaaatgg agcctatttg 240  
 caaacacaca agtaattaaa gtaccaattc tctcttagtt tcttttttta tagttggttt 300

<210> 175  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 175  
 tgganactct ttantatgga aggtgaattt cctgtcaaca tagtccagga caaagcagtt 60  
 ccaattccag agaaaatgag tgaatgggca cctcgacctc cccagaatt tgtccgagat 120  
 gtcatgggtt caagtgtggt ggccggcagt ggagagttcc acgtgtacag acatctgcgc 180  
 cggagagaat atcagcgaca ggactacatg gatgccatgg ctgagaagca aaaattggat 240  
 gcagagtttc agaaaagact ggaaaagaat aaaattgctg cagaggagca gaccgcaaag 300

<210> 176  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 176  
 tataaaacttt attttattct cttctggggt agagttacat gacaagaaat tgaattaatt 60  
 caataaaatt ttagttcggg ttgcttaggt ttttactgct cccattcttg cttttactaa 120  
 tttatccaag attagatgtg attactatct aataataatt tagtcctcac acttacaac 180  
 cacttacaat accagcatgc ttctatcact gtaattctat tcaattctca ggcccatgag 240  
 gcatgccagc cagacgacca gacagcattt atagagaggg cactcaatac cagccacaaa 300

<210> 177  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 177  
 gactggagaa gtcagaagta gaaaagcaga ttgctaggag agacaggatg acagattttg 60  
 gtcagaaaat gggatattgg agtttaaagt atcaaataca gaatagttcc agatgttcag 120  
 agatccagca tgggattagg tactgaaatg gattagaact aaaagtcact agaatttaga 180  
 aattgagaac catgagagtg gatgcaatga cttgttgctt gattgaaaaa taaattaata 240  
 ataataaagg accatgagac tagcctgtta taggggggtat ctccatgann nttgtttttc 300

<210> 178  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 178  
 tcttggtgtc aaacactata aacctttgac cagctgagct gtgactgctg tcacatatct 60  
 gagtcctgtg tgcacagtaa tatcctgggt caggtaaaat ccaggctctc aagttttaag 120  
 gattttttga agaattcggg cttctttaag acgatccatg cccaaatcca caagcttggt 180  
 gacagtggat tacagtttgt gtggcaaagt ccaagttgtt acactgtgct ttaaaaaaaa 240  
 tcttatctgc atgtattgtt aacttagaga ccatgagatc tatttatcag gaccaggaag 300

<210> 179  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 179  
 ctcatgcctg taatcccagc actttgggaa gcagaggtgg caggatcatt ccagcccagg 60  
 agttcaagac cagcctgggc aacacagtga gtgagaccct gtctctatct aagaaaaaat 120  
 aattaagaaa ttttattaaa aaagaagaat caggaaacca agtccaaccc aactaacct 180  
 caaatgaacc agcccctaac acagatgagg ggattttgga ctgataagct ctgtgctgtg 240  
 tccatggccc gtcatttatc aaggctgcag ctttgtaa atgttgctatct ttatgttgtg 300

<210> 180  
 <211> 300  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 180

gtgatctgcc	tgccttggtc	tcccaaagt	ctgggaatac	aggcatgagc	caccgcactc	60
ggccaggagc	tagttttatc	agcatcctgc	tccactgcct	tcctctagt	cagcctggaa	120
gacatggcag	cgggtagctc	ctggggctga	gccagaagca	tcactgcagt	gaaagtctct	180
gcttacctgt	ctggctcagc	ttgggcaagg	gctgggccat	atgtgctcag	ggacgtgctt	240
ctcttgtaag	gcaggaggat	agaagaggac	caagaaggga	gggagctgcc	ctgtggtgca	300

&lt;210&gt; 181

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 181

cccatgccgg	gatcttccca	caccgcctct	cacagatcca	gccccagccc	cttgcttccc	60
aggccatctc	tcagcagcac	ctgcaggatg	cgggcacccg	ggagtggagc	cctcagaacg	120
catccatgtc	ggagtctctc	tccatcccag	cttccttgaa	cgacgcggct	ttggctcaga	180
tgaacagtga	ggtgcagctc	ctgactgaaa	aggccctgat	ggagcttggg	ggtgggaagc	240
cgtctccgca	cccccgggcg	tggttcgtct	ccttggatgg	caggtccaac	gctcacgtta	300

&lt;210&gt; 182

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 182

tttgagtggt	tgtcagaaac	aaataataaa	gccccaaaag	attaactagt	tgaaaaaact	60
ggcaaaatct	gtatacgtgg	aaatttacca	ggacagagac	tgaagaataa	agaaaatgag	120
tttcattgcc	agatcatgaa	atccaaagaa	actttaagaa	agatgagttg	tgtaaatgga	180
actgaaggga	gggaagagct	gccttcgcct	gggacaaaga	aaacatgtgt	atacacatgg	240
gtcaagcagt	gctggtctgt	ggctgcctgt	ccagaggaat	ggaaatatcc	cttgtcttta	300

&lt;210&gt; 183

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 183

cggacccatc	ggagcgtaac	ctggatctcc	gcaggcctgg	cggaggccgg	ccacctggag	60
gggcattgct	tggttcgcgt	ggtagcagag	gagcttgaga	atgttcgcct	cttaccacat	120
acagttcttt	acatggctga	ttcagaaact	ttcattagtc	tggaagagtg	tcgtggccat	180
aagagagcaa	ggaaaagaac	tagtatggaa	acagcacttg	cccttgagaa	gctattcccc	240
aaacaatgcc	aagtccttgg	gattgtgacc	ccaggaattg	tagtgactcc	aatgggatca	300

&lt;210&gt; 184

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 184

ctgttttgca gatgaggaaa ctgaggtaca gaattccttag ggaacttacc caaaatggct	60
tttctgcact ctgccctttg gtattgtccc atgtgaattg tttaaaactt atgtgtatag	120
tggcatgagt aggtgatttc agaaacagaa ctccactttt ttgtttgggtc ttaaaattag	180
gaacttttct tcatctgggc ttcatttccc tgcaccttcc cagctttcta gtcatgcaag	240
ccacatgtct ccacgtgagg ggttcattgg aaagcagcca cagagccacc ccctggctgg	300

&lt;210&gt; 185

&lt;211&gt; 260

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

attatagaga ttaatctcct ttgctcgaag tctattttaa tattagtcac atctaaaaca	60
tacttttaca gcaacatcta gactgggtgt tgaccaaaca actgggcatc atagctgaca	120
cataaaatta accatcacaa ccatgttcta ggcactgttc ctccactgcct gagaagacac	180
cgttatgttt attagggttt ttgagtttta tccacagctt ttgggttatct gcaacctagt	240
ctcccacctt taacatagtt	260

&lt;210&gt; 186

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 186

gataaactct tcagtgcga atattagaaa aagttagtta tacatttgag gaaaactata	60
aaagtaccaa taatgagtag gaaatcactt ctgcagtatt tttggagcat tttccttaag	120
catgacataa aagccaaagg tcacaaggga aaaaactgat agatttgtct gtgatattga	180
gagatgtatg cacatatata tacaacagtc atagtaagac accgttagac aaaagggtgat	240
gtatgaaaaa gaggcaaaac aacaagaaga aaagattgaa aaaatgagag ctgaagacgg	300

&lt;210&gt; 187

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

aaaaagtaaa gcttttcatg agcacaaatc ccttgcattg tttgatgta ctgatattcg	60
taaaatgaat attttttggt ttgttttggt ttattttttt gagacaagtc ttgctttggt	120
gcccaggctg gagtgcattg gcatgatctt ggctcactgc aaccctgcc ttgctgagtc	180
aagtgattct tctgcctcag cctcctgagt agctgggatt acaggcgctc accaccacac	240
ccagctaatt tctgtatttt tagtagacac agggttttac catgttggcc angctggtct	300

&lt;210&gt; 188

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

gagcattcct cctttgttaa cgaagcaaca ttacacaag atggacatta cattattagt	60
gcatgctctg atggcactgt aaagatctgg aatatgaaga ccacagaatg ttcaaatacc	120
tttaaatccc tgggcagcac cgcagggaca gatattaccg tcaacagtgt gattctactt	180

cctaaaaacc ctgagcactt tgtggtgtgc aacagatcaa acacggtggt catcatgaac 240  
 atgcaggggc agattgtcag aagcttcagt tctggtaaaa gagaaggtgg ggactttgtt 300

<210> 189

<211> 300

<212> DNA

<213> Homo sapiens

<400> 189

ctaatatcca gaatctacaa agaactcaac aagaaaaaaa ccaacccac aagcgggcaa 60  
 aggacatgaa cagacatttc ccaaaagaag acatacaagc aacctaaaat aatctaaaat 120  
 aatttttaaa aagaaaaaat gcttgacaga gttttgatag tacttagtaa aaagttatat 180  
 ctagtggctt tttgtttgtt tgtttttgtt ttgtttttaa gaaatagtct ctgtttccca 240  
 agctggagta cagtggcgca atcttggtct actgcaacct cgaactcctg ggctcaagcg 300

<210> 190

<211> 300

<212> DNA

<213> Homo sapiens

<400> 190

aaccactatg gaggcagatg tggtagccac tacactgcct gtgcacgcct gcccaatgat 60  
 cgtagcagtc agcgagtgga cgtgggctgg cgcttggttg atgacagcac agtgacaacg 120  
 gtagacgaga gccaggttgt gacgcgttat gcctatgtac tcttctaccg ccggcggaac 180  
 tctcctgtgg agaggccccc cagggcaggt cactctgagc accaccacaga cctaggccct 240  
 gcagctgagg ctgctgccag ccagggacta ggccctggcc agggccccga ggtggcccca 300

<210> 191

<211> 300

<212> DNA

<213> Homo sapiens

<400> 191

gcggcgctga cccggccggc cccacacccg ctcttctctt tctttgccgc ggactccctt 60  
 tcctgcctcc aagacctggt gtctccact gtgagccag ctgtcccaca ggagtgcccc 120  
 atggacctag actcaccttc cccttgccct tatgaacctc tgctgggccc agccctgtc 180  
 ccagctcccg acctgcactt cctgctggac tcaggcctcc agctccctgc ccagcgagcg 240  
 gcctcagcca ccgcctcccc tttcttcagg gccctgctgt caggcagctt tgcagaagcc 300

<210> 192

<211> 300

<212> DNA

<213> Homo sapiens

<400> 192

gacagaccgt tgagaggacg tggaggcccg agagggggta tgcgcggcag aggcagaggt 60  
 ggccctggga acagagtttt tgacgctttt gaccagagag gaaagcgaga atttgaaaga 120  
 tatggtggga atgacaaaat agcagtcaga actgaagaca acatgggtgg atgtggagtt 180  
 cgaacctggg gatcggttaa agataccagt gatgtggagc caactgcacc gatggaggaa 240  
 cccacagtgg tggaggagtc ccagggcacc ccggaagagg agtctccagc caaagttcct 300

<210> 193  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
 ctcaagaaag gagaagtttt tttgtatgaa attggaggaa atattgggga acgctgcctt 60  
 gatgatgaca cttacatgaa ggatttatat cagcttaacc caaatgctga gtgggttata 120  
 aagtcaaagc cattgtagaa gacttaacaa gctgcagata accatgtgga cttctgtcat 180  
 aattcttgct gagtcaagag tgtaaataaa agaaatggca ggactcatat tattcagttg 240  
 tacccaagta tttaaaaatg actctcttaa gccttaaaaa gtcataagatt tgtgctgctg 300

<210> 194  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 cagaagctta gtcataatttc aaaatgatca aatatcaaga aaaattctga gctgcataac 60  
 ttgtataaag taattttcag tgattttttt catgggttatg ataaaagaac tggattagca 120  
 gaaactttta ccctgaatca agatttaatt tttctttgag ctcactctta ggatatcgga 180  
 acatagggag caaacgatgg tgtggctgcc tcagtgcttg atttttaacg gttttgaaga 240  
 gaatagttac atttcttctc ctagtaagaa ctaataaata cattaacaga aatgaattcc 300

<210> 195  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
 ctctactaaa aatacaaaaa ttagctgggc gtggtggcac acacctgtaa tcccagttac 60  
 ttgggaggct gaggcacaag aatcgcttga acccgaggag cggagggtgc agttagccaa 120  
 gatcgccctg ctgcactcca gcctgggcaa cagagggaga ctctgtctcc aaaaacaaaa 180  
 acaaaaactg ttagtgaagg ttccctggga cttttgatat tttaaaaatt gatcttatga 240  
 ctaagtagat aaattcattg ccataatgag gctagctccc agataaacag cgtattttct 300

<210> 196  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 196  
 tggatactga caatggtggc aggcatttca agccttttaa attagtactt tttgtcgtct 60  
 tgcttattaa aattttgtta atttttagca agaccaattg ttgtgataaa ctggtgtttt 120  
 ttggatgctt caagcacacg ttaaccaatt ttttaattcc ccttttggtt cctcccattg 180  
 ttctaaaata ggactttcat attattaaaa cctcaaaaga tgatccaccc aggatgaaca 240  
 aagatcacca aggggaaaga aaacattttt tatctttaca gaaaacatgt taagattata 300

<210> 197  
 <211> 300  
 <212> DNA



<213> Homo sapiens

<400> 197

atccagatgg gatacctcta aacacgaaaa gaaagaagat tccattagtg aatttttaag	60
tttggctaga tcaaaagccg agccacctaa acaacagtcc agccccttag taaacaaaga	120
ggaagagcat gcaccagaat catccgcaaa tcagacagtc aacaaagatg tggacgcaca	180
ggctgaagga gaaggagcc gcccatccat ggacttattc agggccatct ttgccagttc	240
ctcagatgaa aagtcctcat cctccgagga tgagcaaggc gacagtgaag atgatcaggc	300

<210> 198

<211> 300

<212> DNA

<213> Homo sapiens

<400> 198

gcaacatttg tctacaactc tactgtaaaa ttggaaatgc tttccacag aaaaacctct	60
caaaatgctg aatgcaaaag ttgggatcac agaaacattg tgcctatatt tggctgctg	120
gaaactgtat ttttacaagg taatccctgt tttcaatata gttcctgtct tgccactggc	180
ggttttcttg tagcattttt ctagtcttga gattgctact acccaaagta ttcatttctt	240
tcttactggg gtgtcctctg tcttcacagc ctgcttctgg attgtaggtt ttttcctttc	300

<210> 199

<211> 300

<212> DNA

<213> Homo sapiens

<400> 199

gcaacatttg tctacaactc tactgtaaaa ttggaaatgc tttccacag aaaaacctct	60
caaaatgctg aatgcaaaag ttgggatcac agaaacattg tgcctatatt tggctgctg	120
gaaactgtat ttttacaagg taatccctgt tttcaatata gttcctgtct tgccactggc	180
ggttttcttg tagcattttt ctagtcttga gattgctact acccaaagta ttcatttctt	240
tcttactggg gtgtcctctg tcttcacagc ctgcttctgg attgtaggtt ttttcctttc	300

<210> 200

<211> 300

<212> DNA

<213> Homo sapiens

<400> 200

agtagaaaaa tacaagact gtgatccgca agttgtggaa gaaatacgcc aagcaaataa	60
agtagccaaa gaagctgcta acagatggac tgataacata ttcgcaataa aatcttgggc	120
caaaagaaaa tttgggtttg aagaaaataa aattgataga acttttggaa ttccagaaga	180
ctttgactac atagactaaa atattccatg gtggtgaagg atgtacaagc ttgtgaatat	240
gtaaatttta aactattatc taactaagtg tactgaattg tcgtttgccc tgtaactgtg	300

<210> 201

<211> 300

<212> DNA

<213> Homo sapiens

<400> 201

ttctactttg	ggtccgcgcg	aagccccactc	acgtgtgac	tgtgttgccc	ctctcggtgg	60
tcccaggcga	tccagccatg	ccccctgccc	ctctgcccag	atgcttcagg	ggccccgctt	120
ttcaggcttg	ccctcaccag	cggccgtcag	ccgacactca	gggatgtagc	taacaccact	180
ccgccagtgc	tttcagtagg	aagagctgag	gctgcctggg	aggccccggg	cgaccggaaa	240
agggtctctc	caagtctctga	aaagagaatc	tgccaccaga	tcgaatttcg	acccttgagc	300

&lt;210&gt; 202

&lt;211&gt; 281

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 202

ggccatggga	cagttgcaac	agcagttaaa	tggactgtca	gtcagtgaag	gtcatgattc	60
tgaagatatt	ttgagcaaaa	gtaacctgaa	cccagatgcc	aaggagttaa	ttccaggaga	120
gaagtactga	gcccagaaaag	ctttgaggaa	gacttgtctg	tccccacatc	tggggatagt	180
aatgccccaa	atggtggagc	tgaagagggg	gatggggcgg	gcgaggggtg	cacagcggga	240
aggggagtgg	tggtctcacg	atactgtgac	tctgagtaac	t		281

&lt;210&gt; 203

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 203

gccctcagcc	acccccatcc	ctgccccttc	tgagactcac	agcaccctt	tccttcctct	60
cctcccacct	cctccctcag	cccctcattc	tccttgaggaa	tctgcagagg	gctctgggac	120
tcaactgccg	atgtgaaatc	caggcgctcag	ctgtttccta	ggcaagggca	ggaaagtggg	180
ctccagccct	tgctccactc	atgcctgggg	gcctggggct	gagtggatc	cctacctggc	240
ctccccctgg	cctctggggc	tccagcgctg	ggtttgtcga	gtgagagaga	gagaggagct	300

&lt;210&gt; 204

&lt;211&gt; 269

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 204

gcggactctc	aggacgaaaa	gagccaaacc	tttttgaggaa	aatcagagga	agtaactgga	60
aagcaagaag	atcatggtat	aaaggagaaa	gggggtcccag	tcagcgggca	ggaggcgaaa	120
gagccagaga	gttgggatgg	gggcaggctg	ggggcattgg	gaagagcgag	gagcagggaa	180
gaggagaatg	agcatcatgg	gccttcaatg	cccgtctctga	tagccctga	ggactctcct	240
cactgtgacc	tgtttcagga	gcctcatat				269

&lt;210&gt; 205

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 205

ttctactttg	ggtccgcgcg	aagccccactc	acgtgtgac	tgtgttgccc	ctctcggtgg	60
tcccaggcga	tccagccatg	ccccctgccc	ctctgcccag	atgcttcagg	ggccccgctt	120
ttcaggcttg	ccctcaccag	cggccgtcag	ccgacactca	gggatgtagc	taacaccact	180

ccgccagtgc tttcagtagg aagagctgag gctgcctggg aggcccgagg cgaccggaaa 240  
 agggctctct caagtcttga aaagagaatc tgccaccaga tcgaatttcg acccctgagc 300

<210> 206  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 206  
 gggattacag gcatgaccca ccgcgcccag cctgtaattt cttatacttg gtattttgta 60  
 cttggattat gcttctgata cgctataatt atttatgtac atgttatttt tcttcaatag 120  
 actgtgaact cttcgaatgt aggactccta gagctagata ctcaattatt ttttattaaa 180  
 ttgaatgact tgaaactaca gatcctttat ttaaacttcc caaatttctg ctttatctag 240  
 gcaactcttt aaattctttg atctcatgta gattccaaag gctgaaataa ttgagatttt 300

<210> 207  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 207  
 tcctgaagct cggggggctg caggtcctga ggaccctggt gcaggagaag ggcacggagg 60  
 tgctcgccgt gcgcgtggtc aactgctct acgacctggt caccgagaag atgttcgccg 120  
 aggaggaggc tgagctgacc caggagatgt cccagagaa gctgcagcag tatcgccagg 180  
 tacacctct gccaggcctg tgggaacagg gctggtgcga gatcacggcc cacctcctgg 240  
 cgctgcccga gcatgatgcc cgtgagaagg tgctgcagac actgggcgtc ctctgacca 300

<210> 208  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 208  
 attccaaagg tttcaaagaa cttggtcata aatatgataa tgagaagaca aagtatttat 60  
 attaaaacag tttagtagcc ttcagttttg tgaaaatagt tttcagcaca gaaactgact 120  
 tctttagaca aagttttaac caatgatggt gtttgcttct aggatataca ctttaaaaga 180  
 actcactgtc ccagtgggtg tcattgatgg cctttagtaa attggagctg cttaatcata 240  
 ttgatatacta atttctttta accacaatga attgtcctta attaccaaca gtgaagcact 300

<210> 209  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 209  
 gagacagcag cccccaggga atgaagctga tgccagagtc agacccgagg aggaagagga 60  
 gccactgatg gagatgcccc tccgggatgc gcctcagcac ttctatgcag cactgctgca 120  
 gctgggcctc aagtacctct ttatccttgg tattcagatt ctggcctgtg ccttggcagc 180  
 ctccatcctt cgcaggcatc tcatggtctg gaaagtgtt gccctaagt tcataattga 240  
 ggctgtgggc ttcatgtgta gcagcgtggg acttctcctg ggcataagct ttggtgatgag 300

<210> 210  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 210  
 gtaacgtgac acgtatcttta cttctctttag taggcggaca cactttctta aagtggtaat 60  
 acgtcatggc cctgctataa ggtagtagtt ctagaagact gtttatctaa taattcagac 120  
 taaagctatt tatattgctg tgacaccacg tggaaaactt ttataattcc atctttatttc 180  
 tgatgtatat gttttatctt ctctgccttc ataagaacta aaaaccaaag ttatttacgt 240  
 gaaaacaaga tttttgtttg agttcattta cttgagatat gtttaaaaaa tccaccttct 300

<210> 211  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 211  
 gtccgtcagc tggtagcttt cattcgtaaa agagataaaa gagtgcaggc gcatcgaaaa 60  
 cttgtggaag aacagaatgc agagaaggcg aggaaagccg aagagatgag gcggcagcag 120  
 aagctaaagc aggccaaact ggtggagcag tacagagaac agagctggat gactatggcc 180  
 aatttgagga aagagctcca ggagatggag gcacggtagc agaaggagtt tggagatgga 240  
 tcggatgaaa atgaaatgga agaactgaa ctcaaagatg aggaggatgg taaagacagt 300

<210> 212  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 gcctgctgct tcatgccgcc ggcgtcctgc tccacgtctc tgtgctgctg ggccctgcac 60  
 tgtcgccctt gctgcgagcc cacacgcccc tccacatggc tgcctcctc ctgcttcctt 120  
 ggctcatggt gctcacaggc agagtgtctc tggcacagtt tgccttggcc ttcgtgacgg 180  
 acacgtgctg ggcgggtgct ctgctgtgct gggctgggct gctcttccat gggatgctgc 240  
 tgctgcgggg ccagaccaca tgggagtggg ctcgggggcca gcactcctat gacctgggtc 300

<210> 213  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 ggtatggttg gagtgtagga atgaatattc atgaaatggt tcttattgct tttccttccc 60  
 taattcatac aatgaatgta tttggaatac ttacatatta taaaataaac tatacctctt 120  
 caagaggat cctgttctgt aagatcagat gtttttattg caggtcaata taatactgcc 180  
 agagacagaa aataccccct tatcagtcct ttagtgcctc tttctgtttg tggcatgggt 240  
 agaaaaccca tgctgaaaag attgtacttt gtgatcccaa tcagagggag gagctaactc 300

<210> 214  
 <211> 300  
 <212> DNA

<213> Homo sapiens

<400> 214

ggaaagggcc	ctaaaagaga	tgaacaatac	ccgtatcatg	tggaatgaat	tagaaaccct	60
tgtcagagcc	catatcaaca	actcagagaa	acatcaaaga	gtcttggaat	gtctgatggc	120
atgcaggagc	aaacccccag	aagaggaaga	acgaaagaaa	cgaggaagaa	agaggaaga	180
caaagaggac	aagtcagaga	aagcagtga	agattatgaa	caggaaaagt	cttggcaaga	240
ctcagagaga	ttaaaaggaa	tcttagaacg	tggaaaagaa	gaattggctg	aagctgagat	300

<210> 215

<211> 300

<212> DNA

<213> Homo sapiens

<400> 215

atacttttta	aacctttttt	ggcagctcag	atggtgtaaa	ttttaaaatt	ttgtataggt	60
atttcataac	aaaaatatgt	atttcttttt	tgttatttta	tcttgaaaac	ggtacatatt	120
ttagtatattg	tgcaaaaaa	caagtcctaa	agtatttggt	tttatgtga	ccatccactt	180
gtgccttact	gtatcctgtg	tcatgtccaa	tcagttgtaa	acaatggcat	ctttgaacag	240
tgtgatgaga	ataggaatgt	ggtgttttaa	agcagtgttg	cattttaatc	agtaatctac	300

<210> 216

<211> 300

<212> DNA

<213> Homo sapiens

<400> 216

gcagatatatt	actgaaggaa	tctaggttgt	attttcagtg	gacaatggga	ataaagcatt	60
tctaaagcac	cgactggaga	ggaaggcaac	agagacaagg	agagaagccg	agagacatgt	120
ctgcgtgctg	ccacgcattc	gagcgattgc	tctgtgaaga	gtgtacact	gaacattttc	180
aggggaggct	gtttaccag	gcaatgtcct	caaacaagcc	tgtgccgggg	agtcctggaa	240
tctgtgccag	gactgtgttt	ttagcccttc	acctctcagc	tttagcagga	catgaaccag	300

<210> 217

<211> 300

<212> DNA

<213> Homo sapiens

<400> 217

ccccatctt	cactggttat	tccacttatt	taaaatgtcc	agaataagca	aatctccata	60
tagaggaagt	agattagtgg	ttgcttcggg	atgggaggaa	tggaagatt	gaggctcttc	120
ttttgcagtg	ataaaaatgt	cctaaaattg	actgtagcga	tggtcacaca	actctgaata	180
tgcttaagac	cattgaatta	cacactttac	gttggtgaat	tgtatggtat	gtaaattata	240
gttcaataac	atagttacaa	aagataatca	aaagcatgaa	agcactgttg	atgtggtttg	300

<210> 218

<211> 300

<212> DNA

<213> Homo sapiens

<400> 218

acggcctggt	ggagcagctg	tacgacctca	ccctggagta	cctgcacagc	caggcacact	60
gcatcggcctt	cccggagctg	gtgctgcctg	tggtcctgca	gctgaagtcg	ttcctccggg	120
agtgcagggt	ggccaactac	tgccggcagg	tgccagcagct	gcttgggaag	gttcaggaga	180
actcggcata	catctgcagc	cgccgccaga	gggtttcctt	cggcgtctct	gagcagcagg	240
cagtggaaagc	ctgggagaag	ctgacccggg	aagagggggac	acccttgacc	ttgtactaca	300

&lt;210&gt; 219

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 219

caactagaga	agattggaca	gcaggctgac	agagaacctg	gagatgtagc	tactccacca	60
cggagagaga	agaagatagt	ggttgaagcc	ccagcaaagg	aaatggagaa	ggtagaggag	120
atgccacata	aaccacagaa	agatgaagat	ctgacacagg	attatgaaga	atggaaaaga	180
aaaatttttg	aaaatgctgc	cagtgtctca	aaggctacag	cagagtgatt	tcagcttcca	240
aactggtata	cattccaaac	tgatagtaca	ttgccatctc	caggaagact	tgacggcttt	300

&lt;210&gt; 220

&lt;211&gt; 260

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 220

ggtaagtcag	gtgattgaat	cccggaaagg	ttcattgtct	tcaagctcac	aatactat	60
tgggacaaac	agttgtctag	tgtttgact	catgaaccct	gattcttgag	ggtggtat	120
tactgctttt	gtgatttggt	ttcaacatat	atagtctttt	ctccggagtt	accttaggtc	180
agtggccagt	gtttcagccc	ctggaaaggg	catgggctgc	cactgaggtt	ggtcacaggc	240
ctctcagctc	atggtgggag					260

&lt;210&gt; 221

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

gggttccatc	ccttccaccc	aggaaatgga	ggcacgactt	gcagcgttgc	agggcagagt	60
tctaccttct	caaaccccc	agccggcaca	tcacacaccg	gacaccagga	cccaagccca	120
gcagacacag	gatctgctaa	cgcagctggc	agctgaggtg	gctatcgatg	aaagctggaa	180
aggaggaggc	ccagtgaccc	tccaggacta	tcgcctccca	gacagtgatg	acgacgagga	240
tgaggagaca	gccatccaaa	gagtcctgca	gcagctcact	gaagaagctg	ccctgatgag	300

&lt;210&gt; 222

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 222

gcggtgaccc	acgtgtcctg	catgattgcc	ctactgctgt	ggagacctcg	tgctgaccat	60
ctggcagtg	tcttcgtatt	ctctggcctg	tggggcgtgg	cagatgccgt	ctggcagaca	120
caaaacaatg	ctctctacgg	cgttctgttt	gagaagagca	aggaagctgc	cttcgcgaat	180

taccgcctgt gggaggccct gggcttcgtc attgccttcg ggtacagcac gtttttgtgc 240  
gtgcacgtca agctctacat tctgctgggg gtcctgagcc tgaccatggt ggccgtatgg 300

<210> 223

<211> 300

<212> DNA

<213> Homo sapiens

<400> 223

gccccctctg gatcctgagc tccctgctct agacagtgat ggtgattcag atgatggcga 60  
agatggtcga ggtgatgaga aacggaaaaa taaaggcact tcggacagct cctctggcaa 120  
tgtatctgaa gggggaaagc cctcctgaca gccaggagga ctctttccag ggaagacaga 180  
aatcaaaaaga caaagctgcc actccaagaa aagatgggcc caaacgttct gtactgtcca 240  
agtcagttcc tgggtacaag ccaaaggtca ttccaaatgc tatatgtgga atttgtctga 300

<210> 224

<211> 300

<212> DNA

<213> Homo sapiens

<400> 224

ctggggccgc aggagctgtg gcgggtttcc taatcctgcg aatatgggta gtgcttcgtt 60  
ccatggacgt tacgccccgg gagtctctca gtatcttggg agtggctgag tccggtgggc 120  
ataccactga gatcctgagg ctgcttgga gcttgaccaa tgctactca cctagacatt 180  
atgtcattgc tgacactgat gaaatgagtg ccaataaaat aaattctttt gaactatgat 240  
cgagctgata gagaccctag taacatgtat accaaatact acattcaccg aattccaaga 300

<210> 225

<211> 300

<212> DNA

<213> Homo sapiens

<400> 225

gccccgctcc atgagcagtg actccccagc tccctcctggc accagtcccc agggctctcc 60  
tgttggtagt tccctgctttt cttcttgga attcctcgtg gacctcgaga tctttacctt 120  
aaaatagttc tgttgaattt caccctggca atgtaaattg atagcttacc ttacacagatg 180  
ccagacaatg gacaactcac catcagtcct ctgctcacct gagacaaatg catgtctgat 240  
tgcttcctct gccctattgt ttatgtgaaa atgcagattc actgagccag actaaggcat 300

<210> 226

<211> 300

<212> DNA

<213> Homo sapiens

<400> 226

tatataacaa cttttgcttt caaagttggg tgggactaga acacacaatg gaaggatgga 60  
gtcaggagac ctggattctt gtgcccgtc tggcttttac agtctgccta actctatgca 120  
gtcacttcct gccagcctgt ttctttacct acaagaggga gagacactcc ctggccagcc 180  
tagttctcag ggtgaacgaa aggtcattat cactgcatcc tctagtcatt tgcttcttcg 240  
ctaattaaca catcttgagc acctgcgatg ttccaggaa aggagatggc agcgtgcaag 300

<210> 227  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 227  
 ttgctgaaat gggcacttct gctgtgatgc tagtggtgat tttgctctca gatgaacaca 60  
 atgtctcata ctaaccaaga agcaagaaaa gcccctatgca ttcatttttc acttggagtg 120  
 acaatgggag aggtcaggaa tcaagttcac tttcaagatc taagggagtc cactatctgt 180  
 gcaattgtat ttggcttttt tttgcaactgt ttcaatgctg gtaattgaaa ccattttaat 240  
 atatttggtt gtattcactt tatatgtcct tccaaaaatg ttgttgtgta cataccatgc 300

<210> 228  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 228  
 gctatgtatt gtgtcctacc atgaattcac tccatgctag ccacattggc ctgtatggct 60  
 attccttgga cacacctagg atgttcttgc ctcttagctt gcctaccttt ctctcatcat 120  
 ttgggcctca gcgaggatat catctcctca gagaagcctt ctgtgaccat gctatctaaa 180  
 atactccagc acttcagtc ccccttatcc cattactctg ctttttcaga aacattgggtg 240  
 ctccctgaaa catatttggt tacttgcctta gtgtcttttc tcccgcacta ccatgtaagc 300

<210> 229  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 229  
 gattttcgaa actcttcagc tacttgccct tttttatctg aaaccatcat accttctgaa 60  
 agaaaaaagc atatcttcat tgacataaca gaagttagat ggcccagtct tgatacagat 120  
 ggtacatga tatatatgga gagtggcatt gtgaagataa catctttaga tggcatgca 180  
 tacctctgcc tgcccagatc tcagcatgaa tttacagtac attttttgtg taaagttagc 240  
 cagaagtcag actcatctgc agtgttgtca gaaacaaata ataaagcccc aaaagataaa 300

<210> 230  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 230  
 acttcttggt tgctttttt ataaggaaat gttggagagt tacatcattg ctaatgtaga 60  
 aatgttaagt ggaaaaatat acagtttggt aaaataaact agattctaca tttatttggt 120  
 ggttttttcc cctcctttc tttccacagc acttttgata tcaagcaagt ggcttccttt 180  
 ttgagatatt aaaaaaaaa agaaaaggaa aaaagtaaat gannnnnnnn nnnnnaaccc 240  
 tttctnattn gnattngttt nagnattgng aagttgngtt aanagtnct agntagaaat 300

<210> 231  
 <211> 300  
 <212> DNA



<213> Homo sapiens

<400> 231

tgattctttt	tgtnntttt	tttgatattg	acaaaagctt	anncnttncn	attaaaaang	60
ccactaatta	gactttttan	ntaaaaaang	tagggggttt	taaaactact	ttcctactac	120
caaaaaatca	naaagtatct	agcttttctaa	atnggggaaag	caagcaatgt	tataaaaaacn	180
ctgaagggaat	ctctttcttc	gggacctttt	gttaaactcg	gttnaagctg	taaaccttat	240
ttaaaataaa	atttaccaca	naacaggaaa	tanaacctgg	ggaanactcn	aaatacnctt	300

<210> 232

<211> 300

<212> DNA

<213> Homo sapiens

<400> 232

ggaagccaag	gcctggagct	gcaggtcccc	cgcatctct	ctctgtccc	gcagcccagg	60
atggcctggg	gccccacct	gctgcagcag	gagccccaag	gagtgtctagc	tgagggtggg	120
tgctggggg	gtcctcatgg	acagtggagg	gtgcaagggt	gcactgaggg	tggtggggagg	180
ggatcacctg	ggttccaggc	catccttgct	gagcatcttt	gagcctgcct	tccggtggga	240
gcagaaaagg	ccagaccctg	ctgagttaga	ggctgctggg	atccactgtt	tccacacagc	300

<210> 233

<211> 300

<212> DNA

<213> Homo sapiens

<400> 233

gaggaagagg	cctgctccac	ttgtctggga	acctgggcag	gaggcacaga	ggaagccaag	60
gcctggagct	gcaggtcccc	cgcatctct	ctctgtccc	gcagcccagg	atggcctggg	120
gccccacct	gctgcagcag	gagccccaag	gagtgtctagc	tgagggtggg	tgctggggg	180
gtcctcatgg	acagtggagg	gtgcaagggt	gcactgaggg	tggtggggagg	ggatcacctg	240
ggttccaggc	catccttgct	gagcatcttt	gagcctgcct	tccggtggga	gcagaaaagg	300

<210> 234

<211> 300

<212> DNA

<213> Homo sapiens

<400> 234

ggaacataat	tagcttactg	atttgatggg	tctgtgtagt	tcttgaaact	cttggtctct	60
gtttgccttt	ctttaactct	ggctccttct	ccttcttctg	tttgtgtatc	tgtttaattc	120
attgagttag	gaggacaggc	agaactgtgt	ctgccaagga	ccggatgtac	ttctttcctt	180
gctcttggtt	ttttgctcac	ttttatatgt	aagggtattag	tacaaacctc	aaggagagaa	240
agtagaggat	cagatcattg	ggacttggtc	tggtttcaag	aaagaattaa	caaattgccc	300

<210> 235

<211> 300

<212> DNA

<213> Homo sapiens

<400> 235

gttggtctcaa	gggccaccag	aagcatttct	ttattattat	tatttttttaa	cctggacatg	60
cattaaaggg	tctattagct	ttctttccgt	ctgtctcaac	agctgagatg	gggccgccaa	120
ggagtgcctt	ccttttgctc	cctcctagct	gggagtgcag	ggtgggagtg	tgtgtgcccc	180
ggtgggggtg	tctcctggct	gggaaggagg	gaaagggagg	gagagttttg	cgggggttgg	240
cagtggagag	caggctggag	aggagatggc	taatagctgt	ttaatggaaa	cctgctgggc	300

&lt;210&gt; 236

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

gaatcatcga	aggttgagac	cgtgtctagt	tacatagtta	taaataccca	tctatgtact	60
gatgccttct	aatgtctat	ctccagtatg	gtcttttccct	ttaagctcta	gatccattga	120
caccctcacc	atctctaaaa	ggcatttcaa	actgaacaca	tctgatacag	aacttttcat	180
ttccttccca	actttgccca	cgccagcctg	ctcctccttc	acgctttcca	cttagtatat	240
gatcccacta	ttcactcagt	ctctgaagct	taaaacctag	gattcatcct	tgactactgt	300

&lt;210&gt; 237

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 237

caggacatgg	agcagtacct	gtccactggc	tacctgcaga	ttgcagagcg	gcgagagccc	60
ataggcagca	tgtcatccat	ggaagtgaac	gtggacatgc	tggagcagat	ggacctgatg	120
gacatatcgg	accaggaggc	cctggacgtc	ttcctgaact	ctggaggaga	agagaacact	180
gtgctgtccc	ccgccttagg	gcctgaatcc	agtacctgtc	agaatgagat	tacctccag	240
gttccaaatc	cctcagaatt	aagagccaag	ccaccttctt	cttcctccac	ctgcaccgac	300

&lt;210&gt; 238

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 238

cactggctac	ctgcagattg	cagagcggcg	agagcccata	ggcagcatgt	catccatgga	60
agtgaacgtg	gacatgctgg	agcagatgga	cctgatggac	atatcggacc	aggaggccct	120
ggacgtcttc	ctgaactctg	gaggagaaga	gaacactgtg	ctgtcccccg	ccttagggcc	180
tgaatccagt	acctgtcaga	atgagattac	cctccagggt	ccaaatccct	cagaattaag	240
agccaagcca	ccttcttctt	cctccacctg	caccgactcg	gccacccggg	acatcagtga	300

&lt;210&gt; 239

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 239

atttcctcca	gtcctggggc	ccatccttga	gggccttccc	agccagccag	caggagaggc	60
aagaactggg	ggaacacagg	aacctagggg	aggaggggag	cgctgggcat	cctcaggctg	120
gcggccaagg	cctgcccctg	gaggcactag	aggagggcat	ctgtctgtgg	gagccagag	180

gctgcaggga ggaggaggag ggaggtatct ggtgtgagcg ttgcccctgc gacatttggg 240  
 accacacagg tgggcttcct tattccctga caaagcctct gtttccagct cttccgccct 300

<210> 240  
 <211> 274  
 <212> DNA  
 <213> Homo sapiens

<400> 240  
 catgagtgat attttggctt gggtttcctc ttaagatttt agtttgtctg aattaaggaa 60  
 aaatgttttt aatatacatt cttattttgt cccaccctc cagaaataag ctggaaatct 120  
 taactttttg gggggtcttt tttggtgttt taatgggccc agaactgtgg tttaaatttt 180  
 tatgtatgta ttttcttttt tgtggagtat aaatttataa actggatttg ggacctaaaa 240  
 tactcctcag gttgatgtat tcatgaaagt tttta 274

<210> 241  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 241  
 ctgttgccctg ccaagctcag ggcccattta tcatgcatct tcccatcctt gtctccccc 60  
 actgtccctt acctgagtca caatttcgcc aaagccaaag ggattgtcct aagccaatgt 120  
 tgatttatca ctcttcctgc tcaaaagccc ccaagatcac ctatcaatca cctacttgag 180  
 tgcaagcttt gactctgtca cctgacattc aagtccccct ctgcccccat gccagtctta 240  
 tccccctccc tacatatgcc ctatgcctca gtttgccctc cctccacttt aaaaagcctc 300

<210> 242  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 242  
 ccgctggcta tgtggacgct ggggcagagc caggccggag tcgaatgac agccaggaag 60  
 agtttgccag gcagctacag ctctctgac ctcagacggg ggctgggtgcc tttggctact 120  
 tccagcagga taccaagggg ttggtggact tccgagatgt ggcccttgca ctagcagctc 180  
 tggatggggg caggagcctg gaagagctaa ctctgtctggc ctttgaggta atgggggggtg 240  
 gcggtgggtg ggggtgctta gtggctatgc tcaccccgct ccaggaggcc tattttggta 300

<210> 243  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 243  
 caagatctgg aggaatgcag agaggaactt gatacagatg aatatgaaga aacaaaaaag 60  
 gaaactctgg agcaactaag tgaatttaat gattcactaa agaaaattat gtctggaaat 120  
 atgacttttg tagatgaact aagtggaaatg cagctggcta ttcaggcagc tatcagccag 180  
 gcctttaaaa cccagaggt catcagattg tttgcaaaga aacaaccagg tcagcttcgg 240  
 acaaggttag cagagatgga tagagatctg atggtaggaa agctggaaag agacctgtac 300

<210> 244  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 244  
 agtaaatttt ttatgcatat tttattgcaa taaaaaatga aaacagtttc aatctaggag 60  
 gattttggat gcatctatgc cttgagaaat gaatggtttg atgtaaatgc atggtagcaa 120  
 gaataaataa ttatgttaat tcatataata tgttatatat agttttaaag aaaattctat 180  
 cactgtcttc ctatgggtag ggctataatg tccagttcct tcagggatta agagggtagg 240  
 gtctgaagtt aatccttggt tgtcgtaatg ttattaattt attcaaccaa gacttaattg 300

<210> 245  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 245  
 tagacataga aaacatacag taagaatatg gtattataat cttacgggac cactgtcaaa 60  
 tacgcggtct gtctttgaaa agttgtaatg cggcgcatga ctataaatac ctactgtggt 120  
 agcatttaca ttccttgcca gggagtttga aattttatact atagaaataa ctttaggttt 180  
 taggtagagt taaagaggta aagcacatgt tgccacaacc caggaaagta tttttaagaa 240  
 agattggatt ttcctacctt tagagatcta aaaaaattt aatataaaaa atcattttgt 300

<210> 246  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 246  
 tggaatattt gctgtgaagg gagaaagga gagaaaactc ttctgaggat catttgtcct 60  
 ggtagtatag taaaaccaac cagctgaacc ttccaggcta caagagaacc cggttcggta 120  
 atgtcttttt aagaataatt tttaattgct tataacaagc atattttgtg gcatttgaac 180  
 tatatttact gtcctaatat ccgttatttt ccaaggatt ttgtatcttt ttgaaaatgt 240  
 ttacatcatc agatgatcca cagaattcac tttatgtgag atctcccag agtttccatc 300

<210> 247  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 247  
 gtgttgctca gtgagcagac ccgactccag aaggacatca gtgaatgggc aaatagggtt 60  
 gaagactgtc agaaagaaga ggagacaaaa caacaacaac ttcaagtgtc tcagaatgag 120  
 attgaagaaa acaagctcaa actagtccaa caagaaatga tgtttcagag actccagaaa 180  
 gagagagaaa gtgaagaaag caaattagaa accagtaaag tgacactgaa ggagcaacag 240  
 caccagctgg aaaaggaatt aacagaccag aaaagcaaac tggaccaagt gctctcaaag 300

<210> 248  
 <211> 300  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 248

gagaggatca cttgagctta ggagttcaaa tccagcctga gccaacataa caagactttg	60
tctctaaaca aaacagttat tgtttaaaga atctgaaatc ttcattcttta attcaggtag	120
caatgaatcg agcccaagtt tgtttgatat ccagttccaa gtctggagag aggcattctt	180
atcttattaa agtatcgaga gacaaaatat cagacagcaa tgaccaagag tcagcaaatt	240
gtgatgcaaa agggctatca aaggagggt ttttacagag aactaaggaa gagaaggagg	300

&lt;210&gt; 249

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 249

ctagcctggg caatatagta cgaccctgtc tttactaaaa atgcaaaaat taaccacgta	60
tggtggctca cacctgtagt cctggctact gaggaggctg atgcaggaga atcatttgaa	120
cccaggagggt caaggctgca gtgagctatg attgcaccac tgcaatccag cctggacaac	180
acagtgagac cctgcctcac aaaaattata ttctgatctt ctgagtccat gaacacattg	240
tccaaatgga tttttctagc tcctccaagt tacagatagt tccacgcaca cacagaactc	300

&lt;210&gt; 250

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

aggaagggtg aggggcagga acaggacgga caggccccgg gctctggcac atcctgggga	60
acaagggacc acaaggacgg gggcagtctc cagacttccc ctgggcgctt gaccccaggc	120
cttgacgggg agagagccag ggcctccctc aggtctttgt tcatgtgtgt ttccctgccg	180
tggacaccct tccccgtct cggattctct aaatcctgcc ccatctccca gatcttggtc	240
atgtccaagc tttccagga agtcttagca gctcccacac cgcagagctc gagatgtctc	300

&lt;210&gt; 251

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 251

gaaggcagaa gtgtaaatga acatacagaa gaaggagaaa gcctgctgtg tttggcttgt	60
tcagcagggt attatgaatt agcacaagta ttgcttgcta tgcattgcta tgttgaagat	120
cgagggaata aaggagacat aactcccctg atggcagctt ccagtggagg ttacttagat	180
attgtgaaat tattacttct tcatgatgct gatgtcaact ccagctctgc aacaggaaac	240
actgcgctaa cttatgcatg tgctggagga tttgttgaca ttgttaaagt gtccttaaat	300

&lt;210&gt; 252

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 252

```

gcactttctct ctcaactggaa agagaactgt tctcctttct ctttcttctg cctattaagc      60
ctctgctcct aaactcctca tgtgtgtctg tgctctaaat tttcctggca tggcaggaca      120
aaccctgggt atttaccaca gacaacaaaa ccgcttcact atgatgtatg catgctgcaa      180
aggaagagac agaattcttg tctatcacc ccgctggagt cagtggcacc attgcagctt      240
actgcagcct caaactcctg gctcaaggga tcttcagct tcagcctcct ggtaactag      300

```

&lt;210&gt; 253

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 253

```

gtctgatgca ggagaattgc taaaaccag gagggagagg ttacattgag ccgagattgc      60
gccactgcac tctagcctgg ggcacagagc aagactccgt ctgaaagaa agaaagagaa      120
aggaaattcc ccagggaagt acctcggctt atttcataaa caggtactga aggaagcaga      180
ggcatgtgga ggacttccc acctcgtgca gctatttggg ccgtggcatc tgaaatttct      240
tatttcagag tcacccttt gatgaccttg gcagtgaact gcagtcact gtttaggcct      300

```

&lt;210&gt; 254

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 254

```

atgttacaga catgaaatga gaacagaatg ctaaaagaac ataaaagaat aagagctcct      60
taaagattat aaataaatgg tgatgttaaa gtaatagcac cattggacga agctagggaa      120
tcaacacttg acagaaagat acatattttt ttatacaaa ctacatatat ttgagcaatc      180
aagtagtaga catagagaat tttcttttta tggaagtact ctaataagta aagggtgat      240
agaattatat cagcattttc tagctcctgg ggaattatgc attgggcatc catggctgct      300

```

&lt;210&gt; 255

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 255

```

gctgcctgtg gcatagccac tgctgtacgt ttttggttg tnttaagaaa ctgatgaag      60
aggggtgtca ttctgggctc ggggtggttg ccaatttttc accagaaagg gagccacccc      120
ttgcaaccac ttctgtctcc gttagcccc cctctgcct cctccaagcc aaagcgtggc      180
ctggcttttg tcttccatt tagttttcct cttttaccct tccttttgtg cttaatttat      240
taaaatagtt gctgtataat ttattttcat aaactataaa aaaatactaa atggttaaaa      300

```

&lt;210&gt; 256

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 256

```

acagtctcgg gtttcatatt ttgctgtttt tgatggacat ggaggaattc gagcctcaaa      60
atttgcgtga cagaatttgc atcaaaactt aatcagaaaa tttcctaaag gagatgtaat      120
cagtgtagag aaaaccgtga agagatgcct tttggacact ttcaagcata ctgatgaaga      180

```

gttccttaaa caagcttcca gccagaagcc tgcctggaaa gatgggtcca ctgccacgtg 240  
 tgttctggct gtagacaaca ttctttatat tgccaacctc ggagatagtc gggcaatctt 300

<210> 257

<211> 300

<212> DNA

<213> Homo sapiens

<400> 257

atagaactag gcactgattt gtttatattt atcctgctcg agacacatga tgtttcatgt 60  
 atctgtggct ttttatagtt taaaataatt tctggaaaag tcatagtcac tatctcttta 120  
 accgtccctt ctcttccatt ctctttgttc tctcttcttc gaactcctgt tagtcatttg 180  
 atcctccata tctctgaata tttttgtatt tcttttatta tttatttctt gtctctgcta 240  
 cattttacat tgagtaaaag tgggatgtga cagtgggaaa tcattagtga cttagaaatt 300

<210> 258

<211> 285

<212> DNA

<213> Homo sapiens

<400> 258

tactctatta tattgtgcat gctcctgatt tagctgctct tggcatcatt ggctgcagtg 60  
 gaaccttgaa atgcatctgg ctagatttat gctcaaatca ttctcagtta gccttttagt 120  
 gcctcttcaa aggttttttt ttgtatgttt tctattctta ataaaagctt aggattaatt 180  
 agaaagaatc tgatatgggt atgtttcccc ttgtgtacgc tgacctcatt catacgtttt 240  
 tcatagtcca gtggtctaaa cgctttcaag agcccagctc cttgg 285

<210> 259

<211> 300

<212> DNA

<213> Homo sapiens

<400> 259

gccttctctg gcctcaccaa ttaggtcaaa tgttccttag aatgtgttgt ggggcatggg 60  
 ctctccctgt gaggacctgt ccagctggac ctccgccttc ctgcgactgt attggtgtct 120  
 ttccctctca agcctatgag ctctgcaagg gcagggaccc tgtatgattt tgcctatcgt 180  
 atgtcctcca gccccagca cagcgcttgg tgtccagtga gagctcagca aatactttgt 240  
 gagttaagga caggcggctg ggtagatgga tcgtctgcct agacagggca gttattcgtc 300

<210> 260

<211> 300

<212> DNA

<213> Homo sapiens

<400> 260

gaaaagggag ccgcgcagcg cctacgggag tccggcggca gcagccggta ccggcaacca 60  
 cgggcagctc tcagggaatc tccgtcgtga ggccagaggc tccagtcccc gcgagtccag 120  
 atgcctgtcc agcctccaag caaagacaca gaagagatgg aagcagaggg tgattctgct 180  
 gctgagatga atggggagga ggaagagagt gaggaggagc ggagcggcag ccagacagag 240  
 tcagaagagg agagctccga gatggatgat gaggactatg agcgacgccg cagcgagtgt 300

<210> 261  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 261  
 tttgctttca gtggttggct ttactgaaa gaaagtgtaa aaaaagtcag aatttatagc 60  
 ttctactatg tccaagacta ggactgggtt ataaagattt tcttttgtga aggaaaataa 120  
 aagaaaattt gccactactg catttacttt actattgtaa acttaagatt cattccttag 180  
 tctttggaat ttgatgtct caaaaccaga tgagtgaag tgctgaattt gcaaaataaa 240  
 gctaagaatg cttaactctg cactttaagt tctactctga ccaaattgaa gatgagcaga 300

<210> 262  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 262  
 ttttttaaga gataaggctt tgctatgtta tctaggctgg cctaaacttc tgggctgaag 60  
 tgatcctcct gtgtagctgg gactacaagc atgtgccacc aatgcctggc ttctcacact 120  
 gttttgtaac atagatatgt gaagatgtgt attatagaat tgtttgtaat actgtagtgt 180  
 tgtaggcaat gtgactgtct ataggggaagt ggacagggtta tttgtggtaa atactcatgg 240  
 aaaacgggtca agcagttaaa agcaatcaat tatgggtcacc cagcaatgca gataaatctt 300

<210> 263  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 263  
 agaacagggg gaagagagga agagggagct gcagggtgcc gaagagaaca gggcggactc 60  
 tcaggacgaa aagagtcaaa cctttttggg aaaatcagag gaagtaactg gaaagcaaga 120  
 agatcatggt ataaaggaga aaggggtccc agtcagcggg caggaggcga aagagccaga 180  
 gagttgggat gggggcaggc tgggggcagt gggaagagcg aggagcaggg aagaggagaa 240  
 tgagcatcat gggccttcaa tgcccgtct gatagccct gaggactctc ctactgtga 300

<210> 264  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 264  
 tttaaaggtag ttttagaagg aagtacaaat tggctttcat cttgcaaaca atcgtttttt 60  
 acttcattat cttaatttgc tttgtcactc ataaaaagga aaccatacct gagttgtaga 120  
 caatgaggaa acacttgagg cttctgctgt gtgttctttt gttattgttg ttattgttgt 180  
 tactcagtaa cttgaatatt gtttaatgtg ttgtaagacg tagagtttat ctcaagctgt 240  
 taaaaatggt aatgtacaaa tgtgaataga cacttatcta tataatatgg gtaagttttg 300

<210> 265  
 <211> 300  
 <212> DNA



<213> Homo sapiens

<400> 265

caggaaagtc	ttcctagagg	taatTTTTaa	gctgattgtt	ttagaattag	tagaagcttg	60
ccagatggaa	aagtcaggc	aaagtgtaac	atgaatggga	aaggccacag	tctagaaatg	120
gcagagtgtg	ttcctagttt	gtttgtttgt	ttgtttgtac	ctgccttggt	ccaggaagga	180
tttaatgtgg	tttatattcc	agtcctttaa	tgctggaagg	gctgagatga	gactgaaaga	240
tgggcaggaa	gtatatcatc	acaagctttg	tgtttgatgt	taatgtgtat	gatttttata	300

<210> 266

<211> 300

<212> DNA

<213> Homo sapiens

<400> 266

tgtgccacca	caccagctc	attattatta	ttattattat	tattattttg	agacgaagtt	60
tcactcttat	ccccaggct	ggagtgcatt	gggtgcgatac	tggtcactg	caacctctgc	120
ctcctgggtt	caagcgggtc	tctgccttg	gcaggcacct	gtagtgtcag	ctactcgaag	180
gctgaggtgg	gagaatcgct	tgaacctggg	gggcggagat	tgcaatggtg	tggtctcggc	240
tcactgcact	cgagcctggc	gacagagcaa	gactctgtct	caaaaaaaaa	aaaaaaaaan	300

<210> 267

<211> 300

<212> DNA

<213> Homo sapiens

<400> 267

atataactct	ggaggtcagg	acataggaga	tattgattca	ggacttgcca	gagtatggtc	60
ttgggggtgtg	ccctgatatt	acaaacaggg	atcttagtgg	ctaggtgatg	aggccatggc	120
aaatgtagat	ggaccaagat	caatttgcct	ttctagatga	ggttttctag	gtgaaatggt	180
tttgaaacta	ttttgtagcc	tagtataatt	tataaaagta	gagagaaact	ataaatataa	240
atttggaagg	ggttagctaa	aaggagaaaa	cagcagaatc	ttcatatata	tagaaatgga	300

<210> 268

<211> 300

<212> DNA

<213> Homo sapiens

<400> 268

cctacttatt	ggatgttggc	tctttggtgt	catggagatg	gctttactgt	aggtttgtgt	60
gtgttgcatt	acttttcatt	gggattgaac	tgagaaataa	caaacaagct	ttaagtggga	120
aattaaaaaa	aagaagtaac	ctatgtagat	ccaaacttaa	aatgtgagaa	attattgaaa	180
tttcattttc	tacaaacttg	aaattagcct	gctaattgta	aagttgtttt	aataatgctg	240
acaaatgtca	gttacgtttg	caaaggagtg	tatggttcta	ggtatttgcc	tactgttacc	300

<210> 269

<211> 300

<212> DNA

<213> Homo sapiens

<400> 269

cctacttatt	ggatgttggc	tctttggtgt	catggagatg	gctttactgt	aggtttgttg	60
tggtgcatta	cttttcattg	ggattgaact	gagaaataac	aaacaagctt	taagtgggaa	120
attaaaaaaaa	agaagtaacc	tatgtagatc	caaacttaaa	atgtgagaaa	ttattgaaat	180
ttcattttct	acaaacttga	aattagcctg	ctaattgtaa	agttgtttta	ataatgctga	240
caaatgtcag	ttacgtttgc	aaaggagtgt	atggttctag	gtatttgcct	actgttaacc	300

&lt;210&gt; 270

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 270

cctacttatt	ggatgttggc	tctttggtgt	catggagatg	gctttactgt	aggtttgttg	60
tggtgcatta	cttttcattg	ggattgaact	gagaaataac	aaacaagctt	taagtgggaa	120
attaaaaaaaa	agaagtaacc	tatgtagatc	caaacttaaa	atgtgagaaa	ttattgaaat	180
ttcattttct	acaaacttga	aattagcctg	ctaattgtaa	agttgtttta	ataatgctga	240
caaatgtcag	ttacgtttgc	aaaggagtgt	atggttctag	gtatttgcct	actgttaacc	300

&lt;210&gt; 271

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 271

ccacatttaa	gtgagatatg	ggaaggagga	gcagattggt	tttgaaggga	ggaagagcag	60
ttacttaggg	tcaaattaag	ttgtaaaatc	ccccccggga	ttttgtatgt	aagtcaaagt	120
gaattgtatt	tggaagaaga	actgggggagc	ccacctctgg	tatttttttt	atgtccctca	180
tatggacaaa	taaacctctg	gtattaaatg	aattttcttt	tgggggattc	tatatattcg	240
ggatttcaac	caccaaccta	tctggttttt	cccgctgaaa	tgttgggtga	tggaatcagg	300

&lt;210&gt; 272

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 272

gaacgcttcc	attttatacc	tgtgtctagt	tagtttctgc	ctatctatcc	aagaagcttt	60
tatcaagggg	ccaccatgtg	ccagccactg	aagtagatat	aaatacaagg	atgtgtaagg	120
tatggatgat	ggtatacgaa	ctgtcatctt	actggatttg	tccgctctgt	taaagatacg	180
gttccgaaaa	ctttttaaag	ccctagagag	ggctttaagg	caatgtagca	tcatatatag	240
aggcatcaac	ctgttcatat	ctttctattt	aacagaactg	tgcacctggg	cacaaggggtg	300

&lt;210&gt; 273

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 273

gaatggcgtg	aacccgggag	gcagatggtc	ttaaagtggg	gagacccggg	ttacaggcct	60
gactgcatca	ctaactcgct	gtgtgtccct	gggcaagtca	gtgcagtgca	gtagcctctc	120
cgtctccgac	tgaggagcaa	agccctcggc	tcaagatcct	cacctacttc	acagggattt	180

gaaatagtgc agtcaacagg aaaagaaaag cgctatagaa atgctcgacg ctatcacttg 240  
 gggcccacgt ggaagtatca acgtataaat tggcccaggc agacagaagg atgcagggga 300

<210> 274  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 274  
 ggaaccaggg gctgcagAAC cagccccctcc ccaatgagga cccctcttgg acgccccctcc 60  
 ccatggagaa caccaggagc cacagacccc agaccacagg agcacacagg ggagggcacg 120  
 gggcggcggg ggcagggtgt ctgctgcctc gtttatggga tttgctccgc gtctagcaca 180  
 ctgctgcctg cagtgtcctc gtcccctgca gtggctactc tgggctacg ggcctaatac 240  
 tggttggcat gaaaatgtcc tgaggctact gtgacaaatt tccacaagct gagtggctta 300

<210> 275  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 275  
 ctttgggaag cagaggtggc aggatcattc cagcccagga gttcaagacc agcctgggca 60  
 acacagttag tgagaccctg tctctattta agaaaaata attaagaaat tttattaaaa 120  
 aagaagaatc aggaaaccaa gtccaaccca actaaacctc aaatgaacca gccctaaca 180  
 cagatgaggg gatttgggac tgataagctc tgtgctgtgt ccatggcccg tcatttatca 240  
 aggctgcagc tttgtaaatg tggctatatt tatgttgtgt atagtttcta tcatttatatt 300

<210> 276  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 276  
 tttgtatttt tagtagagac aggggtttctt catgttggtc aggctgggtct caaactccta 60  
 acctcgtgat ccgcctgcct cgacctccca aagtgtctgg attacaggca tgagccacca 120  
 tgcccagcca aagatcattt ttttatatag acttcagccc tttgtaaata ttgtaactgg 180  
 ggagtataga gtagaaaaaa agtatagtta aaacatttgt tctacaaatt aacctttaaa 240  
 aatataatta ctgctaaaaa tagagtgtct ttacacttaa ggaaaattag tgccattttg 300

<210> 277  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 277  
 ctcacacagc atgtgtcaga tccatggggg aggagtcggc cagagacttg gtaacagaca 60  
 gattgtctga tcccaccctc agactctctg attcagttag tttggggtaa ggcgcaagac 120  
 tgaatttttc acaagtttcc cagtgggtgt gatacttctg gtccaggaaac ttagtgggag 180  
 agaacgacta atctagacca tttcacttca cattctgagc ttcttgatca ctgtcacact 240  
 gcaccccttt aacaatgcat tccctatcct attgcaatac tgacatctca tcaatatttt 300

<210> 278  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 278  
 ctgacaactt gattgggttc tccttcaggt ttgaagcgcc ctcgagaagt gtctaaagga 60  
 gacagttgat agccaaacaa cagttttgga ttcactgact gattatgaaa gaagcagtag 120  
 actggtatca agaatcagtc agcaaggagg ccctcaccag acgccagtgc catgttcttg 180  
 gacttctcag cctccatatt catgaactaa gtttttgga tccttaggct tccacgtgtg 240  
 gaaagcctga gctaacctac tggaggatga gccatcacct ggagcagatt caggccatcc 300

<210> 279  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 279  
 ggtaaaccta tttatataat agaaggatga ttataaacat ttaataaatt atatcaaata 60  
 gatattatat attaaatggg cagataatag aaatctgtcc aagcaaaact ctggataatt 120  
 tttatgttgc cttatTTTTT gttttctgtg aactccaaga aaaatgagat accagtttgg 180  
 aacagatgta atattgctga tttacagtt tagggatact cccaagttc aataattttg 240  
 ccaagataca aatttaaag gaacctttta tgaagcttca tagtgtgtga agaacttacc 300

<210> 280  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 280  
 ataactgctt gcgaagatgt agtttctctt tggaaagcta cacacacgag attatacaca 60  
 tcaggcactg gaactatctg taatactgga acctctgcga agtgccaggt ataaagtttt 120  
 tccactgcc aagcatccag agctttggga aatttgga aa tcagagagat cagggcattg 180  
 ttttgctcct ctgatgatga aagtgaaaag caagtactac tgaagtctgg aaatataaaa 240  
 gctgtgcttg gcctgacaaa gaggaggcta gttagtagca gtgggaccct ttctgatcaa 300

<210> 281  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 281  
 caccatcgaa tttttttatt ttttttgaga gacagactct gtcacccagg ctagtcttaa 60  
 actgttggtg aatcttaagt gattctccca cctcagcctc ccaaagtgtc gggattacag 120  
 gcatgagcca ctacccttgg ctgtgatcaa gtatttagtc tgttggttaa tgtttactaa 180  
 atagtctgaa gtagagaaaa tagcacccaa tctaaaataa ggtgaggtct agtcacttat 240  
 ttaaactctac attttaagct atagtttact attagtttaa actttaagac aggtaattgt 300

<210> 282  
 <211> 300  
 <212> DNA

<213> Homo sapiens

<400> 282

gcaaccttcg cctcctgggt tcaagtgtt	ctcctccctc agcatcccaa gtagctggga	60
ctacaggcac gtgccaccac acccagctaa	tttttgcatt tttagtagag gcagggtttc	120
atcatgttgg ccaggctgggt ctcaaactcc	tgatctcaag taatctgccc actttggcct	180
cccaaagtgc tggcattaca ggaatggagc	caccgcgccc agcctgattt ctttttttag	240
gtcttgtcag gaaagatatt gattcttttg	attcgtgaac atgggtttttg gtcgtcttta	300

<210> 283

<211> 300

<212> DNA

<213> Homo sapiens

<400> 283

cccaggtagc tgagactacc cacaccttgg	tcccagctac ttgggaggct gaggtgggaa	60
aatcactttg cccaggaatt caaggccgca	gtgagctatg attgcaccac tgcactccag	120
gcaacagagt gagaccctgt cttaaaaaaa	gaaggagaaa agtgtcagat ggtgatgagg	180
tctggggggg aaatagagaa tggggatcag	gagtgtggat ggtggtattc cctcaccaag	240
aggtgacatg tgagcaggga gctgggaggt	gagggtgtga cccgtgtgga aatcagggaa	300

<210> 284

<211> 300

<212> DNA

<213> Homo sapiens

<400> 284

ggtgtcctcc ccagtgcgcc gcgatttttg	tgtccaagcc ccagagtccc tctgagacca	60
acccccagcc agcacagact tcctgccttc	ccagctcgga agcgccctcg agaagtgtct	120
aaaggagaca gttgatagcc aaacaacagt	tttggattca ctgactgatt atgaaagaag	180
cagtagactg gtatcaagaa tcagtcaggt	ttttggaatc cttaggcttc cacgtgtgga	240
aagcctgagc taacctactg gaggatgagc	catcacctgg agcagattca ggccatccta	300

<210> 285

<211> 300

<212> DNA

<213> Homo sapiens

<400> 285

aattccgttg ctgtcgggcc gccatgtcat	tctggagaga gacagagtaa aacaaagaag	60
gtgatgggta aagcgcagtc gcctgctata	tattgtctat ttttggtttt tcacttacct	120
tttatattta tgtcttttat gtacaacagg	attataagta gcttgagtcc agtgaatata	180
ccatttcatt ttgctatcct tcactgcact	tagcttagag gaaataatca cagcttatta	240
ttgattaatt aattaattaa tagatgaatg	gtgaacacat gactatcatc ccaagaaatg	300

<210> 286

<211> 300

<212> DNA

<213> Homo sapiens

<400> 286

```

agccaatgag gcttttgcct gccagcagtg gacccaagcc attcagcttt acagcaaggc      60
tgtgcagagg gccctcaca atgccatgct ttatggaaac cgagcagcag cctacatgaa      120
gcgcaagtgg gatggtgacc actatgatgc cctgagggac tgcctcaagg ccatctccct      180
aaacccatgc cacctgaagg cacactttcg cctggccgcg tgcctctttg agctcaagta      240
tgtggctgaa gccctggagt gcctggacga cttcaaaggg aaatttccgg agcaggccca      300

```

&lt;210&gt; 287

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 287

```

gggtgacaga gtgaaactcg tatctccaaa caaacaacaa aaaagtcctt aaacatatgt      60
gaacaaaaat tttgtgatgg aaggattcta gttaatgagt attgcatcaa gatttacatc      120
tttcttacta aggaaaagag ttaataaaaa ttgttcttta ttttacaggc agttactgag      180
gctcttccca gatctcagta aacagccact cagccttgaa aatggagtgt tgttgtttct      240
aaacatatat ttatgtcatt tattaagtac agttcactta aataacataa gtagattttc      300

```

&lt;210&gt; 288

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 288

```

accactaaca gcatctactt gactactgat actttgatca tggagttagg gcatgccact      60
tgatagaaat ttgaagagca attatatattt tcaaaaagag ttttgaataa tgtaagata      120
gattgcaaca tgactatcaa ttcttccctt cccatcaaag gagagagtcc gtttatccag      180
cctttgaatc ttgattattc aagtgaactg cttcacccaa tgtaacatta ataagcacia      240
tacaagcaga ggcttgccaa gaacttggtt tgtttcta at gcttagaaga agaattggtg      300

```

&lt;210&gt; 289

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 289

```

tgtccttata tgaaattcag cgatcttcat gaataagcat ttctctgatt gtggnatatg      60
cctttaattt tatttctaga gtgacaaatt tttggttttg acagtttttt tctagcttta      120
tagtttcttc ttggggagag aatatgtcaa cctcactcca tcatgctgaa gtaaatcttc      180
atctcttaat tttatctctc aaaaatatcc taaggattcc ctctggagcc tgataagtaa      240
ttgcagtatc tggtttctat ggttggatga ttcaggattc caggaataat agttactttt      300

```

&lt;210&gt; 290

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 290

```

ggaaccatga gaaccgaagc tagaattgct attgaattac tttattttct cttcccttat      60
tgggtagaga tacatcatta ctggcctcag gggtttaccc aaagaaaggg tatttttgag      120
caaataatgt gatttcctgg ctattttgtt gggggcttaa gatttttttt tttcaaatgc      180

```

atcttttagtc actaaaaatt aactgtcgtc ccatctagaa ctatactgtc cagtaccata 240  
gcctctagcc gtagttagct atttgtatta agattaatgg aaatttttaa tccagtccct 300

<210> 291  
<211> 300  
<212> DNA  
<213> Homo sapiens

<400> 291  
tatgatttta tttttggcct aatataggaa tgtttaaaaa aggcttttct atgaaaatta 60  
gaaatttata cttgaaatta aaagtctaca agggggagga ccttaaagct aagctaccag 120  
taagacaatg aataattcag aagagaacac tattctttta ctgactgagt gccaagatg 180  
ccaatttcca tgaagtcttg atttatatat atgtacacat gttatgcaca tacatgtttg 240  
ttttctaaca gttattcttt aagcttttga gataatttta gacttacaga agagttggaa 300

<210> 292  
<211> 278  
<212> DNA  
<213> Homo sapiens

<400> 292  
cccagaccta tggagtcaga cagtaggttt gaggccagc aatctatggt ttaacaagcc 60  
atccaggtgt ttctgatgca cagtgaaatt ggggtaccac tggattagg tttggtatgg 120  
caacttttct atcacttggt ttatgtagtt gtctgatcaa ttgtgaaaac ataatgaatg 180  
ttggaaatgg aacagtaaaa taacgaaagc caactttttt tttttttttn nnnnnnnnnn 240  
nntgnttttn cccccaggnt gnanngcagg gncccaat 278

<210> 293  
<211> 297  
<212> DNA  
<213> Homo sapiens

<400> 293  
ggaaggcagt gggaggagag gaccaagtct caaactccag aagccccacc tccctgagct 60  
cagctcctct gccaaagccc ctccagcgga agtcctcgtc cagagaaggc aacggcgaga 120  
aacaatcca acatcctggg ctgcttttct ctccccccac tttttaaaag tttggtgtcc 180  
aagtcacttg acaaaccag accctaacaa tgatattttg tgtagaattc tgggatcaaa 240  
atataatttc aaaaataata tattttctga catcccccaa aaaaaaaaaa aaaaaaa 297

<210> 294  
<211> 300  
<212> DNA  
<213> Homo sapiens

<400> 294  
ggaacagttt gagcaaaggc tctcaagtaa taggggtgtct gacttgttca tttttgaaag 60  
tagaactaat aggatttctt attggaacgt aggggtgtaag agaaaagagg agtcaaaaag 120  
agccacaaga tttttggtct cagcaattag aaggatagaa ttgacattta ctgagatttt 180  
tgtttttgtt tttgagacgg agtttcgcta ttgttgccca agctggcgtg caatggcgtg 240  
atctcggctc agtgcaacct ccacctccca gattcaagcg attctcctgc ctccagcctcc 300

&lt;210&gt; 295

&lt;211&gt; 299

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 295

gtaatatgga tgtgattggt gtcgcttgag aaaaaaaggc aacagctgat tctttcaaca	60
actgtcacag aatggctggg ctgagaacgc tgcccagggc cctgcagctg gcgggagnnn	120
nnnnnnnnnn nnnnnngtgcn tgctgcaaca tntgggtana tngtatcctt ccctanagnt	180
gctacnnctt nnatcccctt gtnaatatgt tgagntnnct tngcnttcnn gntnntccng	240
ntnnttgaca cntatgnaan ttntntngtc tngctctgct ngatnncttn nangctgcc	299

&lt;210&gt; 296

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 296

gcagaacctt ttcccctcta ctcttgtcta aaagttctgt gtggcacaca gagatgcgac	60
ctactcaatc tgacttagta aaaccatgct gaaaaathtt ggtctaaaaa ggaccatac	120
ccagcaccca tgaaataaaa gattcatctg taattgggat tcaaagggat taaattcctt	180
tggtcatact cataaatagc actaaagtgt tataacattt tcatttacct atttttagtt	240
ccttcatttt aacttaataa aaatcttgga ttgatattct tttttttttt ttttgggacg	300

&lt;210&gt; 297

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 297

gctaggatta caggtgtgag ccaccatgcc cagccactta tctttaaagg attaagttta	60
tgtttcctac tatgggaaac catcccaccc caaacttgat gaccgcatta tgtgctttta	120
tagaacatgg cacttctcca ggatagcatt tattctgttt tgtaagtgtg aatgtaatta	180
ccctacacac agcatacaca taatcttcat attctttgcc ttgtcttggt aaggcaagg	240
ccatgtctat cttattcgct attagattcc cacatccaac atagtcctgg ggacagcacc	300

&lt;210&gt; 298

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 298

ccaaatctgc ctagagattg agttcacagt gtatgttctg ggggcgctgg tgcagtcagc	60
ggtccagtct ccagcctgca ggcgtgcaca ctggggtgga cgatgggtgg ccccgagggt	120
gtacacattt ggggtggccc ggcccctata cccagtggtt ctctttgate cagtcccgaa	180
acagagggag ccttgtgtac acgcctccaa agtggagctg ggaggtagaa ggggaggaca	240
ctggtggttc tactgaccca actgggggca aaggtttgaa gacacagcct ccccgccag	300

&lt;210&gt; 299

&lt;211&gt; 300

&lt;212&gt; DNA



<213> Homo sapiens

<400> 299

ctccattgtg aagatccagg cattttttccg agccaggaaa gccaagatg actacaggat	60
attagtgcac gcaccccaacc ctccctctcag tgtggtacgc agatttgccc atctcttgaa	120
tcaaagccag caagacttct ctgctgctgt gatctgcaca ccctccaacc tgggcaggga	180
ctgggggggat gcagtgtgtg ttagtgccca tgtggcattg tggcactgtt gcccccatg	240
gcggcatggg caagatgacc ttccattagc ttcaagtctt gttctcttgt ctgtggtctg	300

<210> 300

<211> 300

<212> DNA

<213> Homo sapiens

<400> 300

agcaattcca ctccatgctc caccacagc aattgaaagc aaagacgcaa acagatgcct	60
gtgcacaaaa gttcacggca gcacccttcg ccatagtggc agcatccgct gtcacagcgg	120
catcatcctt catcatagcg gcagcatccg tcgtcacagc ggcagcatcc ttccgccacag	180
cggcagcatc tgtcgtcaca gcggcagcat ccttcgccaa agcggcagca tccttcgtca	240
tagcggcagc atcctttgcc atagcggcaa ggtggaaacc ctgtccatcc actgaggcgt	300

<210> 301

<211> 300

<212> DNA

<213> Homo sapiens

<400> 301

tcacagatat gaaagtccag tcagaggggc tgggcccagc tctgtgcttt tcctgcagg	60
atcttttagga tcagtgcagc ggtgtgtatt tgggaagcatt tcaaattgtg taccatcgtg	120
ttacttccgt gggcacctgg tgttattggg tggactagtc aggattctcc agagcagcag	180
aagcaatggg atgtgtgtgc atgtgtttgt gcagagacag aaagagagat ttttaaggaa	240
tggcttatgc agttgtgggg gctagcaagt ctgaaatttg cagggcgggc cagcaagctg	300

<210> 302

<211> 300

<212> DNA

<213> Homo sapiens

<400> 302

tcaccaggaa tacagtgcac ttaaaagtgt gatatgggtt agctgtgccc ccacccacat	60
ttcaacttga actgtatcta tctcccagaa ttcccacatg ttgtgggagg gacccagggg	120
gaggtaactg aatcatgggg gctgggtctt cccgtgctat tctcgtgatg gtgaagtctc	180
acgagatctg atgggtttat caggggtttc cacttttgtt tcttcatttt ctcttgccac	240
cagcatgtaa gaagtgcctt tggctctcta ccatgattct gaggcctccc tagccatggg	300

<210> 303

<211> 300

<212> DNA

<213> Homo sapiens

<400> 303

gcccctctcca	ttttctgagg	aggtgatatt	tgggcagatt	acaaactgag	gaagcatact	60
ggatagacat	caggatgaag	agaataggca	gttgaaaagt	cccagaaagg	ggagtgtgct	120
tagagtgttt	gaggaacagc	aaggaagcaa	gcccttggtg	aaacagattg	agcaaggtag	180
aaagtggtaa	aagatgaagt	taaagaggta	gctgagagcc	agatcatgta	aagccttggt	240
aaggactgac	ttttatttta	agagggttag	gaagacattg	gtaggttttg	actctggctt	300

&lt;210&gt; 304

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 304

aacaggaata	tggaaagaaa	ctcagagccg	agttagtgga	aaagtggaaa	gcagagagag	60
aggctcggct	ggcaagagga	gaaaaggaag	aggaggagga	agaggaggaa	gagatcaaca	120
tctatgcagt	caccgaggag	gagtcggacg	aggaaggcag	ccaggagaaa	ggaggggacg	180
acagccagca	gaagttcatt	gctcacgtcc	ctgttccttc	gcagcaagag	attgaggagg	240
cactggtgcg	aaggaagaaa	atggaactcc	tccagaagta	tgcaagcgag	accctgcagg	300

&lt;210&gt; 305

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 305

aatagtagaa	agggtcccca	ttcctgctca	gcaccgcacc	tctctacccc	cccacagaca	60
cacatgcaga	cacacacatg	cagacaacac	gcagacacac	acatgcaggc	actcacatgc	120
aggcccatgc	acacacacgt	gcacacacat	gcagagacat	gcagacacgc	aggcacacat	180
gcacacatgc	aaagacacgc	atgcaggcac	acgcagacgc	acacagagac	acacatgcag	240
atacacatgc	acacacacat	acacacactg	gccctgtttt	ttctgtggtg	tcactgggtg	300

&lt;210&gt; 306

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 306

cagcaaagac	tttatTTTTg	tacagaagat	ggtgaagtcc	aagacggtgg	ctcagtgcgt	60
ggagtactac	tacacgtgga	aaaagatcat	gcggtggtgg	cggaaacacc	ggacacgcct	120
ggcagaaaatc	atcgacgatt	gtgtgacaag	tgaagaagaa	gaagagttag	aggaggagga	180
ggaggaggac	ccggaagaag	ataggaaaatc	cacaaaagaa	gaagggagtg	aggtgccgaa	240
gtccccggag	ccaccacccg	tccccgtcct	ggctcccacg	gaggggccgc	ccctgcaggc	300

&lt;210&gt; 307

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 307

gctgcttctg	gctggggggg	ccttggcctt	catcctgctg	agggtgagga	ggaggaggaa	60
gagccctgga	ggagcaggag	gaggagccag	tggcgacggg	ggattctacg	atccgaaagc	120
tcagggtgtg	ggaaatgggg	accccgctct	ctggacacca	gtagtccttg	gtccccatgga	180

accagatggc aaggatgagg aggaggagga ggaggannnn nnnnnnnnna ntggccttnt 240  
gtggcctcca ccagcagctn tnnannatga catggagtcc caactgnacg nctccctcat 300

<210> 308  
<211> 300  
<212> DNA  
<213> Homo sapiens

<400> 308  
agttaagagt gtgaacccta gatttgccat ctgaaagtca tgtgtccttc agtgatgcat 60  
ttaacctctc tgtgcctcaa atttctccct ctgggggatg ttaggagtat acaaattaac 120  
acatgtaaag tgcttagaat agattggtac tgtaaataat gagctaacgt cacatttgat 180  
atttttttaa aaagaaaaaa tcattatgga gtctcagtcc tagagattct gattcattaa 240  
ttctgcttct cggcaaggag cgatttgctg gtgtagacat tccgggtccg tgtaaagggt 300

<210> 309  
<211> 300  
<212> DNA  
<213> Homo sapiens

<400> 309  
ccaacaccca gttctcactc tgtcatccag gctggtgtgc agtggtgcaa tgtgggctta 60  
ctgcagcctt gacctccagg acaagtgatc tcccacctca gcctccggaa tagctgggac 120  
tacagctcaa caacgcccct ctgaaagtag gactcttgga aatgaacctt gttgggagta 180  
aagctgaacc ttcacctctc ctttcagga ttctactcca ttcatacggc ctcacactga 240  
attaatggtt cttagcagcca catcactttg ttaccecaatt gatctagtag taaagtcttc 300

<210> 310  
<211> 300  
<212> DNA  
<213> Homo sapiens

<400> 310  
aggaaacacc cccttataaa accatcatat caggctgggt gatctgacag agctagacac 60  
tgtcaaacaa acaaacaac aaacaaaaaa accccatcac atctcatgag acttatttac 120  
tatcatgaga gcagctcagg aaacaccac tcccgatgatt cagttacatc ccaactgggtc 180  
tgtcccacaa attgtgggag ctacaattca agatgagggt tgggtgggga cacagccaaa 240  
ccctatcacc atgtaaaata atatctaatt tgtagagatt aaagaacaag ataacttaa 300

<210> 311  
<211> 300  
<212> DNA  
<213> Homo sapiens

<400> 311  
ttntgcagat ctccagcaca agcctctgct agttgatctc acggtagaag aagggtcaaag 60  
attaaagggt atgtttggtt cacacactgg tttccatgta attgatgttg attcaggaaa 120  
ctcttatgat atctacatac catctcatat tcaggggcaat atcactctc atgctattgt 180  
catcttgctt aaaacagatg gaatggaaat gcntgtttgc tatgaggatg angggggtgna 240  
tgtaaacacc tatggccgga taacnaagga tgtggtgctc caatggggag aaatggccac 300

<210> 312  
 <211> 275  
 <212> DNA  
 <213> Homo sapiens

<400> 312  
 cctccctgga tgtgcagaca tggaggagga cagaaggccc agctcagtgg cccccgctcc 60  
 ccacccccca cgcccgaaaca gcaggggagc aggcagnnnn nnnnnntaag ngtgttnaan 120  
 tntnnatttn ttcctntttt ttttnnnntn aaatatnntg nnnntttttt ntantantta 180  
 ttatnntntn nttattannn tntttttcnt ntnttacttt gtntttgatt ttanncnttt 240  
 natntttttt ttgtttcttct nttntattnn atctt 275

<210> 313  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 313  
 tcctgtcttc ttgcccaaatt gttgcatttt ccaagaccac tctggcctgc catgccaccc 60  
 attctgtgcc tataaaaacc ctgagacccc agcgggcaca cacacaagcg gctggacgtc 120  
 aagaggaaca cactggcaga agaacacatc gaaagacgct ggcaggccat tgatggtgga 180  
 acgattcgga cgccaaggga aattcgcca aggacagtag gagatcccgg ctgctgagca 240  
 gccagactcc agaggaagac taccttccca tgctatcccc cttctggctc cccagccatc 300

<210> 314  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 314  
 ataagggtgg ggccttaatt cagtagaatt ggtggcctcc taagcagagg aagagagatt 60  
 tttctttctc tctctgccat gtgaagacag tgaggagtgc gccgtctgca agccaagaag 120  
 agcccttatt aggaacagac ttggctagca ccttcacgtg ggacctccag cctccagaat 180  
 tgcaagaaaa tacatttccg tcgttgaaac caccagctct gtggtatttt gttatggcag 240  
 cccaggcaga ctaatacgtg aagcctgctc taaatagata aaataagaaa ttactacaga 300

<210> 315  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 315  
 gtctcagtgt ggcctgtggg gctggtgggc ggcctgcgat tcgagggccc tcaggtacag 60  
 gacggccggg tagtgggctt ccacacagca tgggagcca gcaggccctt ccctgtggat 120  
 atggctggat ttgccgtggc cctgcccttg ctgtagata agcccaatgc ccaatttgat 180  
 tccaccgctc cccggggcca cctggagagc agtcttctga gccaccttgt ggatcccaag 240  
 gacctggagc cacgggctgc caactgcact cgggtactgg tgtggcatac tcggacagag 300

<210> 316  
 <211> 300  
 <212> DNA

<213> Homo sapiens

<400> 316

gaaatgcctc	tatgtaggtg	aagtgttctc	tctgcatgca	acaggaaaaa	ttaatatataat	60
atthttcccca	caaaagaaac	acttaacaga	ggcaagtgc	atthtataaat	ttatatctaa	120
aggggaatca	tgattataag	tccttcagcc	cttggaactct	aaattgaggg	gattaaaaag	180
aattttaaaat	aattttgaac	gaattttattt	tccctcagc	ttttgagggc	attaaaaagg	240
cattaaatca	agacaaatca	tgtgcttgag	aaaaataaaa	ttaatgaaaa	cacagcactt	300

<210> 317

<211> 295

<212> DNA

<213> Homo sapiens

<400> 317

acactgtccc	actccatcac	ccaggctgga	gtccagtggt	gtgatcatag	ctcgtgcat	60
cctccagttc	ctgggttcaa	gccatccctc	ctgcctcagc	ctccccagta	gctggaacta	120
cagggtgtgtg	ccatcacacc	tggttttaca	tttttctgtg	gggacttact	atgttgccca	180
ggccggcctc	aaactcctga	gctcaagtga	tcctctgcct	cagcctccag	agtatctggg	240
attacatatg	tcggctaccg	tgtctggccg	ttcacatctt	tggccactat	ttgct	295

<210> 318

<211> 261

<212> DNA

<213> Homo sapiens

<400> 318

cctgaatata	aagaggagga	ggaagaccaa	gacatacagg	gagaaatcag	tcatcctgat	60
ggaaaggttg	aaaaggttta	taagaatggg	tgccgtgtta	tactgtttcc	caatggaact	120
cgaaggaag	tgagtgcaga	tgggaagacc	atcactgtca	ctttctttta	tggtgacgtg	180
aagcaggtca	tgccgaccca	agaannnnnn	nnnnnnnnnn	nnntngccnn	aacnnttcac	240
caaatncccc	gggggggctt	g				261

<210> 319

<211> 300

<212> DNA

<213> Homo sapiens

<400> 319

gggacctctg	cccaagaaag	cctgggtatt	gaccaaggtt	tccccccac	tgagacagcc	60
tgagatatgg	cctcatggga	agggaaagac	ctgactgtcc	cccagcccga	cacctgtaaa	120
gggtcgggtc	tgaggaggaa	tagtgaagga	gggaggcctc	tttgagttg	agataagagg	180
aaggcttctg	tctcctgctt	gtccctggta	atggaatgtc	tcggtgtaaa	gctgaccatt	240
cccattcgtt	ctattctgag	ataggagaaa	accgccctgt	ggctggaggt	gagatatgct	300

<210> 320

<211> 289

<212> DNA

<213> Homo sapiens

<400> 320

caccttgccct	ggccaagggg	ctagacctcc	caggctaagc	ctcagattca	gtgcaggaca	60
caagctcatg	ccccgtctt	gccagtgaca	cttgaagcct	cccgacttcc	acagagtgtc	120
tcaggacaca	ttttgagtgg	tattttcttt	tcttttttct	ttcttttttt	ttttnnnnnn	180
nnnnntngt	tntgtnnccc	aggetgnann	gcaggggcct	gatntnggnt	aantgnaacc	240
ttngcctcen	agggttaaagc	nattttttng	octaancctc	naaagtacc		289

&lt;210&gt; 321

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 321

gaaagaccga	gatagagaga	gagacagaga	cagagagcga	gaccgtgatc	gggacagaga	60
aagagaacgc	accagagaga	gagagaggga	gcgtgatcac	agtcctacac	caagtgtttt	120
caacagcgat	gaagaacgat	acagatacag	ggaatatgca	gaaagagggt	atgagcgtca	180
cagagcaagt	cgagaaaaag	aagaacgaca	tagagaaaga	cgacacaggg	agaaagagga	240
aaccagacat	aagtcttctc	gaagtaatat	tagacgtcgc	catgaaagtg	aagaaggaga	300

&lt;210&gt; 322

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 322

cgccctttaa	ctgcagttct	gctctatttt	cttttctctc	tctggagctg	agagtcagag	60
ggcccttctc	ctcctccttt	cagcccccaa	cactaagctg	atggattgat	aaatacctca	120
gcccctcgcc	ttcctcaacc	cacctggcaa	gtcttcttag	gatctgatcc	cagttttctg	180
gaagcaatcc	tacccagcc	caagcttccc	aagagtcgag	ccttaatcct	tctcacttct	240
cagtgtcaga	gcagaaatga	atcctggggg	tgactgtgtc	cattcggggt	attagcagct	300

&lt;210&gt; 323

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 323

agattatgag	catgtagaag	atgaaacttt	tcctcctttc	ccacctccag	cctctccaga	60
gagacaagat	ggtgaaggaa	ctgagcctga	tgaagagtca	ggaaatggag	cacctgttcc	120
tgtacctcca	aagagaacag	ttaaaagaaa	tatacccaag	ctggatgctc	agagattaat	180
ttcagagaga	ggacttccag	ccttaaggca	tgtatttgat	aaggcaaaat	tcaaaggtaa	240
agggtcatgag	gctgaagact	tgaagatgct	aatcagacac	atggagcact	gggcacatag	300

&lt;210&gt; 324

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 324

gtctgagaag	tcaaggatcg	gggtgctggc	ctattcagtt	cctggtaagg	gctgtcttcc	60
tggcttgcat	ttgaactact	tcttgctgtg	tcttcacaag	catgccccca	tcctgtgccc	120
ataagaactc	cagacccccaa	actcagctca	tacacacacg	gaagagagaa	gcactctgaac	180

atcaagaaga gaagaagctg ctggacatca gaaactgtga aaggagagga gtttggtga 240  
gctccagggg aagactgcct gcacattcta tcccccttc agttcccat cctgctgtca 300

<210> 325

<211> 283

<212> DNA

<213> Homo sapiens

<400> 325

gtccgaagaa aaagactgtg gtggcggaga tgctctctcc aatggcatca agaaacacag 60  
aacaagtttg ccttctccta tgttttccag aaatgacttc agtatctgga gcacccctcag 120  
aaaatgtatt ggaatggaac tatccaagat cacgatgcca gttatattta atgagcctct 180  
gagcttctta cagcgcttaa ctgaatacat ggagcatact tacctcgtcc acaaggccag 240  
ttcactctct gatcctgtgg aaaggatgcn nggtgtgtagc tgc 283

<210> 326

<211> 300

<212> DNA

<213> Homo sapiens

<400> 326

atgacatcct cattatccac actgcaaagc caaccatccc tatgatgggt tcattgtgga 60  
tcatgactta gtgggtcaag agtttggaag tggctcagct gggcggttct tctgctccat 120  
gtggctgcca gatggtaccc tgctggtggg cagtctggtc tagagggtcc atgatggctt 180  
tactcacatg cctggcatct tgacaggagc agctggaagg caagggtcag ctgggactgt 240  
ccacagagct cctccctgtg gcctttccag catggtgggtc tcagggtagc tggacttcct 300

<210> 327

<211> 300

<212> DNA

<213> Homo sapiens

<400> 327

ggtagactgg ctagggatcc tggacccagg gttccacgta gcaacacctg ctgagttctc 60  
tgggttttct tcctgcctca tgtagcccag acttggagct gaagaagctg gaaacatgga 120  
aacaccaaca gctacagacc aaaaaaagtc ccaacaaagg cctgtcagtc tgccagcctg 180  
ttctgtggat ttccaactca agattgcagc atcaactcac acctgaagtt ctggcttccc 240  
tacaaacttt gaacttgcca gtccccacaa tggcataagc caattcctta aatgaatgt 300

<210> 328

<211> 300

<212> DNA

<213> Homo sapiens

<400> 328

gtcacaggca ggtttaatgg ccagtttaaa acttatgcta tctgcggggc cattcgtagg 60  
atggtgagtg ttccctggg ctttgctcat cacttcggga catcgtggac ttaccgtgc 120  
gcattggagt gtgtgatgg gcctgagtag atctgctggc agagtatgtt gagccagctg 180  
gactgggctg gccgcctgcc gcttcttgag ggtggaagag ggggtgctctg agaagacact 240  
caggcagcag actctgcctc tcacttaagg tgccccccg accccgctcc accatagtca 300

<210> 329  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 329  
 ttttggctcgt cttaaatttg tctcatcagt gcctccatgt gtttttgatg cctttgaact 60  
 ggtattttta aaatttcaat ttctaattgt tcattataga aacacaattg ggttttatat 120  
 attggcattg tattttgcaa ctttcctaaa ctcactagta attctagtag ctttttttgg 180  
 tagattotta aggattttct gtgtaaatag tcatgtcatt tgtgaataaa gccatttttt 240  
 tttccttttc aaattttgtg ctttttattt cttattotta ccatatcaca ttggcaaaga 300

<210> 330  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 330  
 tcaaggatcg ggggtgctggc ctattcagtt cctggtaagg gctgtcttcc tggtttgcag 60  
 ttgaactact tcttgctgtg tcttcacaag catgccccca tcctgtgccg ataagaactc 120  
 cagaccccaa actcagctca tacacacacg gaagagagaa gcactctgaac atcaagaaga 180  
 gaagaagctg ctggacatca gaaactgtga aaggagagga gtttggtgta gctccagggg 240  
 aagactgcct gcacattcta tccccctttc agttcccat cctgctgtca gccacattta 300

<210> 331  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 accgccctgt ggctggaggt gagatatgct ggcagcaata ctgctctgtt actccttgc 60  
 acactgagat gtttgggtaa agagaaacat aaatctagcc tacgtgcaca tctgggcaca 120  
 gtacctttcc ttgaacttat tcgtgataca gattcctttg ctcacatgtt tccctgctga 180  
 ccttcttccc acctgttgcc ctgctacact cccctcgcta agacagtaaa aataatgatc 240  
 aataaatact gagggaaactc agaggccagc gccggtgcgg gtccccccca tgctgagcgc 300

<210> 332  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 332  
 ggaaaaacaa caggtttgag tcctataaag ccataattta actccagtag ctgatgtcag 60  
 acaagcttgt cctatgtcct atttgagtgg cagcagcgcc agcccagcaa gaaggctggg 120  
 ggttgcaag gttgtcccca gaccttgctt gcagtgggtg gagaaccag ggggctgcct 180  
 tgggccctct ggccagaggg aagcgggcag ctctagccct ggagattgtg gtcacattgg 240  
 ggcttgttta ggattggagg gccaggtcac ctccccagcc accctccctt ctctcctctg 300

<210> 333  
 <211> 300  
 <212> DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 333

cctcctactc ccaaacaat ctttggggaa aaaaaaacta ccaactgtca gccatggggc	60
tgacggcgct aagctctggg gctccgtgca ctgacgtggg gccagccaca gggaggcggg	120
gatcaagtag cggaggccag gattttggcc acctccggg caagttgcag ggcagtggcg	180
ccgggagcaa aagcagcatg atgcagctca tgcacctgga gtccttttat gaaaaaacct	240
cctcctgggc ttatcaagga agatgacact aagccagaag actgcatacc agatgtacca	300

&lt;210&gt; 334

&lt;211&gt; 262

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 334

gccatgcccc tttgtttact cattgtctat ggttgctttc atgccctcac agcaaaggcg	60
agtagttgtg atggatcaaa tggcccacaa agcctgaaat atttactctt tgacccttta	120
cagaaaaaaaa ccttgttgac ccctgcttta gagaatgaga agccatgcag ggatcagtga	180
tgccagagga agggaaggaa ctgcttccag ctattgtgac aataataata ataataatat	240
tgggtctttg actagaacgt gt	262

&lt;210&gt; 335

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 335

tctntctcn ntatnttgn gtagtncctc ntttccttgt ncnntnntcn nctnttgnet	60
tttgcgagacc ctcgattcta tctcatatga gtgagaacgc ttaccagtgc agcgaatgtg	120
ggaaagcctt ccgagggcac tggactttt ctaggcatca gagtccaccac agcagtgaga	180
ggccttatat gtgtaatgaa tgtggaaaag ccttcagcca gaactcgagc cttaaaaagc	240
accaaagtc tcacatgagt gagaagccct atgaatgcaa tgaatgtggg aaggctttta	300

&lt;210&gt; 336

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 336

gaggaccac tccccagga ctcccttgaa ggcgtggacg aggacgagtg ggactagcct	60
gcgccccgt cactccacc tcacctgtgc tgccacttcc tagtgacacac ctcacggctc	120
atcctcaagc tggaagatac ctctctggcc cgggcacatg tcaccctgc actcctgcct	180
tcccggtggc acttccacat cctctgggccc tctggcagtt cccagggact gttttcacct	240
ctgctgtctc tggggtcagc tgctgtcat cagctgcccg ctagcatgtg gccaggggtg	300

&lt;210&gt; 337

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 337

agacaaccca	gaaacaaatt	catacatcta	tggtgaccac	ttttgacaaa	ggaatgaaga	60
acatacactg	gggaaaagat	aatgtcttta	ataaatggtg	ctgggaaaaac	tgatatcca	120
tatgcagaag	aatgaaacta	gacccccatc	tcttagcata	tacaaaaatc	aaaattaatt	180
aaaaagttaa	atctaagacc	tcaaactatg	aaacagctaa	aagaaaacat	cggggaatct	240
ctccaggaca	ttggagtggg	caaagatttc	ttgtgtaata	cctgacaaac	aggcaaccaa	300

&lt;210&gt; 338

&lt;211&gt; 292

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 338

tcaataacca	tgaagatgca	tcctaccacc	gtcagggcaa	tcattagata	gctgatcttc	60
actcgcactc	tcatggttat	tgagggaag	aaggctgccc	aaagacacga	gactttaaca	120
agcttgaaat	tagaaaagaa	agctcgtctg	aaagaggaag	cagctatgaa	ggccaaaaca	180
gagtagcaga	ggatccgtg	ttggctggat	tttgaaaatc	caggaattat	gttataacgt	240
gcttgattta	aaaaggatgt	ggtacgagga	tccatttcac	aaagtatgat	tt	292

&lt;210&gt; 339

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 339

gaaatttgca	ctgatggctc	agaaggctta	cgatcatggag	agtatgacct	acctcagagc	60
agggggggct	ggaccaacct	ggctttcccg	actgctccat	cgaggcagcc	atggatgaag	120
tggtcagctc	cgaggccgcc	tggcagtgtg	tgagtgaggg	gctgcagatc	ctcgggggct	180
tggtgctcac	aaggggactat	ccgtacgagc	gcatactgcg	tgacacccgc	atcctcctca	240
tcttcgaggg	aaccaatgag	attctccgga	tgtacatcgc	cctgacgggt	ctgcagcatg	300

&lt;210&gt; 340

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 340

ctcagngcan	cgatcatggc	tcagtgcagc	ctcaaactct	tggtctcaan	canagcgggn	60
acctcaacct	cctgagtagc	taggactata	ggcacacagc	accatgcccc	ggctattttt	120
ttatttttga	gagatggggg	ctcactatgt	tgcccaggct	agtcttgaa	tcctggcctc	180
aagcaatcct	cccacctcgg	cctcccaaag	tgctgggatt	aaaggcgtga	gccaccgtac	240
ctggcccttg	gtggaatctt	taggggtttt	tattcataca	tataaaatca	tatcattggc	300

&lt;210&gt; 341

&lt;211&gt; 296

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 341

atccagggtg	ttctgatgca	cagtgaat	ggggtaccac	tggtattagg	ttgggtatgg	60
caactttttc	atcacttggt	ttatgtagtt	gtctgatcaa	ttgtgaaaac	ataatgaatg	120
ttggaaatgg	aacagtaaaa	taacgaaagc	caactttttt	tttttttttt	ttnnnnnnnn	180

nnnnnnnnnt tnnccccng ncnngnanngc aggggcccac nntnggntnn ntgnanccnc 240  
 cncncceggg ntnnnccct ttntcnngcc taaccnccc nagnacnngg aactac 296

<210> 342  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 342  
 ggcacgatca tggctcattg cagcctctaa ctccggggct caagcaatcc tcccacctca 60  
 gcctaccaag tagctgtgac cacagctgcc cctcaccatg ctaagctaata ttttttaatt 120  
 agatagtaca taaacgtccc aaaattagaa gataaaaaga catgagggat ccatttctaata 180  
 ttgtgttttg agtgtaattg tccagctcca ttcttctgca catggatatc cagttttaca 240  
 caacactgtg aatgtaattg atgccactga atcatacact caaaaatagc taaaatggca 300

<210> 343  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 343  
 gttttcatca ctacatattc tacacacact gggaagctct gacaacttat tccctgctat 60  
 tatcaactaa agatcaccct ttctactgct gtctctggag caggagctgg caaactatgg 120  
 cctgtctgtc gttttgtac agttttactg aaacacagcc atgcccattt gtttactcat 180  
 tgtctatggt tgctttcatg ccctcacagc aaaggcgagt agttgtgatg gatcaaatgg 240  
 cccacaaagc ctgaaatatt tactctttga ccctttacag aaaaaaacct tgttgacccc 300

<210> 344  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 344  
 ccccaacctg cactctaccc acccccatca cctactccag ctcccaactt ttgtggactg 60  
 agcgcccgca gagactgggt cgccttggat tccctctgcc tccgaggacc ccaaaagaca 120  
 ccccaacccc caggccagcc ggccctgtct tggcgcgctc aaaatactac ctagcacagg 180  
 cctctgtctg aggcaccccc aaactaccta tgtatccagc cccagagggc ctccattccc 240  
 aggaagtccc tatgtatccc aacactggca gacaccagc accaccctcc cagaccgcga 300

<210> 345  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 345  
 ccccatcac ctactccagc tcccaacttt tgtggactga gcggccgcag agactgggtc 60  
 gccttggatt cctctgctt ccgaggaccc caaaagacac ccccaacccc aggcagccg 120  
 gcctgtctct ggcgctcca aaatactacc tagcacaggc ctctgtctga ggcaccccca 180  
 aactacctat gtatccagcc ccagagggcc tccattccca ggaagtccct atgtatccca 240  
 acactggcag acaccagca ccaccctccc agaccgcga gaaagtgaat ctactacta 300

<210> 346  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 346  
 gtccacggtg ctgaacatca tcattcttga agactgtagg aaccagtggg ctatgtcccg 60  
 accactactt ggcttgatat tgcttaatga aaagtatttt tctgacctaa gaaacagtat 120  
 tgtgaacagc cagccaccgg agaagcagca ggccatgcac ctgtgttttg agaacctgat 180  
 ggaaggcatc gagcgaaatc ttcttacgaa aaacagagac aggttcaccc agaacctgtc 240  
 agcattccgt cgagaagtca acgactcaat gaagaattcc acttatggcg tgaatagcaa 300

<210> 347  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 347  
 gctctgagcc caggcgaggc cagggacatg gccatggacc tgtgtcggca ggaccccgag 60  
 tgtgagttct acttcagcct ggacgccgac gctgtcctca ccaacctgca gacctgcgt 120  
 atcctcattg aggagaacag gaaggtgatc agaccccatg ctgtcccgcc acggcaagct 180  
 gtgggtccaac ttctggggcg ccctgagccc cgatgagtac tacgcccgt ccgaggacta 240  
 cgtggagctg gtgcagcgga agcgagtggg tgtgtggaat gtaccataca tctcccaggc 300

<210> 348  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 348  
 gttctgtggc tggcatggc tgccctgtac tggagagatc tcctgagaat tcaggtttgg 60  
 attggtgctg tcattcttct gggaatgctt gagaaagctg tcttctatgc ggaatttcag 120  
 aatatccgat acaaaggaga atctgtccag ggtgctttga tccttgacaga gctgctttca 180  
 gcagtgaaac gctcactggc tcgaacctg gtcatcatag tcagtctggg atatggcatc 240  
 gtcaagccac gccttggagt cactcttcat aaggtttag tagcaggagc cctctatctt 300

<210> 349  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 349  
 gtcagctttt gatgaagcta tgatcatactg tcgatatcat ccttccaaag ggnattgggtg 60  
 gcacttcaaa gatcatgaag agcaagataa agtcagacct aaagccaaaa ggaaagaaga 120  
 accaagctct atttttcaga gacaacgtgt ggatgcttta ctttttagacc tcagacaaaa 180  
 atttccaccc aaatttgtgc agctaaagcc tggagaaaag cctgttccag tggatcaaac 240  
 aaagaaagag gcagaacctt taccagaaac tgtaaaacct gaggagaagg agaccacaaa 300

<210> 350  
 <211> 270  
 <212> DNA

<210> 346  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 346  
 gtccacgggtg ctgaacatca tcattcttga agactgtagg aaccagtggg ctatgtcccg 60  
 accactactt ggcttgatat tgcttaatga aaagtatttt tctgacctaa gaaacagtat 120  
 tgtgaacagc cagccaccgg agaagcagca ggccatgcac ctgtgttttg agaacctgat 180  
 ggaaggcatc gagcgaaatc ttcttacgaa aaacagagac aggttcaccc agaacctgtc 240  
 agcattccgt cgagaagtca acgactcaat gaagaattcc acttatggcg tgaatagcaa 300

<210> 347  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 347  
 gctctgagcc caggcgaggc cagggacatg gccatggacc tgtgtcggca ggaccccgag 60  
 tgtgagttct acttcagcct ggacgcccac gctgtcctca ccaacctgca gacctgcgt 120  
 atcctcattg aggagaacag gaaggatgac agaccccatg ctgtcccgcc acggcaagct 180  
 gtgggtccaa ttctggggcg ccctgagccc cgatgagtac tacgcccgt ccgaggacta 240  
 cgtggagctg gtgcagcgga agcgagtggg tgtgtggaat gtaccataca tctcccaggc 300

<210> 348  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 348  
 gttctgtggc tggcatggc tgccctgtac tggagagatc tcctgagaat tcaggtttgg 60  
 attggtgctg tcattcttct gggaatgctt gagaaagctg tcttctatgc ggaatttcag 120  
 aatatccgat acaaaggaga atctgtccag ggtgctttga tccttgaga gctgctttca 180  
 gcagtgaac gctcactggc tcgaacctg gtcacatag tcagtctggg atatggcatc 240  
 gtcaagccac gccttggagt cactcttcat aaggtttag tagcaggagc cctctatctt 300

<210> 349  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 349  
 gtcagctttt gatgaagcta tgtcactatg tcgatatcat ccttccaaag ggnattgggtg 60  
 gcacttcaaa gatcatgaag agcaagataa agtcagacct aaagccaaaa ggaaagaaga 120  
 accaagctct atttttcaga gacaacgtgt ggatgcttta ctttttagacc tcagacaaaa 180  
 atttccaccc aaatttgtgc agctaaagcc tggagaaaag cctgttccag tggatcaaac 240  
 aaagaaagag gcagaacctt taccagaaac tgtaaaacct gaggagaagg agaccacaaa 300

<210> 350  
 <211> 270  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 350

ccatgctgnt aacgggtttc aaggggactc ttgaggaant gccccctaaa atagaacaca	60
gcaatanggn gggttctctg tccccaggnc cccccacag tgctntntgg cactggnaac	120
tctgctangg agngantgna nnnnaccant aannnnnnan nnatcnacan nnnnnnnncn	180
nnnnnnctn tnncnannn ntannctncc ntannnnanc cnnccannan cactcncnat	240
naacgnnnnn ttantgagan nttctcaact	270

&lt;210&gt; 351

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 351

aatgactcc ctgcaaaacc caacccatgc tgctggctgt gggatttttg gtgtaagcct	60
atctatgcac tctatcagcc agaatttggc atttagctct tagttaaatc tagtaaagga	120
cagtctattg tttaaagaga aggtgcattt gttcctcaat caagcaagag cacctgtgtt	180
gtactgcttt atatctcatg tatatttata gtaatgaaa gactttttaa attgtacacg	240
tttcagtgcc tttcttgtgt tatgaaaggc aggtagatat tatagccata ggtaaaaatc	300

&lt;210&gt; 352

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 352

aagaaatgcc tctatgtagg tgaagtgttc tctctgcatg caacagtaaa aattaatata	60
atattttccc cacaaaagaa acacttaaca gaggcaagtg caatttataa atttatatct	120
aaaggggaat catgattata agtccttcag cccttggaact ctaaattgag gggattaaaa	180
agaatttaaa ataattttga acgaatttat tttccctca gtttttgagg gcattaaaaa	240
ggcattaaat caagacaaat catgtgcttg agaaaaataa aattaatgaa aacacagcac	300

&lt;210&gt; 353

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 353

cccacactcg gacactgtgg aattctacca ggcctgtcg accgagacac tcttcttcat	60
cttctactat ctggagggca ctaaggcaca gtatctggca gccaaaggccc taaagaagca	120
gtcatggcga ttccacacca agtacatgat gtggttccag aggcacgagg agccaagac	180
catcactgac gagtttgagc agggcaccta catctacttt gactacgaga agtggggcca	240
gcggaagaag gaaggcttca cctttgagta ccgctacctg gaggaccggg acctccagt	300

&lt;210&gt; 354

&lt;211&gt; 299

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 354

gaaggaggac	ctaggcacac	acatatggtg	gccacaccca	ggagggtagt	ggggagttag	60
atrtcagagt	ccaggcccta	ggttgggacc	cactccaaat	aatctcctcg	gtgtgggtgg	120
tggttctata	gagggataaa	tgaataataa	acattgttaa	aatatacgaa	aaaaaaaaaa	180
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	240
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaacnncn	ncnananaaa	aaaaaaaaaa	299

&lt;210&gt; 355

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 355

actgttcac	ctaagttcca	ctataaacag	gctcatgact	cgggcacaga	cacttcttgc	60
gtgacttttt	cctatgatgg	taatgtcctt	gcctctcgtg	gaggtgacga	ttcattaaaa	120
ttatgggaca	tccgacaatt	taataaacca	cttttttcag	cctcgggtct	ttccaccatg	180
ttccaatga	ctgactgctg	tttcagtcca	gatgataagc	tcatagtcac	tggtacatct	240
attcaaagag	gatgtggcag	cggcaaactt	gttttctttg	agcgtaggac	tttccaaagg	300

&lt;210&gt; 356

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 356

ttcagaaaga	aacattttaat	agggacttac	aaacaaatta	atgtctgagt	ctcagggtggc	60
agcaagacaa	gatggtggat	ccccatgcca	ttacctgcta	gactcagggt	ttatatactg	120
tagtgggaca	gtgattccga	aggaatgttg	taagacaatt	gaagagcagt	aacatcaaag	180
ttatttgacc	taagggcagg	agttacagta	agtatccact	tttatacaag	aaacaataga	240
taaactggaa	atcttgaggc	ccttcctgga	actgggggta	atgagaagtc	aacatgggtgg	300

&lt;210&gt; 357

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

acaaaaccta	cagatggaga	taaaaattac	tactgttatt	caacatgtgt	tccagaacct	60
tattttgggg	agtaaagtca	attgggcaga	ggatcctgcc	cttaaggaaa	ttgttctgca	120
gcttgagaag	aatgttgaca	tgatgtaata	agaattcatt	tctgacatat	tttacatttc	180
tggaatctc	aactcttatt	tggaaatactt	ctgtgcattt	gtctgtccac	cgtaatttta	240
gaaaagcata	tccataacgt	ttacagtgtg	agtacagttg	tggttagtta	tttgtagtgg	300

&lt;210&gt; 358

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 358

ggtgattaca	gaagcccaga	aggttgatac	cagagccaag	aacgctgggg	ttacaatcca	60
agacacactc	aacacattag	acggcctcct	gcactctgatg	gaccctgcac	ttgatggacc	120
agctggcacc	accagatca	ataaactggc	ttatttgaat	ttgcggcccc	ccaccagga	180

actgactcag	tgcaagaaga	cagcttcgac	tccctgtgat	ttcatctctg	accaatccgc	240
actcctggct	cactggcttc	cccaacccat	gaagttttcc	ttaaaaactc	tgctcccga	300

&lt;210&gt; 359

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 359

atcaggtggt	cctcccatgg	caggagggaa	gaaacccagc	aaacggccag	cctgggactt	60
aaagggtcag	ttatgtgacc	taaatgcaga	actaaaacgg	tgccgtgaga	ggactcaaac	120
gttggaccaa	gagaaccagc	agcttcagga	ccagctcaga	gatgccagc	agcaggtcaa	180
ggccctgggg	acagagcgca	caacactgga	ggggcattta	gccaagggtac	aggcccaggc	240
tgagcagggc	caacaggagc	tgaagaactt	gcgtgcttgn	gtcctggagc	tggaagagcg	300

&lt;210&gt; 360

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 360

tctgtctggt	gatttttatt	ttaagtgaac	ctttggatct	atctttaact	ctctttattg	60
tgagtggtaa	attccaattc	tgacgcagat	cagtaaacctc	acagtatttt	tcctgtggaa	120
atctattcaa	taaggaaacc	aagacaggat	aataaaattt	aaaaaaaaac	aactttgaat	180
tcccctgcct	aggtcttcca	gttggtttcc	agcgcatacc	tcaggtatga	ctttgctagc	240
cggggacaaa	attagcacct	tccgattctc	tagtccaaat	gaactttgtg	ctaaataaaa	300

&lt;210&gt; 361

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 361

gtagaacaga	aaatgagcat	ccgatttctt	cactaaagga	gaccaaactg	ttccttgccg	60
tctagtattg	aagaactgga	acttgaaagt	cctccttcta	ccaactccac	ctccaccccc	120
tcattccctt	tctcccaaag	tactactgct	gttgcatgac	aaccccaa	atgttctgtc	180
aacacaaacc	tgcccttggt	gtataaacag	ggcattacag	aatggtacac	cctatatatt	240
tctgttcagt	atccattcac	tagttcttca	tttataaata	tcattcttccc	cattctgctg	300

&lt;210&gt; 362

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 362

actaccccg	ctacggttcc	cccatgcctg	gcagcttggc	catgggccc	gtcacgaaca	60
aaacgggct	ggacgcctcg	cccctggccg	cagatacctc	ctactaccag	gggggtgtact	120
cccggcccat	tatgaactcc	tcttaagaag	acgacggctt	caggcccggc	taactctggc	180
accccgatc	gaggacaagt	gagagagcaa	gtgggggtcg	agactttggg	gagacgggtg	240
tgagagagc	caaggagaga	gaaatccata	acacccccc	cccaacaccc	ccaagacagc	300



<210> 363  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens

<400> 363  
 ggcaattagc ctcgcttaag ttgccttttt tacacaccaa aacttttttac atgaagggct 60  
 ggtttcacat gaatactata ctgaaatctg tgctctcaag atctagcagt gaccagggct 120  
 gcccggcggg ggctctcctg gcaagtcagg aaggtnnnnn nnnnnnnnnn nnnnnnnnnn 180  
 canattantn nctgatcnc tntnangaan nnngantngc tctnttggn nttgtnnnnn 240  
 gncntnnnnt naantnttt ntnatgtngc t 271

<210> 364  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 364  
 agaggaccct gcagttaggg ggtgttactt tgtcgcccag gatggcctgg acccccaggt 60  
 tcagggattc tcccgcgct gcttctctgag tagctgggac ctcaggcttc cgctcgtgc 120  
 ccgcattcct gctgtgttta ggcagcaggt ggtgacctca ctctccctg gcctgagctc 180  
 tccgtcccgc atcccaggcg gaggccctag ggaacacttt gaagctgagc acgggggtgga 240  
 ccctccctcc tgagtgaatg gagaatagaa agggagagga tttctgttct gttctgtggg 300

<210> 365  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
 gttcttcaaa gccaaccaag acaggcttag cagttttaga gcttcagaac aaattgccaa 60  
 aagccagagt tgtttatgct agtgcaactg gtgcttctga accacgcaac atggcctata 120  
 tgaaccgtct tggcatatgg ggtgagggtta ctccatttag agaattcagt gattttattc 180  
 aagcagtaga acggagagga gttggtgcca tggaaatagt tgctatggat atgaagctta 240  
 gaggaatgta cattgctcga caactgagct ttactggagt gaccttcaaa attgaggaag 300

<210> 366  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 366  
 gccagtcctc acctcccta gtctcgtgt gtatttttag agatgcgtgg gtgtggaaca 60  
 gcctcctgcc tccggtccag gtgtactggg gtctgtgtgt tgtgtttctg cgtgttctcg 120  
 gcagaaagtg gcatgctgtc ccgcctgggt gatttgcctt ttacactat tgctgaagga 180  
 caggaacgaa tccctatcca caagttcacc actgcactaa aggccactgg actgcagaca 240  
 tcagatcctc ggctccgaga ctgcatgagc gagatgcacc gcgtggtcca agagtccagt 300

<210> 367  
 <211> 300  
 <212> DNA

<213> Homo sapiens

<400> 367

cattgccaga	gagcgggttc	agcaagctgc	agatctgatt	gatgctgagc	aacgaatgaa	60
gaagtccatg	tggggtcagt	tctgggtctgc	tcaccagagg	ttcttcaa	acttatgcat	120
agcatccaaa	gttaaaaggg	ttgtgcaact	agctcgagag	gaaatcaaga	atggaaaatg	180
tgttgtaatt	ggtctgcagt	ctacaggaga	agctagaaca	ttagaagctt	tggagagggg	240
cgggggagaa	ttgaatgatt	ttgtttcaac	tgccaaaggt	gtgttgagc	cactcattga	300

<210> 368

<211> 300

<212> DNA

<213> Homo sapiens

<400> 368

gcccggcccg	gcgacgctgg	cgacgcttcc	gcccctgagg	tagtttgagg	accgcgaaga	60
agggaaaaag	gcgggcgggc	ggctgtcttc	tcaccgtcct	cacccgcga	ggcccgccc	120
gctcctccgt	cgtggatttc	gcggcgatcc	ccccggcagc	tctttgcaa	gctgcttgaa	180
acttctccca	aactcggcat	ggatacgact	gcgggcgagg	cgctgcctgc	ttttgtggcg	240
ctcttgcctc	tctctccttg	gcctctcctg	ggatcgccc	aaggccagtt	ctccgcaggt	300

<210> 369

<211> 300

<212> DNA

<213> Homo sapiens

<400> 369

gtggggtgtg	cctcgtgtgc	gtggattcgt	gtgtgtgtgt	gtgtcttgta	tatgtgtgcg	60
cagagtgcac	cattttcaga	ctctactatt	tccgtcaagt	attctgtttg	atttgatca	120
tctcaggatc	ggattctgtt	ttagagtgtt	tctgggccag	gatccgggcc	cctgccctcc	180
tctgcacctg	accacactcc	ctactcaggg	ctagtctgtt	cttcccggac	atcttctggt	240
agccgtgcag	gagagggctg	ggtggggcag	aggccacaga	ggggacctgg	tgtgtcacct	300

<210> 370

<211> 273

<212> DNA

<213> Homo sapiens

<400> 370

cagaggctgg	ttcagaaaag	gaggaagagg	cccggctggc	agccctggaa	gagcagagga	60
tggaggggaa	gaagcccagg	gtgatggcag	gcaccttgaa	gctggaggat	aagcagcggc	120
tggcccagga	tgaggagagt	gaggcctagc	gcctggccat	tatgatgatg	aagaagctnn	180
nnnnnnnnnn	nnnnnnnnnc	atcatgtccn	ntgcatggct	acctatccca	tatttnatnt	240
ccctnncgtt	gnntcnaatt	ncacattntc	ttt			273

<210> 371

<211> 300

<212> DNA

<213> Homo sapiens

<400> 371

gatgaggagt	gtttaatcat	tgatacagaa	tgtaaaaata	atagtgatgg	aaagacagct	60
gttgtgggtt	ctaacttaag	ttccagacca	gctagtccaa	attcttctc	aggacaggct	120
tctgtaggaa	accagactaa	tactgcttgt	agtcctgaag	agtcattgtg	tttaaaaaaa	180
cctatcaaac	gagtatataa	aaaatttgat	ccagttggag	agatttttaa	aatgcaggat	240
gagctcttaa	agccaatttc	cagaaaagta	ccagaattgc	ccttaatgaa	tttagaaaat	300

&lt;210&gt; 372

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 372

gggcccgaat	gcagctgccc	tctccagata	cctggcagcc	tcatatatca	gccaaagcct	60
ggctcggcgg	caggggcctg	ggggaggggc	ccccgcagcc	tcccggggct	cctggctctc	120
tgctcccacg	tcacgggcat	cttcgccgcc	ccccagccc	cagccaccac	ctcccgcagc	180
caggcggtc	agctatgcca	cgacgggtta	catccacgtg	ggcgggggtg	ggcggtgcg	240
gccagccaag	gccaggtcc	ggttgaacca	ccctgctctc	ttggcctcca	cacaggaatc	300

&lt;210&gt; 373

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 373

accctttctg	ccttctgttt	gggaccagc	tggtgttctt	tggtttgctt	tcttcaggct	60
ctagggctgt	gctatccaat	acagtaacca	catgcggctg	tttaaagtta	agccaattaa	120
aatcacataa	gattaaaaat	tccttctca	gttgactaa	ccacgtttct	agaggcgtea	180
ctgtatgtag	ttcatggcta	ctgtactgac	agcgagagca	tgtccatctg	ttggacagca	240
ctattctaga	gaactaaact	ggcttaacga	gtcacagcct	cagctgtgct	gggacgaccc	300

&lt;210&gt; 374

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 374

tcaaggccta	cgaacaggtg	atgcactacc	ccggctacgg	ttcccccatg	cctggcagct	60
tgcccatggg	cccggtcacg	aacaaaacgg	gcctggacgc	ctcgcccttg	gccgcagata	120
cctcctacta	ccagggggtg	tactcccgcc	ccattatgaa	ctcctcttaa	gaagacgacg	180
gcttcaggcc	cggctaactc	tggcaccocg	gacgcaggac	aagtgcagaga	gcaagtgggg	240
gtcgagactt	tggggagacg	gtgttgacga	gacgcaaggg	agaagaaatc	cataacaccc	300

&lt;210&gt; 375

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 375

cttcagtgca	cacaacagga	gagaggagaa	agaagaaacg	ctagtaattc	caagcactgg	60
aattaaagtg	ccttcacag	tgtttgcttc	agagtttgag	gaagatgttg	tgattgttaa	120
ataaagcagc	tccagtttca	ggacctcgac	tggattttga	tcctgacatt	gttcagctc	180

ttgatgatga ttttgacttt gatgatccag ataatctgct tgaggatgac tttattcttc 240  
 aggccataa ggcaacagga gaggaagagg gaatggatat acagaaatct gagaatgaag 300

<210> 376  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 376  
 gggagactgg ggtctatttc acccctgcag tctcgacat aagagatggc tacacccagg 60  
 ggggccagtt cagagaccca ctcccagggtg tgcattctct ttctcaagga tgttccttgc 120  
 tgagaaaaag aattcagtga ttttctccc atttgcttgt gaaagaagag aaatgtggct 180  
 ttgttccacc tggctcaccg gcggtcagaa ttttaaggta tctctcttgt ttcctaaaca 240  
 ttgctgttat cctgttcttt tttcaagggtg ccagatttc atattgctca aacacacatg 300

<210> 377  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 377  
 gatcagccca cctcggcctc acaaagtgtg gggattacag gcgtgagcca ccttgcccag 60  
 cccacatcat acagtttgaa atgaaacttt gccacaacca gcctttgctg tagcacacac 120  
 atatatcact gaacctgttt gaaataaagt tttttttctt tttcctctgg tattctgggt 180  
 tctgaagtct ggtattctgg tattctgggt tcaaaagtat gacttgagag tgttgctctg 240  
 gtattctgag agttgctctg tattctgggt tctgaagatt atttgaaaaa taactcctac 300

<210> 378  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 378  
 tcgctgtgat ccaaggataa aaaagttcaa ggaagaagaa aaagccaaga aagaagcaga 60  
 aaagaaagca aaagcagaag ctaaacggaa ggagcaagaa gctaaagaâa aacaaagaca 120  
 agctgaatta gaagctgctc ggtagctaa ggagaaagaa gaggaggaag tcagacagca 180  
 agcattgctg gcaaagaagg aaaaagatat ccagaaaaaa gccattaaga aggaaaggca 240  
 aaaacttcga aactcatgca agacctggaa tcatttttct gataatgagg cagagcgggt 300

<210> 379  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 379  
 aactataga atacaagcta cttgttcttt ttgcaggatc ccatcgattc gaattcggca 60  
 cgaggcagct tcgagccaat ggtgagctcc ttctggatca gctccttcag ctcttcttgc 120  
 ctcaggatgc tgaaattgca aggctgatgg aagacttgga ccggaacaag gaccaggagg 180  
 tgaacttcca ggagtatgct accttctctg gggccttggc tttgatctac aatgaagccc 240  
 tcaagggctg aaaataaata gggaagatgg agacaccctc tgggggtcct ctctgagtca 300

<210> 380  
 <211> 296  
 <212> DNA  
 <213> Homo sapiens

<400> 380  
 acctggacag ggccagctgc tgggggagcg gcactgggga ctggaggctg gaagcgggtg 60  
 gtgtgtgtcc cctgtttact tttagctgag ctggggttgg gtgtacgggt tctgttcctc 120  
 tgagccctgc ggccacctg atgtttacgt gtgtgtgtga gggggggcnn nnnnnnnnnn 180  
 nnnnnnnnnn ngtnatangc ttaacanatg nanagncnac tnactnctga ttntttatnc 240  
 atttgtgcat tnnaactatg cttttncgat cttnctgntg nnatnacngg catgat 296

<210> 381  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 381  
 cagaaaagag tatagtaggg atgaccaagg tcaaagtggg taaagaagac tcatcatcca 60  
 ctgagtttgt agaaaaacgg agagcagctc ttgaaaggta tcttcaaaga acagtaaaac 120  
 atccaacttt actacaggat cctgatttaa ggcagttcct ggaaagttca gagctgccta 180  
 gagcagttaa tacacaggct ctgagtgagg caggaatatt gaggatgggt aacaaggctg 240  
 ccgacgctgt caacaaaatg acaatcaaga tgaatgaatc ggatgcatgg tttgaagaaa 300

<210> 382  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 382  
 gccaccggtc tcttccta atctgcacagac tattttgggt atttctgggc gggcagttcc 60  
 tttgcatgtt tcgggagagg tttgctgatt tggggcttat atgtcaggcc tttgggttgc 120  
 gtcttatttt aggggttgtt tgggggcctg ggtggtcggc ctcacatggg aaggggatgg 180  
 gtagtgatg gggtttctgt tgtatcttgt gggcgggtga ttttgctttt gtttttgttt 240  
 cacattcttc ccctccaca agccaaagtc gtttcatttg gtttccactg tgtggactgt 300

<210> 383  
 <211> 273  
 <212> DNA  
 <213> Homo sapiens

<400> 383  
 gagatttgat attcgagtgc tgggcttagg tctgttgata aatctagtgg agtatagtgc 60  
 tcggaatcgg cactgtcttg tcaacatgga aacatcgtgc tcttttgatt cttccatctg 120  
 tagtgaggaa ggggatgata gttaaggat aggtggnnnn nnnnnnnngc cngcnttnac 180  
 tttnatngcn ctttttcttg atcnacgnen gnnatncnna nnngtntata ntaatncnga 240  
 anantnttt gnnntgcttt atcaantntt cnt 273

<210> 384  
 <211> 259

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 384

aagagaagga	cctagagatt	gagaggctta	agacgaagca	aaaagaactg	gaggccaaga	60
tgttgGCCca	gaaggctgag	gaaaaggaga	accattgtcc	cacaatgctc	cgGCCccttt	120
cacatcgcac	agtcacaggg	gcaaagcccc	tgaaaaaggc	tgtggtgatg	cccctacagc	180
taattcagga	gcaggcagca	tccccaaatg	ccgagatcca	catcctgaag	aataaaggcc	240
cgaagagaaa	gctggagtc					259

&lt;210&gt; 385

&lt;211&gt; 296

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 385

agagcctgca	agtgacaaag	gaagtgaggc	agaggccac	atgccccac	cgttcacacc	60
ctacgtgcct	cggattctga	acggcttggc	ctcggagagg	acagcactgt	ctccgcagca	120
gcagcagcag	cagacctatg	gtgccatcca	caacatcagc	gggactatcc	ctggacagtg	180
cttggcgcat	agcgccacgg	gcagtgtggc	ttgtgcccc	ccaggaggcc	tgaggctggg	240
tctcactgct	ctgaaaaaga	ccnnccaaa	atgggccttg	gggctnnagg	cccttg	296

&lt;210&gt; 386

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 386

gaagaggagg	ctgtgtatga	ggaacctcca	gagcaggaga	ccttctacga	gcagccccc	60
ctggtgcagc	agcaaggtgc	tggctctgag	cacattgacc	accacattca	gggcccaggg	120
ctcagtgggc	aagggtctctg	tgcccgtgcc	ctgtacgact	accaggcagc	cgacgacaca	180
gagatctcct	ttgaccccga	gaacctcatc	acgggcatcg	aggtgatcga	cgaaggctgg	240
tggcgtggct	atgggccgga	tggccatttt	ggcatgttcc	ctgccaacta	cgtggagctc	300

&lt;210&gt; 387

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 387

ccgcagaggg	cctggaagag	gtgctcacca	cgccagagac	tgtgctcaca	ggccacacgg	60
agaagatctg	ctccctgcgc	ttccacccac	tggcagccaa	tgtgctggcc	tcgtctctct	120
atgacctcac	tgcttcgcatc	tgggaccttc	aggctggagc	tgatcggtcg	aagctgcagg	180
gccaccaaga	ccagatcttc	agcctggcct	ggagtcctga	tgggcagcag	ctggccactg	240
tctgcaagga	tgggcgtgtg	cgggtctaca	ggccccggag	tggccctgag	cccctgcagg	300

&lt;210&gt; 388

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<400> 388  
 tggaggctctc ctttcgcccc agcccagggtg gccaaagccca tcctggcctc agaacatgct 60  
 gagcacattt tgtaggggtgg cacccttttta tccaagttac tagctacaca tcagtgttta 120  
 aagagaaaaa agtgaccttt cattttttttt tcttgaaact tgaggaaaca agatacatac 180  
 tactgatttt ttttttctta aaactaaatg catgactgca gagcggtaga ggtgtatatt 240  
 tttcatactg tggggcaaag tatttgtgct gcttttttga gatggactgg aacgtctggt 300

<210> 389  
 <211> 293  
 <212> DNA  
 <213> Homo sapiens

<400> 389  
 gtcaagctgg ccctggatgt ggagatcgcc acctaccgca agctgctgga gggcgaggag 60  
 tgcaggctga atggcgaagg cggttgacaa gtcaacatct ctgtagtgca gtccaccgtc 120  
 tccagtggct atggcgggtgc cagcggtgtc ggcaannnnn nnnnnnnnnn nnnatgaanc 180  
 agntactcct atggnnttag cnttntanct atnacctgcn cnaactannc tnanagtcta 240  
 gnncttgccc caaccctac ttttgtattt atattgtgtg tgcgtgtgtg cgt 293

<210> 390  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 390  
 ctcacacctg ctttggatgc ttcaagcacc tcagccctct gaactacaaa acagangagc 60  
 ctgcaagtga caaaggaagt gaggcagagg ccacatgcc cccaccgttc acaccctacg 120  
 tgcctcggat tctgaacggc ttggcctcgg agaggacagc actgtctccg cagcagcagc 180  
 agcagcagac ctatggtgcc atccacaaca tcagcgggac tatccctgga cagtgtctgg 240  
 cgcagagcgc cacgggcagt gtggctgctg cccccagga ggctgaggc tgggtctcac 300

<210> 391  
 <211> 257  
 <212> DNA  
 <213> Homo sapiens

<400> 391  
 acccgtccgg ggccggccaa tttgcatatt tggaatgctc cgctataaac cgggctgggg 60  
 ttttgcagcg atttcttaga tgtaaaaatg agatctcaat agcagcgggc tgggcacatc 120  
 ctctctctc tccttctctc tctgcccgga gctggtttcc gtctctcggc tcggggctgg 180  
 aactccggcc caacctaggc ggcagccgc cagagatgg cgcacttccg atcaatgtca 240  
 aagccgccgg ggagccc 257

<210> 392  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 392  
 gcgcgagcgt cggctccgcc tgggcccttg cgggtgcctg cgggcaggcg gtgaggctca 60  
 cgcattgtct tacgggcaag aacctgcaca cgcaccatt cccgtcgccg ctgtccaaca 120

accaggaggt	gagtgccttt	ggggaagacg	gcgagggcga	cgacctggac	ctatggacag	180
tgcgctgctc	tggacagcac	tgggagcgtg	aggctgctgt	gcgcttccag	catgtgggca	240
cctctgtgtt	cctgtcagtc	acgggtgagc	agtatggaag	ccccatccgt	gggcagcatg	300

&lt;210&gt; 393

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 393

gcgcgagcgt	cggtccgcc	tgggcccttg	cggtgcgctg	cgggcaggcg	gtgaggctca	60
cgcatgtgct	tacgggcaag	aacctgcaca	cgcaccactt	cccgtcgccg	ctgtccaaca	120
accaggaggt	gagtgccttt	ggggaagacg	gcgagggcga	cgacctggac	ctatggacag	180
tgcgctgctc	tggacagcac	tgggagcgtg	aggctgctgt	gcgcttccag	catgtgggca	240
cctctgtgtt	cctgtcagtc	acgggtgagc	agtatggaag	ccccatccgt	gggcagcatg	300

&lt;210&gt; 394

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 394

gtccatacat	ggagctccct	ggagcccgtg	tgctctcgtg	tgactgaacg	ttttgtgatg	60
aaaggaggag	aggctgtctg	cctttatgag	gagccagtgt	ctgaattgct	gaggagatgt	120
gggaattgca	cacgggaaag	ctgtgtggtt	tccttttacc	tttcagctga	ccatgaactc	180
ctgagccgga	ccaactacca	cttctgtcc	tcaccgaagg	aggccgtggg	gctctgcaag	240
gcgcagatca	ctgccatcat	ctctcacnag	gngaccatat	tggtttttga	cctggagacc	300

&lt;210&gt; 395

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 395

gcaaaatcaa	tgtggactga	acataaatca	cctgatggaa	ggacttacta	ctacaacact	60
gaaaccaaac	agtctacctg	ggagaaacca	gatgatctta	aaacacctgc	tgagcaactc	120
ttatctaaat	gccccctggaa	ggaatacaaa	tcagattctg	gaaagcctta	ctattataat	180
tctcaaacaa	agaatctctg	ctgggccaaa	cctaaagaac	ttgaggatct	tgaagcaatg	240
atcaaagctg	aagaaagcag	taagcaagaa	gagtgcacca	caacatcaac	agccccagtc	300

&lt;210&gt; 396

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 396

aagagcacaa	gaggaagaga	gagaccctca	ctgctgggga	gtccctgcca	cactcagtcc	60
cccaccacac	tgaatctccc	ctcctcacag	ttgccatgta	gacccttgta	agaggggagg	120
ggcctaggga	gccgcacctt	gtcatgtacc	atcaataaag	taccctgtgc	tcaacaaaaa	180
aaaaaaaaaa	aaaaacnnnn	nnnnnnnnnn	nnntnngggn	gnctnntnnc	nnaaanccan	240



ncttnataaaa anccttngnt natttggaac aaccncann taaanngcag ggaaaaaaag 300

<210> 397

<211> 300

<212> DNA

<213> Homo sapiens

<400> 397

gataaatacc	tcagcccctc	gccttctctca	accacactgg	caagtcttct	taggatctga	60
tcccagtttt	ctggaagcaa	tcctacccca	gcccagctt	cccagagtcg	agccttaatc	120
cttctcactt	ctcagtgtca	gagcagaaat	gaatcctggg	gttgactgtg	tccattcggg	180
ttattagcag	ctaagaagcc	cagacgagta	gtgtgagctg	ccttgggagc	ctcagtgagg	240
gcactgggac	tggcctcact	ctcttgcccc	cagcctagtg	ggctttctcc	tctgtctctc	300

<210> 398

<211> 300

<212> DNA

<213> Homo sapiens

<400> 398

ctgaacccta	aaggaaagcc	agcaaaccag	ctgcttgctc	tcaggacttt	ttgcaattgt	60
tttggtggcc	aggcaggaca	aaaactcatg	atgtcccaga	gggaatcact	gatgtcccat	120
gcaatagaac	tgaaatcagg	gagcaataag	aacattcaca	ttgctctggc	tacattggcc	180
ctgaactatt	ctgtttgttt	tcataaagac	cataacattg	aagggaaagc	ccaatgtttg	240
tcactaatta	gcacaatctt	ggaagtagta	caagacctag	aagccacttt	tagacttctt	300

<210> 399

<211> 300

<212> DNA

<213> Homo sapiens

<400> 399

gctgacctac	agcagaagct	gctggatgca	gaaagtgaag	acagacccaa	acaacgctgg	60
gagaatattg	ccaccattct	ggaagccaag	tgtgccctga	aatatttgat	tggagagctg	120
gtctcctcca	aaatacaggt	cagcaaactt	gaaagcagcc	tgaaacagag	caagaccagc	180
tgtgctgaca	tgcataagat	gctgtttgag	gaacgaaatc	attttgccga	gatagagaca	240
gagttacaag	ctgagctggt	cacaatggag	caacagcacc	aagagaaggt	gctgtacctt	300

<210> 400

<211> 300

<212> DNA

<213> Homo sapiens

<400> 400

ggctagcgat	ttctacctgc	gctactacgt	agggcacaag	ggcaagtttg	ggcaccgagt	60
ttctggagtt	cgaatttcgg	ccggacggaa	agcttagata	tgccaacaac	agcaattaca	120
aaaatgatgt	gatgatcaga	aaagaggctt	atgtgcacaa	gagtgtaatg	gaagaactga	180
agagaattat	tgatgacagt	gaaattacaa	aagaagatga	tgctttgtgg	cctccccctg	240
atagggttgg	ccgacaggag	cttgaaattg	taattggaga	tgagcacata	tcttttacca	300

<210> 401

<211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 401  
 acccccttca tggacagatc cccacagcc tggggcagaa gaggcgtcga gggcgccaga 60  
 agtggcggca gcagcagccg cagcagccaa agagaggcaa gagaaagaga aagcgggagg 120  
 tggaggggtc ccggaagagc tgggtcccggt gggtgagctg gtccccgtgg ttgaattgga 180  
 agaggccata gcccagggct cagaggccca gggcgctggg tctgggtggg acgcgggggt 240  
 gcccccaatg gtgcagctgc agcagtcacc actagggggg gatggagagg aagggggcca 300

<210> 402  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 402  
 ggatcctttc cagacagaag accccttcaa atctgaccca tttaaaggag ctgacccttt 60  
 caaaggcgac ccgttcgaga atgacccttt tgcagaacag cagacaactt caacagatcc 120  
 atttgagggg gacccttca aagaaagtga ccattccgt ggctctgcca ctgacgactt 180  
 cttcaagaaa cagacaaaga atgaccatt tacctcggat ccattcacga aaaacccttc 240  
 cttaccttcg aagctcgacc cctttgaatc cagtgatccc ttttcacctt ccagtgtctc 300

<210> 403  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 403  
 aattccgttg ctgtcggaca gattgcccta gtacccaccc acctatcagg gttatgcaat 60  
 ggaacatcct cgcccaagct cttggagaag gcaaagacaa ctttgtacag tgccctgttg 120  
 aagcactcaa atgggaagaa aggaaatgtc tcatcctgga agaaatcctg gcctaccagc 180  
 ctgatataatt gtgcctcaa gaggtggacc actattttga caccttcag ccactctca 240  
 gtagactagg ctatcaaggc acgtttttcc ccaaaccctg gtcaccttgt ctgatgtag 300

<210> 404  
 <211> 300  
 <212> DNA  
 <213> Homo sapiens

<400> 404  
 agtgggataa aatgagacga gccctggaat ataccattta caatcaggaa cttaacgaga 60  
 ctctgtgcaa acttgatgag ctttctgcta agcgagagac tagtggagaa aaatccagac 120  
 aattaagaga tgctcagcag gatgcaagag ataaaatgga ggatatcgaa cgccaagtta 180  
 gagaattgaa aacaaaaatt tcagctatga aagaagaaaa agaacagctt agtgctgaaa 240  
 gataagagca gattaagcag aggactaagt tggagcttaa agccaaggat ttacaagatg 300

<210> 405  
 <211> 856  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 405

tggtgccngt	tcctattccg	tgctntcgt	ctnccnccag	ancnangcgt	ntcgaattcg	60
gcacgaggaa	ggaggaccta	ggcacacaca	tatggtggcc	acaccagga	gggtagtggg	120
gagttagatt	tcagagtcca	ggccctaggt	tgggaccac	tccaaataat	ctcctcgggtg	180
tgggtggtgg	ttctatagag	ggataaatga	ataataaaca	ttgttaaaat	atacgaaaaa	240
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	anaanaaaaa	300
aaaananaaa	aatnaaaaaa	annanaaaaa	aaaaaaaaaa	aanncccctn	cncctataaa	360
nattcngggg	ggntttttcc	tccannccnn	ntntttaata	nnctnctnt	tgnttcttng	420
netcaccnnt	tcttttggtg	ggcnntaana	naaaatnttn	nttttttttn	ggntanaaat	480
ncnntnnng	ttttttntnn	ttttttttcn	aaaccctcct	ntntnctc	ncgtntcnaa	540
aaanntnttt	ntccnncn	nttnntnt	nctntttcta	ttttnttct	ttntncaann	600
tccnangtg	nnnngngtnt	nntgnggctt	gtttnttttt	ncnncctngc	gtcatccnnc	660
caataatttc	ttnnccccc	nannccnnt	ttttntnnc	ctctatntnn	gnngngnnat	720
atnantcccc	tttatnttn	atnantagtc	ntntnttttn	ttntccntng	tnatannatt	780
ttntntcccn	ntntaanttc	ctcannnnat	ttntntnncn	ncngntata	tttnangnta	840
ntcnnccggg	gttntct					856

&lt;210&gt; 406

&lt;211&gt; 843

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 406

tnntnnnnnc	gnangctggn	nnnttctncc	cntttctaata	ngttntctaata	actanggatn	60
gtcacgagg	tcceangtag	gcatagcgca	ctgctgtacg	tttttggttg	tttttaagaa	120
actcgatgaa	gaggggtgtc	attctgggct	cgggggtggt	gccaattttt	caccagaaag	180
ggagccaccc	cttgcaacca	cttctgtctc	cgttagcccc	ccctctgccc	tcctccaagc	240
caaagcgtgg	cctggctttt	gtcttcccat	ttagttttcc	tcttttacc	ttccttttgt	300
gcttaattta	ttaaaatagt	tgctgtataa	tttattttca	taaactataa	aaaaatacta	360
aatgggttaa	atagacttgc	aggccaatct	taaatggggg	gggaggggtc	tgagggtggg	420
atggggaaag	ggaaagaggt	tttgatntaa	acaaaacaaa	tgacttttgg	gtgtgtnnng	480
gnattttnt	ggggatanan	ggggtggggg	nnnnngnann	nnnnnnnnnn	nnnnnnnnnn	540
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	600
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	660
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	720
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	780
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	840
ncn						843

&lt;210&gt; 407

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 407

tgggcngggn	ctantngngg	gctctogact	tctacganc	ttccaatggt	tngngggcac	60
gagcccccat	cttcactggt	tattccactt	atttaaaatg	tccagaataa	gcaaatctcc	120
atatagagga	agtagattag	tggttgcttc	gggatgggag	gaatgggaag	attgaggtct	180
ttcttttgca	gtgataaaaa	tgctctaaaa	ttgactgtag	cgatgggtcac	acaactctga	240
atatgcttaa	gaccattgaa	ttacacactt	tacgttggtg	aattgtatgg	tatgtaaat	300
atagtttcaat	aacatagtta	caaaagataa	tcaaaagcat	gaaagcactg	ttgatgtggt	360

ttggatctgt	gtcctcaccg	agtctcatgt	tgaaatgtaa	gccccctggt	gggaggcgat	420
gggattatgg	ggcagagtcc	tcacaaacgg	tttacaccac	ccgctcagtg	ctgggtctcct	480
gatattgagt	cctcatcaca	tctggttgct	tcaaagtgtg	tggtgcctcc	cctctatctc	540
cctnctgctc	tgcccatata	agatgtgcct	gcttctcttc	gccttctaac	atgattgnaa	600
gtttcctgag	gcctncctag	aacaaaactg	ctgtgctttc	tgnncccatc	tacaggaccc	660
ggagccaatt	naaccctttt	tctttataaa	aaaaaannnn	nnnnnnnnnn	nnnnnnnnnn	720
nnnnnnnnnn	nnnnnnnnnn	nnt				743

&lt;210&gt; 408

&lt;211&gt; 746

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 408

tgtccgnttc	ttangntgng	ctctngcttc	ctaggagtnt	cnaatcgctt	ggtgcagacc	60
tccagcacaa	gcctctgcta	gtngatctca	cggtagaaga	aggtaaaga	ttaaaggtna	120
tttttggttc	acacactggg	ttccatgtaa	tngatgttga	ttcaggaaac	tcttatgata	180
tctacatacc	atctcatatt	cagggcaata	tcactcctca	tgctattgtc	atcttgccca	240
aaacagatgg	aatggaaatg	cttgtttgct	atgaggatga	gggggtgtat	gtaaacacct	300
atggccggat	aactaaggat	gtgggtgctc	aatggggaga	aatgcccacg	tctgtggcct	360
acattcattc	caatcagata	atggctgggg	cgagaaagct	attgagatcc	ggcagtgga	420
caggacattt	ggatggagta	ttnatgcata	agcgagctca	aagggttaaag	tttctatgtg	480
aaagaaatga	taaggnatat	tttgcatctc	gtgcgatctg	gaggaagtag	cccaagtgtt	540
tttcatgacc	ctcaacagaa	attccatgat	gaacctgggt	accagaagaa	ccccttgcca	600
cttatcttca	tggcgttatt	ctaatttaaa	aagaacataa	ctcatgngga	cttatgccca	660
gtctagaggc	agaatcagaa	ggcttgggtg	gaacatatcg	ntttcctttt	tcctttcctt	720
cggccctncc	agnccagtcc	atnttt				746

&lt;210&gt; 409

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 409

ggatccgggt	tccaatgctc	gggcncctga	gctncctaag	annttgctaa	tgcttgngg	60
ngtgccctcg	gtgcgtggat	tcgtgtgtgt	gtgtgtgtct	ngtatatgtg	tgccgagagt	120
gcatcatttt	cagactctac	tatttccgtc	aagtttctgt	ttgatttga	tcattctcagg	180
atcgattctc	gttttagagt	gtttctgggc	caggatccgg	gcccctgccc	tcctctgcac	240
ctgaccacac	tcctactca	gggctagtct	gttcttccc	gacatcttct	ggtagccgtg	300
caggagaggg	ctgggtgggg	cagagccagg	aggggacctg	gtgtgtcacc	tgccaccac	360
ctggctcatc	cctcangccc	accctgaccc	tacattacat	aggttacgtc	agcctactgt	420
ggctgttgag	caaagcattt	ctcctttctn	gggcctcatt	gcactagatg	ggcctgtggg	480
cccaaagtag	gtcagtaggt	tggggttgct	gacaccctt	gggtgcaact	ttgggacaag	540
atgaantggc	tctgtcctgt	cactggcctc	tccttgcttg	ggggctatgt	gcacttcaaa	600
accctggcca	agctcaagcc	catgaagnat	tggagaacac	cctgggcccc	caagaactgg	660
angcaccggg	ccanttcccc	tgggattcca	nctttgcca	ggtgaacctt	tcttttacc	720
naaacttntg	tccccctgnt	tccacttcca	aaaanaactg	g		761

&lt;210&gt; 410

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 410

gatgccggtt	cctatgatgn	gctctcggtt	tcctaggagt	tccaanactn	ggctngcncg	60
aggncttnta	aatatatctn	ggntttanta	ggtgataagt	nctgtcantt	agtancatct	120
gaaaaancag	ctttgtcctg	ggtgaaaaag	gatgccaaaa	ttgcctggaa	aagagcagtg	180
anaggagtcc	gggagatgtg	tgatgcntgt	gaagcancat	tgtttancat	tcactgggtc	240
tgccaaaaat	gtggatttgt	ggtctgctta	gattgttnca	aggcaaagga	aaggaagagt	300
tctagagata	aagaactata	tgcttggatg	aagtgtgtga	agggacagcc	tcatgatcac	360
aaacntttaa	tgccaaccca	aattatacct	ggttctgttt	tgacagatct	tctagatgcc	420
atgcacactc	ttagggaaaa	atatggtatt	aatcccat	gncattgtct	aacaaacaga	480
atttacaagt	tggaaatttt	cctncatgaa	tggtgtatct	caagtttaca	gaatgtctta	540
atcacagtat	aaaattctct	gngcatgcct	gagtctcagc	gccaaaatcc	tcctccgaag	600
tctgagaaaa	atggtggcag	cnnccccana	aagtgatgtt	nggcnccaga	ttaccaggtt	660
aacttcctcc	agaatnccag	tcaccactgn	actggnatgc	anatcttgcc	gagccaaaaa	720
gcccnaagng	ggaaaaaaa	aaaaaaaa				748

&lt;210&gt; 411

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 411

gnangnnngn	ttcntagtgc	ccgtgggagt	cttagatncc	ctaaaaaatt	gntaatgctn	60
ggtcggcacg	agtcaggcc	tacgaaacag	gtgatgcact	accccggtta	cggttcccc	120
atgcctggca	gctnggccat	gggcccggtc	acgaacaaaa	cgggcctgga	cgctcgccc	180
ntggccgcag	atacctccta	ctaccagggg	gtgtactccc	ggccattat	gaactcctct	240
taagaagacg	acggtctcag	gcccggctaa	ctttggcacc	ccggatcgag	gacaagtgag	300
agagcaagtg	ggggtcgaga	ctttggggag	acggtgttgc	agagacgcaa	gggagaagaa	360
atccataaca	ccccacccc	aacaccccc	agacagcaat	cttcttcacc	cgcttgcaac	420
ccgttcgctc	ccaaacagag	ggccacacag	atacccccag	ttctatataa	ggaggaaacc	480
gggaaaagaa	tataaagtta	aaaaaaaagc	ctccggtttc	cactactgng	tagacttcct	540
gcttcttcaa	cacctgcaga	ttctgatttt	ttgtgtgttg	gttgttctct	ccattgctgn	600
tggtgcangg	aagtcttact	taaaaaaaa	aaaattttgn	gagtgcactc	gtgtaaaacc	660
atgttanttt	taacagaacc	nanaagggtt	gncctattgg	ttaaaaaaa	aaaaaaaaa	720
aaacttngng	cctttagaac	tattannngag	nccnatctac	nttaatecan	nct	773

&lt;210&gt; 412

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 412

gnannccgga	ttcntagcgn	tcgtggaagt	gcatcgggctg	ntaacaattt	gctaattgctt	60
ggagtcccaa	ttccagagaa	aatgagtga	tgggcacctc	gacctcccc	agaaatttgt	120
ccgagatgtc	atgggttcaa	gtgctggggc	cggcagtgga	gagttccacg	tgtacagaca	180
tctgcgccgg	agagaatata	agcgacagga	ctacatggat	gccatgggctg	agaagcaaaa	240
attggatgca	gagtttcaga	aaagactgga	aaagaataaa	attgctgcag	aggagcagac	300
cgcaaagcgc	cgaagaagc	gccagaagtt	aaaagagaag	aaattactgg	caaagaagat	360
gaaacttgaa	cagaagaaac	aagaaggacc	cggtcagccc	aaggagcagg	ggtccagcag	420
ctctgcggag	gcatctggaa	cagaggaggga	ggaggaagtg	cccagtttca	ccatggggcg	480

atgacaatgt	ttgccacagc	ctctgcctgg	aacctggctc	gtgctgtgac	cagaagggaa	540
agggcgctgt	ttggctcttt	cttccccgca	aggaccccg	ttaccgctg	gatggagagc	600
aaaggagacc	cccttccgag	cccgtcaca	gtcctgtatt	tggcaagggt	tgggaacctg	660
aaagggccaa	tntnccttga	cacttanang	cacttgccct	tcagacacca	ttccngcgt	720
ctggtaaaag	gggacaagaa	aagccttaac	cttggcnnca	tattttgaca	gggg	774

&lt;210&gt; 413

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 413

gnngnnnnnn	tttctaatac	ttgggnnnnn	ngtcnatgcn	taagagccan	gggntcgaa	60
ttcggcacga	ggcgggccc	gccagcgga	gcccctg	ccgcgccatg	tcaaagaaaa	120
aaaggactga	gtgcagaaga	aaagagaact	cgctgatgg	aaatattttc	tgaacaaaa	180
gatgtatttc	anttaaaaga	cttggagaag	attgctccca	aagagaaaag	ctttactgct	240
atgtcagtaa	aagaagtcct	tcaaagctta	gttgatgatg	gtatggttga	ctgtgagagg	300
atcggaactt	ctaattatta	ttgggctttt	ccaagtaaag	ctcttcacgc	aaggaaacat	360
aagttggagg	ttctggaatc	tcagttgtct	gagggaaagtc	aaaagcatgc	aagcctacag	420
aaaagcattg	agaaagctaa	aattggccga	tgttgaaacg	gaagagcgac	caggccttagc	480
aaaagacttt	cttcacttcg	agaccaaang	ggaacagcta	aaggcagaag	tagaaaaaat	540
ncaaagactg	tgatccccga	agttgtngga	agaaatcgcc	aagcaaatna	agtagcccaa	600
ggaactgctt	acagatggac	tgattacata	ttcgcaataa	aatcttnggc	ccaaagaaaa	660
attnnggggt	tgaaggaaaa	ttaaattggg	tngaaccttt	tgggaatttcc	cgaagacttt	720
ttgcctncnt	ngacttaaaa	tatttccatg	gnggtgaaag	gttgtccaan	ctt	773

&lt;210&gt; 414

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 414

gnagnnnnnn	nttctaatac	ttgggnnnnn	nngtcaatnc	ctnngancna	ggcggntcgc	60
tcattccagaa	angtcagatc	ancaaagaag	tccangaaaa	antgcgaccc	agctngaccn	120
tttgatccca	ggcttagcac	acgattgcat	ggcntccct	ttagccactt	naaccactgc	180
agacntccag	gaagctggac	tctctctca	gtcctccag	acttctggcc	accacagant	240
gaaaacccca	ttttcaactg	agctatcttt	gctccagcct	gatactccag	actgtgctgg	300
agatagtcat	acccactgg	cttttccctt	caccgaggac	ttggaaagt	cttgtttgct	360
agaccgaaag	gaagaaaaag	gggattctgc	caggaaatgg	gaatggcttc	atgagtctaa	420
gaagactatc	agagtatgga	gaaacacacc	aaactacctg	gggacaaatg	ctgtcagccc	480
ttaggcaaga	ctaaattgga	aagaaagggt	tctgccaaag	aaaacaggca	ggcccctgtc	540
ctccttcaaa	catacaggga	atcctggaat	ggagaaaaa	tagaatcagt	gaaacaaacc	600
cgtagtccag	ttctngttt	tcctgggata	tgaagaaga	gaccanggac	tnctggagtc	660
aacttttcac	ttgaagaatc	tcaaggccac	cggtcattgg	ccacacactn	gaactccttt	720
ttaagatgta	cccattactg	gaattgggct	taggg			755

&lt;210&gt; 415

&lt;211&gt; 852

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 415

gnagnaannn	ttctaagtct	tgggnnnnnn	ngtcaaacct	tannaacctg	gcntgncgaa	60
ttcggcacga	ggtcacaggc	aggttttantg	gccagtttaa	aacttatgct	ntctgcgggg	120
ccnttcgtag	gatggtgagt	gtttccctgg	gctttgctca	tcacttcggg	acatcgaggga	180
ctttaccgtg	cgcnttggag	tgtgtgatgg	tgcctgagta	gatctgctgg	cagagtagtt	240
tgagccagct	ggactgggct	ggcgcgctgc	cgcttcttga	gggtggaaga	ggggtgctct	300
gagaagacac	tcaggcagca	gactctgcct	ctcactagga	ggtgcccccc	cgaccccggt	360
ccaccatagt	caaggctgca	ggctgccccg	ggagaagtgg	ctcccccttct	tgcgcctgtc	420
ttccattcgc	ttcaccgggg	gganaagacn	ttgggcttgg	ttggcacagc	ntgacccttc	480
tgcccatctt	naaggcagnc	ccggaantgg	gaaaaatatt	tctttaaatg	gtggcctttt	540
nttttttttt	nctttnaaag	gggttgaagt	tccannaatg	natttcccaa	tttccctccc	600
gaattgggnc	ccaaagggcc	ccaatggggc	antcggctct	ttaaaaagna	accttttttg	660
acctgggaag	aagaaaatca	cccagattgt	tgggaaatat	tttggnatt	aaaataaant	720
aatggaaaac	ctnaaaaaaa	aaaaaaaaaa	aaaactcgag	cccnttaaaa	acttttagtg	780
agtcnnatta	ccnttanatc	canacnttga	tangaanctt	tggataattt	tgggncaaac	840
cnnaacttng	at					852

&lt;210&gt; 416

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 416

ggnnnnnnng	tnaaaccttc	cnaannaggc	tnggcgtcac	tgnccccggg	caacaaaccc	60
acttttatga	cagttttctt	ccgcagcttg	gctnttaaat	tttactggca	ggtgtatggt	120
tgttgagggg	ttcctagtga	gttgggggac	ctggcantan	agctgcttgg	ttggagggaag	180
tgaanctggc	ttantaccag	cagctgatct	cttccacgtg	ctgctgcttt	ttttgccact	240
ctgatactaa	accagagaaa	gctgcaggtg	gataaagaag	ctgtggctgt	ttttgcttt	300
tgggtggcaa	tgagaaagag	tcacagtgtg	ggttaaaggg	atctgcagtg	gggccaagga	360
tgccacccca	ccctcagctg	tangcaagct	tgacataaa	taacccccgt	cagtggagtg	420
ttcgggatgc	agggggcant	atagtgttct	tggactttgt	ccgtcctggg	gcagttttta	480
agttctttat	atttaagtgg	ggtcagtgcc	aagtgtacc	actttcccaa	taaangaatg	540
ggggaccan	aaggctgggg	tccctggcta	cctgttatg	aaggttttgn	tnnttctctg	600
acaaganttg	ctttggaaaag	ancctgtttt	taggggatta	ttttttgnat	accccgatgg	660
gganccaggg	ttctnctcaa	aaccttaca	accttagga	tcatagggaa	aaggggccc	720
tnnttttctg	ctggcttncc	caacttaaaa	acnt			754

&lt;210&gt; 417

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 417

ngtntatagc	ttntaatgc	ttcntancga	attcggancg	agagaagccn	tgagcagcaa	60
agtctntcgc	gacaccctgt	acgaggcggg	gcgggaagtc	ctgcacggga	nccagcgcaa	120
gcgccgaag	ttcctggaaa	cggtgaggtt	gcagatcagc	ttgaagaact	ntgatcccca	180
naaggacaag	cgcttttcgg	gcaccgtcag	gcttaagtcc	actccccgcc	ctaagttctc	240
tgtgtgtgtc	ctgggggacc	agcagcactg	tgacgaggct	aaggccgtgg	atatcccca	300
catggacatc	gaggcgctga	aaaaactcaa	caggaataaa	aactgggtcaa	gaagcttggc	360
caagaagtat	gatgcgtttt	tggcctcaga	gtcttttgat	caagcagatt	ccacgaatcc	420
tcggcccagg	tttaaataag	gcaggaaagt	tccttttct	gtnacacaca	acgaaacatg	480

gtggccaaag	tggatgangt	gaagtnca	atcaagttnc	aatgaagaa	ggtgttatgt	540
ctggctgtan	cttgttggtc	acgttgaaga	tgacnngacg	atgaancttg	gggtataaca	600
ttcacctggc	tgtcaacttc	ttggnggtca	attgcntcaa	agaaaaaact	tgggcagaaa	660
tgttccnggc	cttatnttnt	caagaaccnc	catggggcna	agccccaacg	ccctttnttt	720
aaaggcncat	ttggaattaa	attcntnttt	ncccg			755

&lt;210&gt; 418

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 418

tggggntnn	nttctaattgc	tgggatgttc	taaangntgg	gtactcgtt	ctttccgcag	60
ganccntcg	attcgaattc	ggcacgagga	aagggtggcg	gcttctcacg	gttgagttgc	120
tgcgcctgca	gacggaagct	ccccacaggc	agagctgctt	ggatgtgtga	gtcatgaagc	180
cagagaagcc	ccgctccatg	agcagtgact	ccccaggccc	tgtgacctcc	ctcctgtctt	240
gcagctcctc	ctggcaccag	tccccagggc	tctcctgttg	gtagtccctg	cttttcttct	300
tggaaattcc	tcgtggacct	cgagatcttt	accctaaaat	agttctgttg	aatttcaccc	360
tggcaatgta	aattgatagc	ttatcttcac	agatgccaga	caatggacaa	ctcaccatca	420
gtcctctgct	cacctgagac	aaatgcatgt	ctgattgctt	cctctgccct	attgnttatg	480
tgaaaatgca	gattcactga	gccagactaa	ggcatcagtg	actgttcctc	tactgcctct	540
cacatggaga	ttgtgtattc	agtgaaggc	tgatcaaaga	ccccaaagga	atgcaccagt	600
ttatctctta	tctacctatg	acctgcgagc	tgncaccac	ccccagttgt	tgcgcctttc	660
cagacagaac	cagtgtcatc	ttacacgtat	taattggatg	tcctgngnct	tccttaatat	720
gtatcaaaac	aagctngcct	tgaacacctt	gggcacn			757

&lt;210&gt; 419

&lt;211&gt; 738

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 419

gnnnngcgtt	cnaattncgn	ggntctttc	tngccnanna	nnannngcgt	gngngaattc	60
ggcacgagac	tgttcatcct	aagttccact	ataaacaggc	tcagtactcg	ggcacagaca	120
cttcttgctg	gactttttcc	tatgatggta	atgtccttgc	ctctcgtgga	ggtgacgatt	180
cattaaaatt	atgggacatc	cgacaattta	ataaaccact	tttttcagcc	tcgggtcttc	240
ccaccatggt	cccaatgact	gactgctggt	tcagtccaga	tgataagctc	atagtactg	300
gtacatctat	tcaaagagga	tgtggcagcg	gcaaacttgt	tttctttgag	cgtaggactt	360
tccaaagggg	gtatgaaata	gacatcacag	atgcgagtg	tgttcgtg	ctgtggcatc	420
caaagctgaa	ccagatcatg	gttggaaactg	gaaatggatt	ggctaaagtc	tattacgacc	480
ccaacaagag	tcagagggga	gcaaaattat	gtgtgggttaa	aaccancgg	aaggcaaac	540
aagctgagac	tctactcagg	actacatcat	caccctcat	gccttgccct	tgttcccg	600
agccccgnca	acggagtaca	aaggaaacag	ctggagaagg	acagactgga	tcctgaagt	660
cgcattaacc	tgaacctcct	gtancangcc	cangtcgtgg	tggccgattt	ggaacccacg	720
ggggcactnt	tttttct					738

&lt;210&gt; 420

&lt;211&gt; 739

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 420

```

gcgntnntat tagcgtgggc tcgntctcgc tcnacncanc nngngctggn cgaattcggg      60
acgagaatca gaggaggctt cttcatcctt caactccatg atgaactcct atatgaagtg      120
gcagaagaag atgttggttca ggtagctcag attgtcaaga atgaaatgga aagtgcgtga      180
aaactgtctg tgaaattgaa agtgaaagtg aaaataggcg ccagctgggg agagctaaaag      240
gactttgatg tgtaactgtg ctggtgatga agtcctccca gggaagcctg tgcagatgca      300
gtcacctgga aagaacagag attccctttc acctacctca gcaaaacaaa ctttcaagtc      360
ttgatagact tagcctagta attttatagt gagagtttca aactatatat caagtgtcta      420
tagcatcaaa aactttctggg ggcgtggggg aaagtagaat accaagtata atagttacat      480
tcactttcaa agagcatcta tgaatttgcc ttttgtaact tactgtggct ttaaacatat      540
tcagaacaga tgcttgaaat atgcacttag cactttgggt ccacatctgt ctgggtaaac      600
catgaagaaa atgaagctgc tgcctcaatc gancccagac agcagccata ggcagataaa      660
gatttnggtt cacccttggg ggtgggaggc atcgtgtgtg cctttttttc ctctaataac      720
aattttacag tccgggaan

```

&lt;210&gt; 421

&lt;211&gt; 727

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 421

```

gtgatctttn tgagtggggg ccntnctngc tctannanac aggttngngg ggctagcgat      60
ttctacctgc gctactacgt agggcacaaag ggcaagtttg ggcacgagtt tctggagttc      120
gaatttcggc ccggacggaa agcttagata tgccaacaac agcaattaca aaaaatgatgt      180
gatgatcaga aaagagctta tgtgcacaag agtgtaatgg aagaactgaa gagaattatt      240
gatgacagtg aaattacaaa agaagatgat gctttgtggc ctcccctgat agggttggcc      300
gacaggagct tgaaattgta attggagatg agcacatata ttttaccaca tcaaaaatag      360
gttctcttat tgatgtaaat caagtcaaag gatcctgaag gccttcgagt attttactat      420
ttggtacaag acttgaaatg tttagttttc agtcttattg gattacactt caagattaaa      480
ccaattttaa ttgtatgttt tcaagctggg tgnatattta attaaaggga tgggaagggg      540
ttatttgtca tttacagtat tggggtttta tgaatgtgaa gcaacacaaa aaaatttnaa      600
tgtaaaactg gaaaatagga aaattcatta ncagcttaat gggatccctt acttgatnctn      660
ctgggttttg aagtccccac acacattaaa tctgtaatga aancnctttt ggttaaaatt      720
tctctat

```

&lt;210&gt; 422

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 422

```

gtntngnnng nngtttnatt atatggntcg nctnnctcna nnancnangc ttngctgac      60
aacttgattg ggttctcctt caggtttgaa gcgccctcna gaagtgtcta aaggagacag      120
ttgatagcca aacaacagtt ttggattcac tgactgatta tgaaagaagc agtagactgg      180
tatcaagaat cagtcagcaa ggaggccctc accagacgcc agtgccatgt tcttgactt      240
ctcagcctcc atattcatga actaagtttt tggaatcctt aggcctccac gtgtggaaag      300
cctgagctaa cctactggag gatgagccat cacttgagc agattcaggc catcctagtt      360
gaagcctccc taggccaagc aaccgtccaa ctaccagaca ttgaccattc agccttgaaac      420
attcagcaca aagacaaaac agaccagacc agaagagtcc cacagaatag gggaaactat      480
tcagagaaaa cttaaagccac taagttttat ggtgttttgt tcttgtagcc agaagcatag      540
gcatactggc caatacaaac cgaaatcctt ctaacgtant ggaccctttt caggccagca      600

```

ttttttccct	tgaaaacctg	ggagccttgt	attccatctt	attagcagaa	gatcactttc	660
accaatgggt	tgggctcttg	at ttggaatt	gatgatgtaa	tgagcctnta	ttcnanatgn	720
gacttaatac	ctctgcgaat	tgactggatt	ccn			753

<210> 423  
 <211> 844  
 <212> DNA  
 <213> Homo sapiens

<400> 423		
nggnnnntnn	nnnnnatncc	ntgatcgtgt
ntcgttcttt	ctncaggatn	nnntcgtttc
60		
gaattcggca	cgaggaaaag	ggagccgcgc
agngcctacg	ggagtncggc	ggcagcagcc
120		
ggtaccggca	accacgggca	gctctcaggg
aatctccgtc	gttgaggcca	naggctccag
180		
tccccgcgag	tccagatgcc	tgtccagcct
ccaagcaaag	acacagaaga	gatggaagca
240		
gaggggtgatt	ctgctgctga	gatgaatggg
gaggaggaag	agagtgagga	ggagcgganc
300		
ggcagccaga	cagagtcaga	agaggagagc
tccgagatgg	atgatgagga	ctatgagcga
360		
cgcgcancn	agtgtttcag	tnagatgctg
gacctggaga	agcagttctc	ggaagctaaa
420		
nggagaagtt	gttcaaggga	acgacttgan
tcanctgccg	gnttgccggc	tgggaaggaaa
480		
ntgggggggc	ttgaanaaga	agcccctgga
atnccaccgg	aagccccctt	ttgggggggg
540		
gccttgcaaa	cggggaancc	ctttnaaagg
aatttcngcc	antttcaang	gttgggccaa
600		
ggggaatcnt	accnaagggg	ccttctnngc
cttggnatgg	tgaatccang	gnaaattaag
660		
gtneccaatt	gntgaancct	tccaanggga
ancccaaacc	agcacccttg	naanaagttg
720		
agaaaacttg	cttgcntctt	ntgacacccc
tncnaggggg	aacttcaagg	aaccggttcc
780		
tnaggcttgg	aaggaggacc	cccananccc
tggancctaa	attnttaaat	gggtnggacc
840		
accn		844

<210> 424  
 <211> 799  
 <212> DNA  
 <213> Homo sapiens

<400> 424		
ggagnnnngn	ntccnaattn	nntgggnnnn
nnngtcaaan	nctngctact	cgttctttcc
60		
gcaggatccc	atgcgattcg	aattcggcac
gagcccagac	ctatggagtc	agacagtagg
120		
tttgaggccc	agcaatctat	ggtttaacaa
gccatccagg	tgtttctgat	gcacagtga
180		
attgggggtac	cactggtatt	aggtttggtg
tggcaacttt	ttcatcactt	gttttatgta
240		
gttgctgat	caattgtgaa	aacataatga
atggttgaaa	tggaaacagta	aaataacgaa
300		
agccaaacttt	tttttttttt	tttgagacgg
agtcttgctc	tgtcgcccag	gctggagtgc
360		
agtggcgcca	tctcggtcca	ctgcaagctc
cgcctcctgg	gttcacgcca	ttctcctgcc
420		
tcagcctccc	gagtagctgg	gactacaggc
gccccncacc	acgcccggct	aattttttgn
480		
attttttagta	gagacggggg	ttcaccgtgt
tagccaggat	ggtctcgatc	tcctgacctc
540		
gtgatccacc	cgcctnnggc	ttccaaagtg
ctgggattac	aggcgtgagc	caccggggccc
600		
gggccaagaa	ccaactcttt	atgcctagaa
aatattgtgc	accctatgac	ccaagcccat
660		
tgaatttttn	cngggaaatt	tatggtaaat
tattgaaatg	gatggtacct	ttaaaaagtt
720		
at ttggcaca	ttccccttgg	gttacctttg
gnatggtttg	ccagggaatt	naaaactttg
780		
ggntnaaacc	ttttttann	
799		

<210> 425  
 <211> 750  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 425

gangccggat	tccaattntc	nggctnctct	naaannctgt	ntaatgcttg	gtccgcanga	60
ncccatgcga	tctgtggagg	tctcctttcg	ccccagccca	ggtggccaag	cccatcctgg	120
cctcagaaca	tgctgagcac	atthttgtagg	gtggcacctt	tttatccaag	ttactagcta	180
cacatcagtg	tttaaagaga	aaaaagtgc	ctttcattht	tttttcttga	aacttgagga	240
aacaagatac	atactactga	tttttttttt	cttaaaacta	aatgcatgac	tgagagcgg	300
tagaggtgta	tatttttcat	actgtggggc	aaagtatttg	tgctgctttt	tgagatgga	360
ctggaacgtc	tggtttctgt	ccccggggcc	ggcagctacg	tctattttct	gtagaagggtg	420
ccacagtgag	acctggagcc	accccttctc	gcctggcgcc	gtttanagct	gggagcccgt	480
ggactccggc	ctgtttctac	cttctattca	accactctga	cgtggggaga	caagaagaaa	540
tagaactttt	tgatagtgtg	gtaaaaacat	tggattttga	actatttttag	taaaaggagt	600
taccaacaag	aatgtnatag	gtgctacttt	gagctagata	aataaaggct	ctttgtgagc	660
ctcctgaaaa	aaaaaaantt	nnnnnnnnnn	atnannnnnn	annaaaaaaa	ctggnccttt	720
aaaactttan	gggncgttta	cctanaccct				750

&lt;210&gt; 426

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 426

gnagnncggn	ttcttatgat	cgtggctnct	cntctannng	ttgtgtaatg	ctnggtcnnc	60
angannnnnt	gcganncgaa	ttcggcacga	aggggggttc	ccaatagtag	aaaagggtcc	120
ccattcctgc	tcagcaccgc	acctctctac	ccccccacag	acacacatgc	agacacacac	180
atgcagacaa	cacgcagaca	cacacatgca	ggcactcaca	tgacggccca	tgacacacaca	240
cgtgcacaca	catgcagaga	catgcagaca	cgcaggcaca	catgcacaca	tgcaaagaca	300
cgcagtcagg	cacacgcaga	cgcacacaga	gacacacatg	cagatcacat	gcacacacac	360
atacacacac	tgccccctgt	ttttctgtgg	tgctactggg	tgccagcaac	tcgggtatctn	420
ccaccttcca	ctaaaacctg	ggccttaatt	tctctcccgt	ccccaccctc	aaattcctga	480
tgatgaacc	tagagctgtc	ctgtccactc	caggccggac	tgacgtancc	tatgggcccc	540
gcaggtccag	ggcccacgtt	ttaatttctt	tttnaaaagc	tttaggtctt	ggcngggccg	600
ccggtgggtc	acgccttggg	agttcccagc	atthtttngg	aaggccnaag	gccgggttgg	660
attcacaag	gtcaagcaag	tttcaaggaa	ccaagccttg	aaccaggcca	ttgggtgagg	720
aaccctgggc	ttnttactng	ggnaaattcc	caaaaaaaa	ttggccttgg	gccnaagggt	780
gggcaagggc	acccttgttg	gggtccccaa	antttacct			819

&lt;210&gt; 427

&lt;211&gt; 750

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 427

gagnnngatt	cnaattnctg	ggctnctctc	ttnttatnta	atgctgggtc	cgcangancc	60
nttgcgattc	gaattcggca	cgaggtccaa	ggacaacttc	gagacatttc	tttttgccac	120
cgtatctaac	agggagcagg	aagatctctg	ccgaggaatt	gtccagctct	gcttcaatga	180
gcaaagccaa	cagctgctag	cagaggtcca	gccctctgac	tctttcctca	tggtagagac	240
aactgcatac	tttgaggcct	acaggcacgt	cctggaagga	ctccaggagg	tccaggagga	300
agatgttccc	ttccagagga	atatcgtgga	gtgtaactct	catgtgaagg	agccaaggta	360
cttgctaattg	gggggcagat	atgactttac	ccccttaata	gagaatcctt	cagccactgg	420
ggaatttcta	agaaatgtcg	agggtttgag	acatcccaga	attaatgtct	tagatcctgg	480
ccagtggccc	tcaaaagaag	ccctgaactg	gatgactcca	gatggaagcc	ttgcagtttg	540

ctctcacaag ggaactggct attattcaag gaccttctgg aacaggcnaa acctatgtgg	600
gtctnaaaaa ttgttcaagc ccttctacca acgagtcttg tttggcaaaa ttaaccttca	660
gaaattccca tcttggttgn gtgtatacta atcatgcttt ggaccanttc tggaangctt	720
ttccattgtc agaaaaccan atttgcccg	750

&lt;210&gt; 428

&lt;211&gt; 943

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 428

gnngnccggt ttcctattct cnggcanctc tcttctnctn acctattanc tggactctaa	60
anaaaagnnt gnnngcggtg gctcaagggc caccanaaca tttctttatt attattattt	120
tttaacctgn acatgcntta aagggtctat tacctttctt tccgtctgtc tcaacagctg	180
aaatggggcc nccaaggagt gccttccttt tgctccctcc tactgggact gacggntggg	240
antgtntggn cccanntggg ggtgtctcct gnetgggaag ganggaaagg gaggcanaag	300
tttgccgggg ttgcanntng acancangct gnanaggana tggctaataa ctgtttaatg	360
gaaacctgct tgggcttggg nggaacttag nctgaathtt cccgacttcc tctgccagtt	420
attgacacan tctctttnta agacangaaa taaactaaac cccaccccaa ggnantnatn	480
ncangcngaa aacnncncat ngcccacatt nctnatccc ntancacnn ctctntnttt	540
nncccaanac tntctccan ntntncncnt ttaccntan ncntntntnt atcccnctaa	600
tnctnannnn cntntntnt cennatnctt acnncncnn ntntnncccn nntcttntnn	660
cccaaancn nctcncnnt tcnctnaac cntntnnnca nnaacaccc tctnatnnc	720
ccanntctn cacntntnt ntctcennnt nnnncennnt ntctntnnna nancntntnn	780
nanancnate tntnncncnn cnantntnt tcanctacn ctctntnnnn tntancnat	840
tnnccntenn tnnccntta nnnctntnn nncnaantnn nnnnancctc ncnncnnc	900
canntntnt nnnnnncnt cnaacncn nnnntctatn ccc	943

&lt;210&gt; 429

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 429

gnangnnnnn nntttctaan tnttggggn nnnngtcann gattngcta aagggtngga	60
tcnncgcag naangctgtg gcgtccatt gtgaaagatc caggcatttt tccgagccag	120
gaaaagccca agatgactac aggatattag tgcattgcac ccacctcct ctacgtgtgg	180
tacgcagatt tgcccatctc ttgaatcaaa gccagcaaga ctctctgtct gctgtgatct	240
gcacaccctc caacctgggc agggactggg gggatgcagt gtgtgttagt gccatgtgg	300
cattgtggca ctgttgccc ccatggcggc atgggcaaga tgacctcca ttagcttcaa	360
gtcttgttct ctgtgtgtg gtctgtttaa tatgtgggtc actagggtat ttattctttc	420
tcccatcctt acactctgga tcattgtgca gacttaatac gggttttaac gctttcattn	480
nnnnnnnnnt ttttttgagc tcaaagaaag ttctcatttt cctattcaa ctaataccca	540
tgccgngttt tttaccttg atttaaaggc acctangtt ggggcaacag attctcactc	600
atgtttaana cctggnatc ancttcataa gaccaaagan ggagctttcc cttctcttt	660
acctctnagg attctcatcc ttacannntn gactttttcc aggccaattt cccatnnaat	720
ctgcnanncc cngccttttg ncccaagctt ttntgntngn cccccattt acccn	775

&lt;210&gt; 430

&lt;211&gt; 763

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 430

ngggtgnnnn	nntttcta	nctggggnn	nntnnnnnn	ntttccta	ncttaggn	60
tcgttctt	tccangc	nnngcgtt	gcgacagc	tccaatac	aggttaat	120
tgaaaaat	tccaagac	ttattgca	agtttaatt	ttgaaaac	gctactgc	180
tgtgttt	gacgtgtg	gtttaggc	tgtagcta	ggacattt	aagggccc	240
gatcgttt	tcccaggg	agcagaag	aaaatgtt	atatgtct	tacccggc	300
attccctt	cctaaata	agggctgg	tctgcacg	acctatta	gtattttc	360
caatgatg	gatttcag	gggatgac	catcatca	ttcagggc	ttttttcc	420
cacaaaccc	agggcagg	ccactctt	ctaaatcc	ccccgtga	gcaataga	480
cctctggg	gctcanga	gggtgtgt	agtctata	tataagct	catataatt	540
gtagacaag	atggctct	cgtatctc	cttcctag	gaggagtgt	aacaaggag	600
ttagataag	caccctta	accattcc	ttttccag	gacctacc	tcacaggca	660
aggccccaa	atgagaagt	tgtaacct	tttctcat	ttttacta	ctcaaanga	720
ntgacagc	tcagggac	acattcatt	cttnatac	tcc		763

&lt;210&gt; 431

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 431

tggtgttnn	ntccta	ttggnngn	ggtannct	ctaatact	tggggctc	60
tctntctc	nnngcnng	cgtnnca	tcggcacg	cttgaagc	tggttttct	120
cgaagcaat	cttattat	tgtaaaca	ggaaagat	accagatg	aacagacca	180
gattctcag	gattaaag	attaagag	gtagctgg	ctagagtgt	tgacgaacg	240
aaggaagaa	gcatctct	aatgaaag	acagaggg	aacgggaaa	aatcaatga	300
ttgttaaaa	acattga	gagattac	actctag	aagaaaagg	agaactag	360
cagtatcag	agtgggata	aatgagac	gccctgga	ataccatt	caatcagg	420
cttaacgag	ctcgtgcc	acttgatg	ctttctgt	agcgagag	tagtggaga	480
aaatccag	aattaaga	tgctcanc	gatgcaag	ataaatgg	ggatatcg	540
cgccaagt	gagaattg	aacaaaaa	tcagctat	aagaagaaa	agaacagct	600
aatgctgaa	gacaaga	cn gattaag	cag aggact	aat tggagc	ttaa agcccc	660
ttacaagat	aactaccg	gc aatagt	gaac aaagg	aaaacc	gttttttaa	720
aanctgctt	g	aaaaaaa	aaactc	ggcctnta	n t	761

&lt;210&gt; 432

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 432

gnngantnn	tcttatt	atc gtgng	ctct nactnn	ctct aaatana	att gtgtt	gnngg	60	
aattcggc	ac gaggcc	accg aagctt	cagg atgacat	ctt agactc	tctt ggtcag	gggga	120	
tcaatgag	tt aaagact	gca gaacaa	tca acgagc	atgtt caggcc	cc tttgtg	cagt	180	
tctttgtc	aa gattgt	gggc cattat	gctt cctatat	caa gcggga	agca aatggg	caag	240	
gccacttc	ca agaaaga	tcc ttctgt	aagg ctctg	accc caagac	caac cgccg	atttg	300	
tgaagaag	tt tgtga	agaca cagctc	ttct cacttt	tcat ccagga	agcc gagaag	agca	360	
agaatcct	cc tgcagg	ctat ttcca	acaga aaatac	ttga atatg	aggaa	cagaag	420	
agaagaa	acc aaggg	aaaaa actgt	gaaat	agagct	gtg	gtgaata	aga	480

ctacacacca	tttctggact	tcagccctg	ccagtgtggc	aggatcagca	aaactgtcag	540
cttccaaaat	ccatatcctc	actctgagtc	ttggtatcca	ggtatttggt	tcaaactggg	600
gtctgagatt	tgatccctg	gnattggatt	tcttaaggac	ttttggangg	ctcttgacac	660
catgcttcac	agaacttggg	cttcanaagc	ttcanttttt	tgcanagggtg	ccccagggtta	720
ggaaaacagt	tntncttggt	ttgtannt				748

&lt;210&gt; 433

&lt;211&gt; 769

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 433

gggnaaaagt	ttnnnnannng	ggnagnnnng	ntnnaccntt	cctattactt	tggagctcga	60
actcgcncca	canannnagt	gnctgtngct	gttttgcaga	tgaggaaaac	tgagggtacag	120
aattcttagg	gaacttaccc	aaaatggctt	ttctgcactc	tgcccttttg	tattgtccca	180
tgtgaattgt	ttaaaactta	tgtgtatagt	ggcatgagta	ggtgatttca	gaaacagaac	240
tcacttttgt	tgtttggctt	taaaattagg	aacttttctt	catctgggct	tcatttccct	300
gcaccttccc	agctttctag	tcattgcaagc	cacatgtctc	cacgtgaggg	gttcattgga	360
aagcagccac	agagccaccc	cctggctggg	ttcttcccca	gctctgcttc	ctccttcccc	420
aagtcttgca	gctgctctct	ccatggcaga	accacttctc	cccttactgg	aggggaggtc	480
cactgaacaa	atccaggaga	ggaatcattg	tgttttccac	agaagagaaa	gtacactgga	540
ctttctgtgc	aacctgttac	tacattttca	caganactca	tatttgtgca	ntgtaactca	600
atttgaaacc	cagcaaaatt	aggctcccgt	gtctccataa	aaggccacca	tgatggtaac	660
cgttggactt	caccttgtgt	ttnggacana	ngctgattgg	attttaccca	tcattcacanc	720
cgtgtcttac	attctcnttt	cctgggcttt	ggaccctgn	tanaaaaaa		769

&lt;210&gt; 434

&lt;211&gt; 764

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 434

ctanccttcc	taaannctng	gctactcgnt	ctttctnman	ganncnnttg	cgatncgaat	60
tcggcacgag	caccttgcc	ggccaagggg	ctagacctcc	caggctaagc	ctcagattca	120
gtgcaggaca	caagctcatg	ccccgtctt	gccagtga	cttgaagcct	cccgacttcc	180
acagagtgtc	tcaggacaca	ttttgagtgg	tattttcttt	tctttttttc	ttcttttttt	240
tttttgagat	ggagtctcgt	tctgttgccc	aggctggagt	gcagtggcct	gatctcggct	300
cactgcaacc	tctgctccc	aggttcaagc	gattcttctg	cctcagcctc	cagagtagct	360
gggactatag	acatgcacca	ccacgcccgg	ctaattttgt	atttttggtc	gagacggggt	420
tttgccatgt	tagtcangct	ggtcttgaa	tnctgacctc	aagtgatcca	ccactcggcc	480
tccaaagtgt	tgagatgaca	ggcacgagcc	accagcccaa	cctgagtggg	attttcttta	540
gggaccangt	agactttaaa	acgagggtaa	gagaaaaagc	ccagtgggtc	tttctgangg	600
taaataaatt	tctgcccagg	aaacnttncc	aagccccaac	cagcaagcca	acccttaaaa	660
aaaaaatcac	ttcgtgttcc	ccaangggan	ctttnttaaa	gctttggggg	cttccaggna	720
aatcatttc	cagtnnaant	ttggaagaat	tcannagnat	ttnt		764

&lt;210&gt; 435

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 435

```

gnnnnntttc taatgtggnn nngnnngnta annttctaaa ncttgggntc tegtcttttc      60
tncagatncc ntcgattcga attcggcacg agggatcctt tccagacaga agacccttc      120
aaatctgacc catttaaagg agctgacccc ttcaaaggcg acccgttcca gaatgacccc      180
tttgacagaac agcagacaac ttcaacagat ccatttggag gggacccttt caaagaaagt      240
gacccattcc gtggctctgc cactgacgac ttcttcaaga aacagacaaa gaatgacca      300
tttacctcgg atccattcac gaaaaaccct tccttacctt cgaagctcga cccctttgaa      360
tccagtgatc ccttttcac ctcagtgctc toctcaaaag gatcagatcc ctttggaacc      420
ttagatccct tcggaagtgg gtccttcaat agtgctgaag gctttgccga cttcagccag      480
atgtccaagg gtgcctgggg aagagccact ggcgatgta tctttgggtg tactccagtg      540
ttgaacanag agctggtcag aggcagtgc tgcganagag acattaataa gggaaatcctt      600
tgaatcccta ancagcanca gcttttctga nggggccnat gatgccagtg acctnttcan      660
ggnaagtctg ggacattggg accaccctgg ggggaagaac ttgtgggatg tggtctttct      720
tttatgaata aagtactttg agttggttgn aatcn                                     755

```

&lt;210&gt; 436

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 436

```

aaggctggnn nnnnnntgc nnnncttct attantctgg gggctcgtnc tctctcnann      60
nagnnaggcg ntgngaattc ggcacgagct caagaaaagg agaaagtgtt tttgtatgaa      120
aattgaggaa atattgggga acgctgcctt gatgatgaca cttacatgaa ggatttatat      180
cagcttaacc caaatgctga gtgggttata aagtcaaaag cattgtagaa gacttaacaa      240
gctgcagata accatgtgga cttctgtcat aattcttgcg gagtcaagag tgtaaataaa      300
agaaatggca ggactcatat tattcagttg tcccaagtat ttaaaaatga ctctcttaag      360
ccttaaaaag tcatagattt gtgctgctgc cagaattata ttaattatta ttaattggtat      420
tattagaaaa aaaatttctg gaggtagagt naagangctt aattagtttg tgggcagttt      480
tcatatgctc tgtgaaatgt gtccagatgt gacataagtt ttttttttta atatggngga      540
aatgncttct ctttccattt cttttctcct aaaaatcata tatactggga atatatgcct      600
ctnttacctc tattaccctc ctcacattta ccttttccca gttngggttt gctttttnac      660
caaaaagatt ccaatnccna ggtattggca agtntnaaa accgcccntt aaacatccct      720
aatttcncag natccnncn ttgccaaatn ttngtntcnn                                     760

```

&lt;210&gt; 437

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 437

```

ggnnnnngnn ngntnncgtt ccctattant caggngctcg ntctntctcn annnancnng      60
gcgtgtncga attcggcacg aggatcttcg aaactcttca gctacttgcc cttttttatc      120
tgaaaccatc ataccttctg aaagaaaaaa gcatatcttc attgacataa cagaagttag      180
atggcccagt cttgatacag atgggtccatg atatatatgg agagtggcat tgtgaagata      240
acatctttag atgggtcatg atacctctgc ctgcccagat ctcagcatga atttacagta      300
cattttttgt gtaaagttag ccagaagtca gactcatctg cagtgttgtc agaacaatat      360
aataaagccc caaaagataa actagttaga aaaactggca aaatctgtat acgtggaaat      420
ttaccaggac agagactgaa gaataaagaa aatgagtttc attgccagat catgaaatcc      480

```

aaagaaactt	taaagaagat	gagttgtgta	aatggaactg	aagggagggg	aagaactgcc	540
ttcgccctgg	acaaagcaca	catgtgtata	cacatgggtc	aagcagtgc	ggtctgtggc	600
tgncgtgtcc	gangaatgga	aatatccctg	gcttttagcac	ttcattttca	taataaaaatc	660
agcaattntg	tctaaaaaaa	aaaannnana	aaaaactnga	gcctntanaa	ctntagtgag	720
tcgtattacg	tagatncnna	catgataa				748

&lt;210&gt; 438

&lt;211&gt; 823

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 438

taatccttnn	tattgntcgg	gtactngntc	tntctcnaag	annntntcgt	tncccccagg	60
tagctgagac	taccacacac	ttgggtcccag	ctacttgagg	ggctgaggtg	ggaaaatcac	120
tttgcccagg	aattcaaggc	cgcagtgagc	tatgattgca	ccactgcact	ccaggcaaca	180
gagtgaagcc	ctgtcttaaa	aaaagaaggg	agaaaagtgc	agatgggtgat	gaggtctggg	240
ggggaaatag	agaatgggga	tcaggagtgt	ggatgggtgt	attccctcac	caagaggtga	300
catgttgagc	agggaaactg	ggaggtgagg	gtgtgacccg	tgtggaaaatc	agggaaaagc	360
attnacgct	gagggacagc	caatgcanag	gccgtgaggt	ggccagtgcc	actgagcagt	420
gagcttgagg	tagggggcan	gtgangaggc	tggagagcgg	ggtcagacaa	accaatatgc	480
ttatttaaaa	caaggttgtt	ncagcaccct	tgctttaaag	ccttgagcct	gnaanctnga	540
aaaatttggg	cacnttcaaa	agcanggang	gaaaccaaaa	gaagattggg	agggaaaagc	600
ccttncttcc	ccttancagg	aaatgaagtt	nccacccttn	aaaacaggnc	caggaccttt	660
ttgggacctt	tttggccttt	tgggtccctt	gaatcctctt	ggtngcttnn	gaatnaaaag	720
gnaaaagggg	cctttaaggg	gggatcccat	tntttccaaa	attcaaaggg	ggctttccct	780
gggcttacct	aaaatttctt	ggncttaant	aaaaaaattt	ntt		823

&lt;210&gt; 439

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 439

gnnnnnngntt	ctaagtctgg	nnnnnnnngg	taccctttcc	aaaacctggg	ctctcgntct	60
ttctncangn	agccnngcga	ttcgtctgtc	tgggtatgtt	tattttaagt	gaacctttgg	120
atctatcttt	aactctcttt	attgtgagtc	taaattccaa	ttctgcagca	gatcagtaaa	180
ctcacagtat	ttttcctgtg	gaaatctatt	caataaggaa	accaagacag	gatantaaaa	240
tttaaaaaaa	ancaactttg	aattcccctg	cctaggtctt	ccagttgttt	tccagcgcct	300
acctcaggta	tgactttgct	agccggggac	aaaattagca	ccttccgatt	ctctagtcca	360
aatgaacttt	ggctaaataa	aaaattatta	tactacataa	taaagttnc	gatagcagga	420
aatgcaagag	ctaggagatt	cctagattat	atctggccaa	gccaataacc	ttaaacatcc	480
acctggaaat	cctctacccc	ctcttctgag	ataatttgcc	cagccctttc	ttccacacac	540
ctcactcaat	gtcaccctct	tctaataccc	aaaactgttt	ttgtggcctt	ggtagcctat	600
agtagtttct	cacatctttt	cccctanact	tttctgtttt	cagtttcaga	ccaaaaaac	660
tcttcaactt	ttttccagtg	gggtcttctt	taccagtaac	tttaccactt	gnaatcttat	720
ttcattgaaa	aaaccttaaa	tgggntggga	aaaggcttgc	cnncann		767

&lt;210&gt; 440

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 440

nagnnnnntt	tctaatgctt	ggnnnnnnnn	tcnatgcttc	caaaagcngg	gngctcgttc	60
tttctccaag	atncnngcgn	tnccaattcg	gcacgaggat	ggatgagact	gttgctgagt	120
tcatcaagag	gaccatcttg	aaaatcccc	tgaatgaact	gacaacaatc	ctgaaggcct	180
gggatttttt	gtctgaaaa	caactgcaga	ctgtaaat	ccgacagaga	aaggaatctg	240
tagttcagca	cttgatccat	ctgtgtgagg	aaaagcgtgc	aagtatcagt	gatgctgccc	300
tgtagacat	catttatatg	caattcatca	gcaccagaaa	gtttgggatg	tttttcagat	360
gagtaaagga	ccaggtgaag	atgttgacct	ttttgatatg	aaacaattta	aaaatcgttc	420
aagaaaattc	ttcagagagc	attaaaaaat	gtgacagtca	gcttcagaga	aactgaggag	480
aatgcagtct	ggattcgaat	tcctggggaa	cacagtacac	aaagccaaac	cagtacaaac	540
ctcctacgtg	gtgtctactc	ccagactncg	tacgccttca	cgtntcctn	catgctgang	600
cgcaatacac	cgcttcttgg	gtcangaatt	agaagctact	gggaaaatct	accttccgac	660
agaagagatc	atttttagatn	taccgaatga	anaaaagcttg	cattagtgc	attgaaaggg	720
aaataaaaat	tcctacagtc	naaaaaaaaa	at			752

&lt;210&gt; 441

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 441

gnagccngat	tccaaaacct	gggnnccgat	ccaatgcttn	ccaattactt	gggagctcnn	60
actngcncna	ncaanctngc	cntgcgaatt	cggcacgaga	agnaggcgga	gcttgcgagt	120
agctgagatc	gcgccactgc	actccagcct	gggcaacaga	gtgagactct	gtctcaaaaa	180
aaaaaaaaaa	aaatggaacg	cagggcaaga	actcgtnttt	ggaaggagat	gggggaaagg	240
anccgtatta	tacctatgtt	gnatttgcag	gcaaatgaga	tgganccctc	tctgtaaaga	300
agagtcattt	gtgcaagtag	acggggctctg	tgggtgcang	ccctggaggg	gcacacaatt	360
gcctgnangc	ttctgtgana	tcgggagang	gaggagaagc	agtctcttga	caaaataaag	420
tattttttatt	cattngtatt	tattaaatga	aaaaacaatc	ccatgggtgtc	ccttggtgtg	480
ggtggaacct	aatgactgtt	gaaataaagt	ctgngttttc	ccttcaaaaa	aaaaacncnn	540
anaanaaaaa	ctcgagccct	ntaaaacctn	tnngngagtcc	gnattacctn	anatcccnga	600
cnttgataag	gatccattga	tnaantttgn	cccaacccca	actnngaagt	ccnngaaaaa	660
aaattgcttt	atttgggaaa	tttgcnaatn	ctttgcttta	ntttgnaccc	antttancnt	720
cannnnccaa	gttacnancn	ncaattgcnt	tcatttangg	ttcaagggttc	aaggg	775

&lt;210&gt; 442

&lt;211&gt; 804

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 442

gagnnngntt	ctatacctgg	gnnccgatcca	aancttnccct	attaccttgg	atcttnngct	60
atctcnaann	aaaangcttn	cgaattcggc	acgaggccac	ctgcactgag	gtctgggccc	120
ggggacaggg	tgcttttagcc	aggcttgtct	gcgcctcagg	gaaggggtgag	cagcccaggg	180
accagatgca	agttggtggg	cccctccacc	cntccnacgc	cactccccag	tgtgctgggt	240
cctaaccagt	cgctctatgg	gagcagtcag	ccttcctctc	ctcctcaggg	cagctctccc	300
acctgctgnt	ccccgcacac	agaacctcat	tgtcttgagc	agttgcttat	tacctcagttg	360
ttgaaaaact	agcatgtgan	ggccggggcgc	ggtgggtcac	gcctgtaatc	ccaacgcttt	420
gggangccaa	ngcgggtgga	tcatgangtc	aggagatcaa	gaccatectg	gcttaacacn	480
gtgaaacct	gtctctacta	aaaatataaa	aaagtancca	ggcgtgggtg	tggcccctgt	540
agtnccaann	tacttgggaa	gctnangcan	gaanaatggc	ntgaacccaa	gaaggaagaa	600

```

cnttgcantg aanccttaaaa ttgcgcccac tggaatttca aaccttgggc cnanaanaat 660
tgaagaatcc cgtcttaaga aaaaaggaaa aaanttttnc nttntnaaag gcccggccac 720
aantnggctt taacgcccctg gtaaatnccc aancactttt tggggaaggc ccaaaggcaa 780
ggccnggatt caatttttna aggg 804

```

&lt;210&gt; 443

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 443

```

gnagccggat cttattattg gcnncgnttt aatgctggct aatntntcgt aatncttggg 60
nnccccaann annnaggngg ggngaattcg gcacgagcac catttttatt ttgatgctta 120
cactcattta ttctgttttt gtaaaacagt ttcaagaatt taaaaatcct tccagttaat 180
agagcttttg ttattatatt ataattttgt aaaccactt tgttttccc actttaaagc 240
cacagggtcg actcatggat gatacctcta ttgctgctgc atgatgttca agaccggccc 300
ttggctgttg ttacagagat gttgggcaga gctatgcagg tgtttcattg ngaactctag 360
ctttgatcat ggtaaaaagt taaccctttc ttttttttaa tggatgttat accaactatt 420
cagaggactc atacttcaaa aatattagga aaatctgtct tatagttctc taataaatat 480
ctgaaatctc aagtaagaca tgaaagaatg tcagaccatt gntattgggtg aaagtcattt 540
gatgaatggn aaattctatg aaaagtaagt ggatttgcac ggattaatat cagggaaaat 600
ttaagccttc ccaagtgtga ctgggcaaaa gagagccaga tgccccagc gcctgtgccc 660
ataaagtctc cgaatcccc aatgggggtct nttttcaaaa acttggncca gacccggaaa 720
ataaaancat tcntcataaa ttcaannggg gncctcanga aacacnttcc cccancaacc 780
cttngg 786

```

&lt;210&gt; 444

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 444

```

gnagnccggt tcnnangcnt nggctnnatc caatgctggc taaagttcna ananctggca 60
acnccaggan ncangcgttg cgaattcggc acgaggagga attacaggta gcaaattatg 120
gagttggagg acagtatgaa ccccatTTTT actttgcacg gaaagatgag ccagatgctt 180
tcaaagagct ggggacagga aatagaattg ctacatggct gtttnatatg agtcatgtgt 240
ctgcaggagg agccactgtt tttcctgaag ttggagctag tgtttggccc aaaaaggaa 300
ctgctgtttt ctggtataat ctgttgccag tgggagaagg agattatagt acacggcatg 360
cagcctgtcc agtgctagtt gcaacaaatg ggtatccaat aaatggctcc atgaacgtgg 420
acaagaattc gaagaccttg tacgttgtca gaattggaat gacaaacagg cttccctttt 480
tctcctatng gtgnactctt atgtgctgat atnccatttc ctagtcttaa ctttcaggag 540
tttacaatng ctaacactnc atgatngatt cantcatgaa cctcatccat gttcatctgn 600
ggcaattgct taccttgggg gntcttttaa aaagtaccac gaaatcatca tattgcatta 660
aaacccttaa agtttctggt gggnatcaca gaagacaagg ccnaanttna aagnggagga 720
attttattat ttaaaagaac cttttgggtn ggatnaaaan 760

```

&lt;210&gt; 445

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 445

tggtgcccgt	tcttantctg	ngctctcgtc	ttcctttctta	tacctgggca	ncncttgccg	60
gccccnaggn	tcccangnag	ccnngcngng	ncngattcgg	cacgagattc	caaagggtttc	120
aaagaacttg	gtcataaata	tgataatgag	aagacaaagt	atttatatta	aaacagttta	180
gtagccttca	gttttgtgaa	aatagttttc	agcacagaaa	ctgacttctt	tagacaaagt	240
tttaaccaat	gatgggtgtt	gcttctagga	tatacacttt	aaaagaactc	actgtcccag	300
tggtggatcat	tgatggcctt	tagtaaattg	gagctgctta	atcatattga	tatctaattt	360
cttttaacca	caatgaattg	tccttaatta	ccaacagtga	agcactacag	gaggcaactg	420
tggcattgct	tccttaacca	gctcatgggt	tgtgaatggt	ataaaattgt	cactcagata	480
tatttttttaa	atgtaatggt	atataagatg	atcatgtgat	gtgtccaaac	tatggtgaaa	540
agtgccagtg	gtagtaactg	tgtaaagttt	ctaattcaca	acnttaattc	ctttaaaatn	600
cacanccttc	tgctctcgtg	tttggaagtt	gtcagtncaa	ctcatcaaag	aaaactgcct	660
aatntnaaaa	tcatattntg	ggaataattt	ccctcttttg	tagtctgccc	aagatcctta	720
aagattggat	ttttattact	atttaacca	gtggattaat	n		761

&lt;210&gt; 446

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 446

tgggnnnnngn	ccnaangcng	gggannnggt	ccccgttcca	anactggaan	ncttggcann	60
cgaactcgct	cnannagnaa	ggccgggnga	attcggcacg	aggccccgct	ccatgagcag	120
tgactcccca	gctcctcctg	gcaccagtc	ccagggtct	cctggttgta	gttccctgctt	180
ttcttcttgg	aaattcctcg	tggaacctga	gatctttacc	ctaaaatagt	tctgttgaat	240
ttcaccctgg	caatgtaaat	tgatagctta	tcttcacaga	tgccagacaa	tggacaactc	300
accatcagtc	ctctgctcac	ctgagacaaa	tgcattgtctg	attgcttcct	ctgccctatt	360
ggntatgtga	aaatgcagat	tcaactgagc	agactaaggc	atcagtgact	ggctcctctac	420
ctgcctctca	catggagatt	gggtattcag	tgaaggctg	atcaaagacc	caaaggaatg	480
caacagttta	tctcttatct	acctatgacc	tgcganctgc	caccaccccc	agntggngcg	540
cctttccaga	cagaaccagt	gtacatctta	cacgtattaa	atngatgtcc	cnggggctcc	600
cnaanangna	tcaaacaagc	ngggcctcga	ccaccttggg	cacatatccc	nanngacatc	660
annctggagg	ctngngncac	tggcattggc	cctnaccctn	ggcaaaataa	accttctaaa	720
attggnaaaa	aanaaanaa	aaaaacctng	nccctntna	naacnntacg		770

&lt;210&gt; 447

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 447

tggtatnntt	tnaangctgg	nngnnnggcn	ccgttccaat	gnctggganc	nttggcaatc	60
gctctttccg	nangatccca	tcgattcggg	ctgatgcagg	agaattgcta	aaaccagga	120
gggagaggtt	ncattgagcc	gagattgcgc	cactgcactc	tagcctgggc	gacagagcaa	180
gactccgtct	cgaaagaaa	aaagagaaa	gaaattcccc	aggggaagtac	ctcggcttat	240
ttcataaaca	ggtactgaag	gaagcagagg	catgtggagg	acttccccac	ctcgtgcagc	300
tatttggggc	gtggcatctg	aaatttctta	tttcagagtc	acctcttga	tgaccttggc	360
agtgaactgc	agtcattctg	ttaggccttt	ccatggccca	cgtcaatgcc	ggatatttctg	420
tttggtgcac	atttgatttc	cttggtgttg	gcatttagaa	ggccccccgt	ttcccagatc	480
acaccacggg	catggaccac	agagattgca	tcttgtagt	ctgtagaaat	ggtcaaggcc	540
ttgtcctctc	ttaagtccag	agctcangtt	aatgcaaaat	tttncggnc	atctgtgctg	600

aaatcccttt	ggggaagctc	ctggctgggt	tccctgtaggt	aggacagcta	cacgtnctgc	660
cctttattgg	cttcttttca	tgaagctcct	gccatntacn	aaacatgtct	cccttcttga	720
atcacatctc	tggtattgna	actctanaat	cgccccgg			757

<210> 448  
 <211> 770  
 <212> DNA  
 <213> Homo sapiens

<400> 448						
gggtgnnnng	tttctaattg	ttggtngnnc	nggnccnacb	tttctaattg	tccgaanggc	60
ttggctactc	gntctttctn	cangnagccc	ntcggtncca	attcggcacg	aggtgtcttc	120
atcttaccca	gtggaacctc	agaaattaaa	ttctccagaa	gaaactgctt	ttcagacacc	180
aaaatctagc	cagatgcctc	ggccttcagt	gccaccatta	gttaaaacat	cactgttttc	240
ttcaaaatta	tctacacctg	atgttgtag	cccatttggg	acccatttg	gctctagtgt	300
aatgaatcgg	atggctggaa	ttttgatgt	aaacacctgc	tatgggtcac	cgcaaagtcc	360
tcagctaata	agaagggggc	caagattgtg	gacatcagct	tctgatcagc	aaatgactga	420
atcttcta	ccttctccat	ctacctctat	tagtgctgag	ggtaagacaa	tgagacaacc	480
cagtgtgatt	tattcatgga	ttcagaataa	acgtgaacag	attaagaatt	tcttgtcaaa	540
acgggtgctg	ataatgtatt	ttttcagtaa	gcaccagag	gcctncattc	aggctgtttt	600
ttcagatgcc	caaatgcata	tttgggcatt	agaaaggtct	gtcgactta	gtagcagcat	660
cattttacag	aggatagatt	tggagttgtc	cagacgacac	taccagctat	ccttaatact	720
ttgttgacac	ttgcaagang	cagtcngaca	agtactttaa	cttcctcatg		770

<210> 449  
 <211> 792  
 <212> DNA  
 <213> Homo sapiens

<400> 449						
ngagaaangt	ttctaattgt	ggnnnnngna	gntcancctt	tctaattgtc	taataacttg	60
ganntcgaac	tntcncnaca	cagnnangcn	ntgcgaattc	ggcacgaggn	cnnctcnatn	120
atnacttgnt	cncancggnc	tggcatcnac	ncgncacacc	tacntnagcg	cntttagcgg	180
caatatncac	ctnntnaaac	ccnnnagtc	cagggctctg	ccnnnnnact	gntcaactga	240
cnaacnacnn	nctancncaa	cntnnnnnta	ngccnctgnc	tgntctctatg	gcacctnncc	300
tncctncn	cntnaccnc	tacgtctcagg	gctatataca	atgggaacct	tnccaacagt	360
aanccntgga	tctnaggnat	ggccttgnc	tggcgatca	cagccttnna	gcntatcagn	420
atcttgagga	agacaccatt	ccgtcccnga	ttntgaccaa	ncnctcggat	gtgnctatgg	480
gctcnattga	ggnacaacaa	ctnnnactgc	nnataggcca	tcctcnnnan	nctacacatg	540
ngactttncn	nnncatntna	aatgnnnana	tgtctctcnc	aagcatcacc	cnetgtccct	600
ncgncntcnt	ggaagacctt	ctgnncaact	ganctccttc	ntgnnnnnnn	ngattnttnc	660
nnncnnaata	tnctncccc	aatgnccttg	tnnnnattt	atnangggnt	ttccaatttg	720
ggntaattca	ntnccnccg	nannctannn	ncccatnaac	cntcngngcc	ttcttgnaac	780
cttttnnct	gg					792

<210> 450  
 <211> 848  
 <212> DNA  
 <213> Homo sapiens

<400> 450

gnatgncccg	atttccttaa	tgatgggggn	nnnnngagcg	anncttccga	aantttccaat	60
annctgggng	ntcgcaactc	ntcnanaca	gnaaggncgn	gggctttgct	ctctccattc	120
caagttgntc	tctgttctag	aaagcagatg	tagtagacat	ctactgttgt	tgctgaaca	180
gaatcccttt	gtcctttttt	tgntaaaagt	actcatccct	aatattcatt	gtncgtgaag	240
gactgaaaat	acagaactca	caccatgatc	ggccgggaca	atcagattat	ttcattccnc	300
agcaaacgga	gatcganccg	aaaagtggaa	anatgagcnc	ttctttggng	ttggcatatg	360
gacctgaga	gaaagaactn	tnattntttc	tcttggaactg	caataaagta	tagctgccta	420
aaatacgntt	cctgacactt	ggaggnttgt	ccacaatcgg	ngaaataaag	gcgagaccgn	480
acactggatg	aaaaaanaa	gnnnccngnn	gaanaccac	tnnnccannn	nccnnnccnn	540
tncccanng	nnganccnnn	tanccgnnan	nagggcnnng	cnntngcnnn	nnngccnnnn	600
nnnnnngggn	aaaccnncnn	gnnnnnccnn	nnnnnnnnnn	nnnnannnnn	nnncnnncng	660
nnngnncn	nnnnnnnnnc	cccnnccncc	cnnccnccnn	nggnaanncc	nnnnnnnnnn	720
annnnngggn	nnnnnnnnnn	ccnnnnnnnn	cannnnnnnn	cnnnnngggn	nnnnnnnnnn	780
nnnnnnnnnn	ncnnngnnnn	acnnnnngnn	nnnnccnnnn	nnnnnnncng	nnnnnnnnnn	840
nnnncccc						848

&lt;210&gt; 451

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 451

gnnnnnnnntt	tcctaaatgc	ttgggnnnnn	nnngagnnn	nttnccnagt	ttcctaanta	60
gcttnggcna	ctcgttctnt	ctncangcag	nnntgctgn	gnccgaattcg	gcacgagcat	120
tcctcctttg	ttaacgaagc	aacattttaca	caagatggac	attacattat	tagtgcattc	180
tctgatggca	ctgtaaagat	ctggaatatg	aagaccacag	aatgttcaaa	tacctttaaa	240
tccttgggca	gcaccgcagg	gacagatatt	accgtcaaca	gtgtgattct	acttcctaaa	300
aaccttgagc	actttgtggt	gtgcaacaga	tcaaacacgg	tggtcatcat	gaacatgcag	360
gggcagattg	cagaagcttc	agttctggtg	aaagagaagg	tggggacttt	gtttgctgtg	420
ccctctctcc	cgtggtgaat	ggatctactg	tgtaggggag	gactttgtgc	tctactggtt	480
cagtcagtca	ctggcaaact	ggagagaact	ttgacagtgc	acganaagga	tgtgattggt	540
attgcacatc	accctcatca	gaacctgatt	gctcctacag	tgaagatgga	ctcctaaagc	600
tctggaaacc	ataattcaac	ttttcttttt	taaatcaact	cgaaagcatg	tncttaaagt	660
aacatattca	tgtaangggc	tttttttttt	tgncactttt	ctaagcaa	agatggctga	720
attagtcacn	gaataaattt	gngaaaatca	tggttaaatn	ccaac		765

&lt;210&gt; 452

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 452

nnngnnnnnn	ntttcctaaa	tgcttggggg	nnnnnnngnn	nnnnnttctn	atgttcttan	60
ngcnnnggng	ctcgttctnt	ctncacgnng	ccngtgcgg	gnccggtctga	ttgaaagctg	120
ttcaggttta	tcattgcaaat	cctcgctctc	ggctacggct	ggctgaatgc	tgcatgtctg	180
ccaataaggg	gactttctgaa	caagaaacta	aaggccttcc	cagcaaaaaa	ggaattgtnc	240
agtctattgt	tggtcaagct	atcatcgtaa	aatagttttg	gcatcacagt	ctatacagaa	300
tactgtttat	aatgatgggc	agtcttcggc	cattcctgta	ccagtatgga	gtttgcagcc	360
atatgtctca	gaaatgcctt	gttgctgctc	ctgaagaaca	gcaagatcca	aagcaggaaa	420
atggggctaa	aaatagtaat	caattaggtg	ggaacacaga	gagcacgaaa	gcagtgaac	480
ttgcagcagt	naaagccatg	atggagatna	attcattcca	gcttcacctt	cttctccatt	540

gagaaaacag	gaattagaaa	acttaaagtg	ctccatactt	gcttgacgtg	cctacgtggc	600
tctggccttt	gggtgatacc	tcatggcttt	gaatcatgcn	gatnaacttc	ttcagcagcc	660
caagctgcag	gatctcttaa	gttttgggac	atztatatgc	tgcagaaccc	ttatcttctt	720
cgaacgaatn	tctgtgccnt	tctcacttga	ccccgagaat	gtncct		765

&lt;210&gt; 453

&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 453

gngtnnnnnt	ttctaangtt	cntaatannt	tnggctactc	gttctttctc	caggnatccc	60
ntgcgattcg	aattcggcac	gagagaaacg	ttctcaggtt	gaccagctgc	tgaatatctc	120
tttaaggagg	gaagaactta	gtaagtcatt	gcagtgcatg	gataacaatc	ttctgcaagc	180
ccgtgcagcc	cttcagacag	cttatgtgga	agtcaagagg	ctacttatgc	tcaagcagca	240
gatactatgg	agatgaatgc	actgaggacc	catagaatac	agattctaca	ggggattaca	300
agaaacatat	gaaccttctt	gagcacccca	ggttttggca	ttagaaaatg	ggtacccttt	360
ggttcaaaaa	tgaacaaaga	aagccttaga	tttgatggg	ggaacctgat	ctgtccagtc	420
tagaaggatt	ccagtgggga	aagtgtttcc	atttccttng	tcccctggct	tggccaagga	480
aagcgaaagc	cctttcttga	anagcaaccg	tggatcattn	gaccaggaac	ttccttctgg	540
ggtattaagc	ttctttcaan	tggaaaggga	aggttccang	gccaaaggaa	aaatggaagc	600
cccccaaccng	atgggtttca	ccctaantaa	cctcaattgg	aagggttgg	accaagaacc	660
cnggaaaggc	nanccattgc	acccttaaaa	ncaaggaaag	tggaccacct	ttggggcttg	720
ncnttcctnt	ccgaaccagg	ttgaaaangg	gcttgaaaaa	tggttgctta	cccaaaaggg	780
cgnacnttaa	tggcaccaat	tattcctntg	gacnnttttt	aatanccttt	ngn	833

&lt;210&gt; 454

&lt;211&gt; 737

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 454

gnngnnnnnt	ctaagttcct	aatnctgggc	tactngttct	ttctgcaggn	atccccatcga	60
ttcgcaaaaa	tcaatgtgga	ctgaacataa	atcacctgat	ggaaggactt	actactacaa	120
cactgaaacc	aaacagtcta	cctgggagaa	accagatgat	cttaaaacac	ctgctgagca	180
actcttatct	aaatgcccc	ggaaggaatn	caaatacagat	tctggaagcc	ttactattat	240
aattctcaaa	acaaaagaat	ctcgtttggg	ccaacctaaa	gaacttgagg	atcttgaagc	300
aatgatcaaa	gcttgaagaa	agcagtaagc	aagaagagtg	caccacaaca	tcaacagccc	360
cagtccctac	aacagaaatt	ccgaccacaa	tgagcaccat	ggctgctgcc	cgaagcagca	420
gctgctgttg	ttgcagcagc	agcagcggca	gcagcagcag	cagctgcagc	caatgcta	480
gcttccactt	ctgcttctaa	tactgtcagt	ggaactgttc	cagttgttcc	tgacctgaag	540
ttacttccat	tgggtgctact	gntgtagata	atgagaatac	agtaactatt	tcaactgagg	600
aacaagcaca	acttactagt	acccctgcta	ttcaggatca	aagtgtggaa	agtatncagt	660
aatctggaga	agaaacatnt	taaccaggaa	actgtanctg	atctttacttc	caaaaaagaa	720
gaagaggaga	gccacct					737

&lt;210&gt; 455

&lt;211&gt; 718

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 455

ggnnnnnnntt	tnnnngttn	cntaaaaanc	tgggctactc	gttctttctn	cangnagccc	60
ntgcatncg	aattcggcac	gaggatgagg	agtgtttaat	cattgatata	gaatgtaaaa	120
ataatagtga	tggaaagaca	gctgttggtg	gttctaactt	aagttccaga	ccagctagtc	180
caaattcttc	ctcaggacag	gcttctgtag	gaaaccagac	taatactgct	tgtagtccctg	240
aagagtcattg	tgttttaaaa	aaacctatca	aacgagtata	taaaaaattg	atccagttgg	300
agagatttta	aaaatgcagg	atgagctctt	aaagccaatt	tccagaaaag	taccagaatt	360
gcccttaatg	aatttagaaa	attctaaaca	gccttctgtt	tctgagcaat	tgtctggtcc	420
ttcagactcc	tctagtggc	ccgaaatctg	gatggccttc	tgcatctcag	aagccaaaag	480
gacgattgcc	atatgaactt	caggactatg	ttgaagatac	atcggataac	ctagctcctc	540
aggaaggaaa	ttttggttat	aagttattta	gcctgcaaga	cctgttggtc	tcgtcgctgc	600
agtgtncaga	ggatagagnc	agaccacgtt	ctaaaacnga	gaaatcagaa	gacatttnca	660
gttatgtctc	caaaagtgg	tntcagctgt	atgagttgac	tctgctgaaa	gtgacttg	718

&lt;210&gt; 456

&lt;211&gt; 739

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 456

gtggnnnnntt	ctnnngtttc	aatangntgg	gtctcgttct	ttctnnacga	tcnnntgcga	60
ttcgcttggg	aggctgagtc	aggagaaatt	gcttgagccc	aggagatgga	ggttgagctg	120
agccaagatc	atgccactgc	actccagact	gggcaacaga	gggagactcc	gtctcaaaaa	180
ctaaaaaaaa	aaatncattt	agtataccgg	ggggtggggg	ggagaaataa	tgttattttcc	240
tatgcgaaat	gacgtgtatc	cctgtaccca	tgggtaaatg	taaatatact	gtgtctcttt	300
tgggagagcc	ttttagtaga	ggagtcttat	atgaagtctc	tcataagtag	ttcacttgag	360
ttttgcagtt	tgaatcttta	aaggagcttt	aattgacatt	tattatacca	attaagcttg	420
gaatggggca	atggatgcac	ttccaaaacg	tgtgaaagcc	taacagctta	tattgctgaa	480
tgagaatctc	ctgggtgtaa	tttancactt	agggaactgc	gtgaacactc	ccagccatta	540
tgatgctggt	accagcttta	ntgtntaaat	gccatganta	ttctttctgn	tctgttttgt	600
gctctcttgg	tncattttatt	ttacccttta	cngaataatt	tcttgtaaaa	tcntaaaaaa	660
tnntttggcat	ttaaaagtcc	nntcttggan	tnaanann	nnnaaaaaa	ancttncccc	720
tttanaaactt	tnngggct					739

&lt;210&gt; 457

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 457

gtgnnnntnt	tctnnngttt	ccaattantc	tggngctcg	ttctttctcn	anncnnnnan	60
tggttgncga	attcggcacg	aggnnanagg	gnagctacat	gnntnacnt	nttngnnctc	120
tcagccangc	tcnnctnnnn	ctggctctac	tgtacatag	aacacttggt	ntncnnggna	180
actnntntat	gtnnccnnga	ntctctgnna	ctngtttaaa	tgtanttgta	taacaggcta	240
tgcaaggnc	gnaagtggan	agcgtcatca	ttcatcatnc	ntnttanctn	gantnnntgt	300
atcctacatg	ctttgattgg	taaatngcn	tcagactggg	actctcaata	aatgnatata	360
gangancttg	ctgtggaaan	ctgtcctctc	ntatctntnc	atgngnaant	tccactncag	420
tntgaactcc	aaatgcnntn	atngngnanc	cctncttgta	tagtgggtgc	cattccaanc	480
tgnagggnc	tagaaaccgt	cggetntngg	aaacnatgg	gnnagttgan	ctggtagang	540
cngttntcac	ctgcanctac	cataaaatgg	gnntacccaa	gctttatcat	ggaatggnta	600
taaaaaacgc	attnattgng	cctttntaan	cccattatnt	gttnaatttn	acttatggtt	660

ccccccattn aaattatnca attgggnann gangettca gtcnccatnt ttnaatggnn 720  
 tttncaaaaa aacgnnttttt ttt 743

<210> 458  
 <211> 906  
 <212> DNA  
 <213> Homo sapiens

<400> 458  
 gnngnnnnnn ntttctaag cttgggnncn cgtttctann nnnnnnnnaa nntttcctaa 60  
 ttggttaggn gtcggnctn tctccacnaa gnnnngcggt gcgaattcgg cagcaggctg 120  
 aatcaaggat cacaaactnc acatttngca cnttggctcn cacatncntg gttngggcag 180  
 tcncagtnaa catggctntg gaaactnatn ttngnctngc ntcaaccatc tcgttccng 240  
 gggaccann ntccnnatc ncgnnttnc tcgnnatng gagngctnct tngnccannn 300  
 atgggctccc nanaatangn ntncnnngn nnatncancn ncngncaann ggntcnnct 360  
 nnnnnngccc tnttncctna tggnnngctn catgncccat nnnnnngggn ancaataann 420  
 naaanggtct ntcccnega nccccnnnnn ccnctaacan ngnacctcgc aaagggcccc 480  
 aggcnttnc tngnaaacca nnttngccaa nggtanttca aaggngcct tngggacctc 540  
 ccnannnngc cntggnnnta ccccggnnaa anggtngnaa acccnnccnn ngntgccnnn 600  
 cccggnncng gaaanaaatt tccnngnac ccagnntncc nccgnaannn anantannnc 660  
 ccncccnnaa cnttngccc ncancnttn gnnntgnaa tcnncnncc ctttnnntn 720  
 nccaanncgg ccnggnnacn nctttnacc tnttncncn naanngacnc caantcctn 780  
 nannaaagg nggnnnnnnn nnncttnc nnggnagcc cnnnnncct nncntnncn 840  
 aaaaattcnn cnntgnancn cccctnnnt nangngccc natnnnnnnn nngnaaanc 900  
 nnacc 906

<210> 459  
 <211> 765  
 <212> DNA  
 <213> Homo sapiens

<400> 459  
 gnngnnnnng nttcctaang ctggggnccg ntctnnnnnn nnnnnnnngt tcctaaanac 60  
 ctagngctc gntctngctc cagcagncn gggcggtggc gaattcggca cgagcttctg 120  
 ttgattggtt tgtttaaagt acctaagtac tacccttga ctccctacca aaagtcttt 180  
 tgttttttaa acaactttta tttgtgactt actttcttga gaagngttct taatgaattg 240  
 cataaaatag tggtagcagc ttatttctta agtnctnat tattggggtt ttaccattca 300  
 ggtcttatct ttaaccctta ttactcagt tttccatctg aatgaccta tctctaaatn 360  
 aaggatttaa taaatgctgc aaattgtcca ctttgcaaat ngccaaaag ctttagtttt 420  
 ggacctgng aacttttttt ttaataacac attatttggg cccggtcgtg gtggctcaag 480  
 cctgtaatcg cagcactttg gaatgcctag gcagacagat cacttaangc ctggagtctg 540  
 agaccagcct ggccaatgtg gtgaagacct cgggttctat tactaaaaat nctaaaaaat 600  
 tancaaggca tggnggtgca cgcctgnaat ctcagctact tgagangcaa atcnggagaa 660  
 atgcttgacc ngggangcan anatganccn anattgcacc actgcattcc acctggggan 720  
 nanantgaga anctggctca aaacccaaaa acccaaaaaa aaaa 765

<210> 460  
 <211> 677  
 <212> DNA  
 <213> Homo sapiens



&lt;400&gt; 460

```

gtttncgctg ggagccacca acatagcaga ttaccatgtg aagttgccac tgctgcatct      60
cctgaaacct ggctgatggg agaggtctca ttttgtgtct gagaatgtcc aggttgtctg      120
cagaccacag cactgatttc ccattagcag ttattatttc ctggccattt ctccctgaag      180
gttttgtggt taaactccct gtcctcaata ttttatcagc agtagggctg tcattcttct      240
ggttatcaac ctctacatta tgaagtaagg ttcaaccctt ctgcttttct caggccccc      300
aaacggttcc tatccaatcg aacacaaaaa cgggtattga gaaggaattg gcagggtca      360
gtggctgttt ccgttgctcc tacctcatgg agactcttac tcatgctgga tttattgaga      420
gaacttctaa ctgaccactc acccccaccc actcttatgc agtctgttca ttcctgaaaa      480
caccactttc atccctcctg cacacaaccc atgagggatt gctacttcct ataagattcc      540
tcagtga gcc ttatagagtt gctgcgagaa ttacatttgg tcatgatgtc aagtgtctgg      600
tatgtagctn atgcttattg aacacatagt aattttattg aataattgnc atgatcactg      660
gatgagaata tagcccn

```

&lt;210&gt; 461

&lt;211&gt; 787

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 461

```

gnnnnnnnnag ggnnnngngg ggcctcncaa agcccngncn acaggtcccc gttccaaagc      60
ntggnganc gcnncgcccc ancagnaagg cgggggaang cggcacgagg acatcatcnn      120
cttattctag taagagaaag tacacagatt caactttaga gaggacnggg gggnnnncng      180
gagcnaaatc aaggaaggan tatcacnggg cnccccnga atataannnn gaagctgnga      240
acagnaccat cagnaacann nnatggacag ctctgatggg gnnnatacca cggcactctn      300
cnnaccnnng gnggaagcna tccggagnna tgactgangan gnaaagnggn nnaactgnna      360
aanccngng ngctaggann ctgggagagn cactttcang aagnnaccng gcgangagnc      420
atcanaagaa cccgganaag ngagaagacn ggaaaaagnn cncancgnac ngagcccagn      480
nannnnnct gagccanggg ctncgaaang ccccacnga agcnccatca canggnacaa      540
ggnnngggaa aaggaancna cnnngcngac angnccncn aanagngcca aanacngcn      600
nngccncnc gcccaaagaa nacnggacng cnggcncna ncanaaggag cncnanggcc      660
cnnngnaang aaactncnag nagcccaanc ccaaaggccc cnanggannc cncncaaggg      720
gaaacanna nncaccaag gggcctgggc naanaaggcn nccacncng gccncncnc      780
nnnaccg

```

&lt;210&gt; 462

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 462

```

ctaattgctt ggnnnnnnng nnnnccgntt cttaattgnc ttgggcnct cgctctntct      60
ccannnagnn nntgcgttng cgaattcggc acgagcctca gcccacacc agctctattt      120
caggggtgag agtcagagag cactgcaata tgtgcttcat gggatttoga ttcgaagatc      180
ctagaccagg gagacactgt gagccaggga tacaacaaaa tactaggtaa gtcactgcag      240
accgacctcc ctgcagtttg ggaaagaagc tgggtttgtg gagaatcaga gcatcttgac      300
atgactgctg acctaaagat ccctggcatt ggccagggat cctgtggaac ctcttctagt      360
tcaggggtgt gagcattaga ctgccagttg tctagtgaac tctgatgctt gctgtgaact      420
ttaagatcc ccgaatcctg agcacctcaa tctttaattg ccctgtattc cgaagggtaa      480
tataatttat ctggatggaa attttaaaga tgaatcccc tttttctctt tctnctctct      540
tttcttctct tctcccttct ttctttgctt tctaaatata ctgaaatgat ttanatatgt      600

```

```

gtcaccaatt aatgatcttt tattcaatct aagaaatggn ttaagttttt ctcttttagct 660
ctatggcatt tcaactcaagt gggacagggg aaaaagtaan tgccatnggc tccaaagaat 720
tnntttatgt tttagctatt taaaaaa 747

```

```

<210> 463
<211> 750
<212> DNA
<213> Homo sapiens

```

```

<400> 463
tncctttcta angcnntng nnaanngtcn ccgttctaan tncctgggca gnnccgtctn 60
tctncannca gncnntgcgt tgcgaattcg gcacgagcg agatgaagct acactgtgag 120
gtggaggtga tcagccggca cttgcccgcc ttggggctta agaaccggg caagggcgctc 180
cgagccgtgt tgagcctctg tcagcagact tccaggagtc agccgcccgt cagagccttc 240
ctgctcatct ccaccctgaa ggacaagcgc gggaccgct atgagctaag ggagaacatt 300
gagcaattct tcaccaaatt tgtagatgag gggaaagcca ctgttcggtt aaaggagcct 360
cctgtggata tctgtctaag taaggattcc atatggctct catatcattc cattccatct 420
ctgccaaagt ttggataccg caaaaatttg tgttngngga agattctgnc tgaactcttt 480
cattcaagga actactacca tgaatctgca ttctgntgcc cacactgagg ncttagtaga 540
taattgggtg gtctgaaaca cctattatct cttatntctg gtctctangc tggnatgtta 600
attcctctga aatgntaaaa gtaatgggtg anaccngaaa aagaaatttc aatnacagat 660
caanntggg ngcatgtatn attttcaagc gtcaaaatgg aataaggga gantnctgga 720
tacctgcttg gaaaaggaag natgtgtatn 750

```

```

<210> 464
<211> 748
<212> DNA
<213> Homo sapiens

```

```

<400> 464
gnngtgcctt tgnaaagcct ttggggaann gncnccttct aatgcttggc tategntctt 60
tacgcagnnc ccatcgattc gaattcggca cgagccggc cggcgacgct ggcgacgctt 120
tcgcccctga ggtagtttg cgaccgcgaa gaaggaaaaa gggcgggcgg gcggctgtcc 180
tctcacctgc ctcacccgc gagcccgcc ccgctcctcc gtcgtggatt tcgcgcgat 240
ccccccggca gctctttgca aagctgcttg aaacttctcc caaactcggc atggatacga 300
ctgcgcggc ggcgctgct gcttttgttg cgtcttctg cctctctctc tggcctctcc 360
tgggacggc ccaaggccag ttctccgag gttgntgct tcttctgtc tctcctctgg 420
gggctctgaa gtttcaccag gtggacgctg gggagcggc tcccagcac ttgtctacct 480
nccgccagtc ctgacaactt ttctggcaa cctaccagc ttcgcttggc tggcgagcgc 540
atctgctgct ggggttcgag gtgcaaatgg agacgcagtg gtggccagag ggtgatggag 600
aagacgggaa aagcgacagc cacgctnctg gcttgaagcc gcaggacgca aataacttac 660
tttgacctg acagttctac gttgntgttg angccctgtt tcttggaat aaaactcaaa 720
atggtggttt ttggaaaaa aaaaaaat 748

```

```

<210> 465
<211> 863
<212> DNA
<213> Homo sapiens

```

```

<400> 465
gggnnnnnnn aanggnnnnn ggnnnnngtc ccgttccaan gaccnngaga tcgnngnccg 60

```

tccanaagaa	aggcgggtgng	aattcggcac	gagacctgta	ccgcctggcc	actggctgtc	120
accggcgtaga	tgagctgccg	gtgtttgaac	gcngcctatg	cnngggacttt	cccggcanan	180
nggcnnngaan	atggccncca	tncaggaagc	cgcccagAAC	ctcctngggn	acacnacttn	240
agngccttcn	agtccgntgg	nacccggncc	aagccccggc	aancnctgcc	ccgggtcncc	300
gttcccaagg	ccaaccagcc	ctgggnaccc	ccggggagcc	gaaacnctgg	ggctnggana	360
ccngantga	gagncnact	ttcnntgta	nacacgggcc	cagganacan	ctntgtctgt	420
ggccccgggg	naaaannnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	480
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	540
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	600
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	660
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	720
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	780
nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	840
nnnnnnnnnn	nnnnnnnnnn	ncc				863

&lt;210&gt; 466

&lt;211&gt; 713

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 466

ngtctttcga	gcntggngnt	cggtctngct	cnannanatt	ggttgnggga	attcggcacg	60
agcctcagcc	ccacaccagc	tctatttcag	gggtgagagt	cagagagcac	tgcaatatgt	120
gntcatggg	atttcgattc	gaagatccta	gaccagggag	acactgtgag	ccagggatag	180
aacaaaatac	taggtaagtc	actgcagacc	gacctccctg	cagtttgagg	agaagctgg	240
gtttgtggag	aatcagagca	tcttgacatg	actgctgacc	taaagatccc	tggcattggc	300
cagggatcct	gtggaacctc	ttctagttca	ggggtgtgag	cattagactg	ccagttgtct	360
agtgcacatc	gatgcttgct	gtgaactttt	aagatccccg	aatcctgagc	acctcaatct	420
ttaattgccc	tgtattccga	agggtaatat	aatttatctg	gatggaaatt	ttaaagatga	480
atcccccttt	tttcttttct	tctctctttt	ctttccttct	ccctttcttc	tttgcttctt	540
aaatatactg	aaatgattta	gatatgtgtc	aacaattaat	gatcttttat	caatctaaga	600
aatgggttta	attttttctc	tttactctat	ggcanttcac	tcaantggac	aggggaaaaa	660
agtaattgcc	atgggcttcc	aaaagaattg	ntttatgntt	tagctatttn	aaa	713

&lt;210&gt; 467

&lt;211&gt; 732

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 467

gnnnggtntt	ctaatncttg	nnnnnnnnntc	ncccttctaa	gcentggngct	cgnetnnccn	60
acnancnggc	ttncgaattc	ggcacgaggc	gagatgaact	acactgtgag	gtggagggtga	120
tcagccggca	cttgcccgcc	ttggggctta	ngaaccgggg	caagggcgtc	cgagccgtgt	180
tgagcctctg	tcagcagact	tccaggagtc	agccgcccgt	ccgagccttc	ctgctcatct	240
ccaccctgaa	ggacaagcgc	gggacccgct	atgagctaag	ggagaacatt	gagcaattct	300
tcaccaaatt	tgtagatgag	gggaaagcca	ctgttcgggt	aaaggagcct	cctgtggata	360
tctgtctaag	taaggattcc	atatggctct	catatcattc	cattccatct	ctgccaaagat	420
ttggataccg	caaaaatttg	tgtttgtgga	agattctgtc	tgaactcttt	cattcaagga	480
actactacca	tgaatctgca	ttctgntgcc	cacactgtgg	tcttagtaga	taatttgggt	540
ggtctgaagc	acctattatc	tcttatttct	ggtctctagg	ctggtatggt	aatcctctga	600
tatgttaaaa	gtaatgggtg	agaccngaaa	aagaaatttc	aatacngatc	aantttgggg	660

tgcattgttga atttgcaacc tcaaattgga gtaagggaan attctggata cttgctggaa 720  
aggaggaatg tn 732

<210> 468  
<211> 748  
<212> DNA  
<213> Homo sapiens

<400> 468  
gnnagnnttc taatngcttg tnnnnnnnna gacgttctaa nnctttggcn atcgttnttt 60  
ctncagnann cnttcgattc gaattcggca cgaggccggc cggcgacgct ggcgacgctt 120  
tcgcccctga ggtagtttgg cgaccgcgaa gaaggaaaaa gggcgggcgg gcggtgtcc 180  
tctcacccgc ctcaccccg c gagcccgcc ccgctcctnc gtcgtggatt tcgcggcgat 240  
ccccccggca gctctttgca aagctgcttg aaacttctcc caaactcggc atggatacga 300  
ctgcggcggc ggcgctgcct gcttttgttg cgctcttgct cctctctcct tggcctctcc 360  
tgggatcggc ccaaggccag ttctccgcag gttggttgct tcttctgctt tctcctctgg 420  
gggctctgaa gtttcaccag gtggacgctg gggagcgggc tcccgagcac ttgtctacct 480  
tccgccagtc ctgacaactt ttctggccaa cctaccagc ttcgcttgcc tggcgagcgc 540  
atctgctgct ggggttcgcg gtgcagatgg agacgcantg gtggccagag ggtgatggag 600  
aagacgggaa aaagcgacag ccaagctcct ggctgaaacc gcaaggacgc aaaataactt 660  
actttgnacc tgacagtttc tnacgtttgt tgtggangcc ctgtttcctg ggaaataaac 720  
tcaaattggt ggtttcttg aaaaaaaa 748

<210> 469  
<211> 776  
<212> DNA  
<213> Homo sapiens

<400> 469  
ggngntctat atgcttgnnn tgattctccg tctataacng gntaatnctt ggnccctacna 60  
aaaggctang ngaattcggc acgagacctg taccgctgg ccaactggctg tcaccggcgt 120  
gatgagctgc cgggtgttga acgcaaccta tgcctggactc tcccggcaga ctgcctggat 180  
atggctcgcca tgcaggaagc cgcccagcac ctctcggca cacacgactt cagcgccttc 240  
cantccgctg gcagcccgtt gccgagcccc gtgcgaacgc tgcgcccggg ctccgtttcc 300  
ccaggccaag ccagcccctt ggtcaccccc gagagagca ggaagctgcg gttctggaac 360  
ctggagtttg agagccagtc tttcctgtat agacaggtac ngaggatgac ngctgtgctg 420  
gtggccgtgg ggcttnaann tnannnnnnn nnnccnnnac caantctncn nannannnnn 480  
ccnacnnnta aaantnncnn ncnnnnnncan nnnnnnnnnc cnnnnanncc nnnncttnnn 540  
naancnnnnn nnnnnnnanc nnnncancna nnnnnnnnna nnnnnnnnnc nnnnnnnncn 600  
nnnnnnnnnn nannccnnnn nnnnantnnn nnannnnnnn nnnnnnnnnn aaannnnnnn 660  
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720  
ccnnnnnnnn nnnnnccnnn nnnnnntnnn nnnnnnnntn nnnnnnnnnn nnnnnnc 776

<210> 470  
<211> 765  
<212> DNA  
<213> Homo sapiens

<400> 470  
tatgnntttn ctaaaatncn tgggcaanac gtcctcncctt tcctaanagn ttnggcanaa 60  
cccttggcaa nacgccngtn acccanacnc agnnnggccg tggcgggcga gcgggcaaca 120

gctcttgagg	agtgagactg	cnggagatnt	gggccgtgcc	aaagagatgg	atgagactgg	180
tgctgagttc	atcaagagga	ccatcttgaa	aatcccatg	aatgaactga	caacaatcct	240
gaaggcctgg	gattttttgt	ctgaaaatca	actgcagact	gtaaatttcc	gacagagaaa	300
ggaatctgta	gttcagcaact	tgatccatct	gtgtgaggaa	aagcgtgcaa	gtatcagtga	360
tgctgccctg	ttagacatca	tttatatgca	atttcatcag	caccagaaaag	tttgggatgt	420
ttntcagatg	agtaaaggac	caggtgaaga	tgttgacctt	tttgatatga	aacantttaa	480
aaattcgttc	aagaaaattc	ttcanagagc	attaaaaaat	gtgacagtca	gcttcagaga	540
aactgangag	aatgcannct	ggattccaat	tgcccgggga	acacagtaca	caaagcccaa	600
ccagtcaaac	ctacctacgn	gggggactac	tccagactcc	cgnacncctt	cacgtcctcc	660
tccatgctga	ggcgcaatca	cgccttctgg	gncaagaagt	tanaaacnct	gggaaaaact	720
acctncgaca	agaaggggan	catttanatt	taccnnaaat	gaana		765

&lt;210&gt; 471

&lt;211&gt; 820

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 471

cnnnnngggg	nnngngggc	cntccnaaan	cgggggagac	agngccnnng	ttccaacaga	60
ccngngnggc	cgncngngcc	ccanacagca	ngggnggggc	nnnggggnnn	cnnngcnnnn	120
cnnancnaca	aagaactcaa	caagaaaaaa	acnaaccca	caagcgggca	aaggacngna	180
acagacantn	cccaaaaaga	gacatacaag	caaccnaaaa	taatcnaaaa	taagnnncaa	240
aaagaaaaaa	ngcnagacag	agnngngana	gnactnagna	aaaangnana	tctagcggn	300
annagnangn	nngnnnacgg	ncngnnncna	agaaanagn	nctggnnccc	aagcnggagn	360
acagcggcgc	aagcnnngcn	cactgcaacc	gcgaacnccc	gggctcaagc	gaaccnccag	420
cctcagcctc	ccaagnagcn	gnnaaaggca	ngcaccacca	cacccgacna	aaatanncgc	480
nancaanaac	ananaanggc	nccccngngc	nnanncagga	aanaaacacn	cnnangcnn	540
ngaaaaanaa	naancncn	cnnnacaaaa	aaacnnnagc	cnnagaacaa	nnnggaggc	600
ggaanacggn	nnancccgac	anganaanga	nacnanngan	gganganngg	gaccaaacn	660
cancccgga	anggcnnngn	aaaaaaaang	ccnnnaaann	gggggaaaan	ncggngnang	720
ccnaaagggc	cnnaaanggg	gaaaccnann	naaaangccg	ggcanannan	aaccnagcnn	780
nancnancn	nccaangggg	nannncn	nncnaggccg			820

&lt;210&gt; 472

&lt;211&gt; 738

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 472

gnngtgtctc	taatgcttgg	ctactngttc	tttccgcoga	acncttgcta	atgcttggn	60
ntcgttcttt	ctccacnnac	nnngcnnntc	gaattcggca	cgaggtcaca	ganatnaaag	120
tccaatcata	ggggctggnc	cnactctnt	gctnntccct	gcangantca	tangatcagn	180
nanaccgtgc	gnntttgnaa	gcntttcaaa	tgtgntacca	tcgngttact	tncnnnggca	240
cctgntgann	tnggtgnac	tnnncnggat	ntcccaaanc	caccnnnnnc	atgggntnng	300
tgngcatgng	ntggnncann	nacagannta	ganactttaa	ngaannngnt	tntgcaaccn	360
tnggnnctag	caancntgan	antnccaggg	nnggccacna	agctgaaaat	nnatgttana	420
ncnnatgntg	naatctctag	natgacttcc	ncannnancn	aaactnangc	anggtcgna	480
tgttagaanc	tanaggccna	atttctntc	natgnaacca	ntntatgctt	ttaagaccnt	540
caactgtinn	natgaagccc	atntacatna	ttncggtaat	anggctatnc	ttaaannnaa	600
ctgctgaaaa	tntgatnca	nctacgaaat	cctnnncanc	ncatntggct	naatcattac	660
caaccatttg	acaccnncat	ngnctaccca	cntgcattnc	catgaccnan	tccantgcca	720

cccgcncaga tntacctt

738

&lt;210&gt; 473

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 473

tatgnntncc taanagagtt ntgnnacacg gcccgccttc tnaaancttc ctaatncttg	60
ggcgctcggt ctntctncac ncagnnntg cggtnCGaat tCGgcacgag gtccttttga	120
accaccccaa agaactcaac atggcaaagc aaatggtaaa agcttcccgga ctgttctact	180
ttgggtccgc gcgaagccca ctcacgtgtg atctgtgttg cccctgggag gcccggggcg	240
accggaaaag ggtctcttca agttctgaaa agagaatctg ccaccagatc gaatttcgac	300
ccctgagctt gttcggacgt atggtccaaa ttcagattaa ggtggtcacc caaccgaga	360
tgtcaggaaa ggccttctgc agagaaaatg tccccacc cgccatctgc agccaggtgt	420
gtgccacacg gcagccttcc cgaaacatag tatggatttt aaaaatgtgt ntatttttgg	480
ttctcaacca ctttataacg tattttttta tttattttgt aatgtcttgt tttgaagtat	540
tgtgtctatc cttggtatcc ttcacctggg ttttatctact ganttatctt gngaaagttg	600
ncactaatgt tctatgtcaa aatcaaaagt atttaataaa atactanctc tatttaaatgt	660
ggntatggaa ccagctggaa acacaaaaca aacagtgatt gacancaagc tgggccaag	720
agncaggtca ttttgnacat atgccaataa ac	752

&lt;210&gt; 474

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 474

ttgcanacnn aatanttgct gtaaaagtcc cnnctttttn ccctttctaa tgnttgngcg	60
ctcgnctctnt ctccacnagn nnntgcgttn cgaattcggn tctnagccca tgccgggagc	120
ttccacaccc cgtcctcaca gatccagccc cagccctgtt cttcccaggc catctctcag	180
cagcacctgc aggatgcggg caccggggag tggagccctc agaacgcac cagtgaggag	240
tctctctcca tcccagcttc cctgaacgac gcggcttttg ctcagatgaa cagtgagggtg	300
cagctcctga ctgaaaaggc cctgatggag cttgggggtg ggaagccgct tccgcacccc	360
cgggcgtggt tcgtctcctt ggatggcagg tccaacgctc acgttagaca ttcatacatt	420
gatctccaaa gagctggaag gaacggaagt aatgatgcca gtttgactc tggcgtagat	480
atgaatgaac caaaatcanc ccggaaggga angggagatg ctttgtctct gcagcagaac	540
taccgnccg tccaagagca ccancagaaa gancctcanc ccagacagc acggnctaca	600
cgcancctcg gnacctggat gacntggaac anaatgggtan cnaatgtggg accacngnct	660
tgtanccna ggacaaggcc ctncnangct tgnatggang gtcnantcng anaaatggng	720
gccactgccc aaccgcgag aaganaacaa nn	752

&lt;210&gt; 475

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 475

gntttctntt aatncttttn naaangcggn ntttaacntt ctangnntgn gntcgttct	60
ttccacacna nnnnncggtg cgaattcggc ncgaggtgaa acagaaagtg gagatgcttt	120
ccttgacctg aagaagcctc ctgcctccaa atgcccccat cgctatacaa aagaagaact	180

```

cttggatata aaagaactcc cccattccaa acagagcctt catgcctttc tgaaaaatat 240
gacagtgatg gtgtctggga ccttgagaag tggcatgcct ctctctaccc agcttcaggg 300
cggagctcac cagtggaaag tctgaagaaa gagtgggata cagaccggcc ttccttggtg 360
cgcaggatag tagatccacg agagcgtgtg aaagaagatg acttanatgt tgttctcagc 420
cctcagagac ngagcttttg agggggctgc cacgtgacag ccgctgtcag ctcccggcgc 480
tcangaagtc cattagagaa agatagtgat gggcttcgtc tgcttggtgg acgtaggatt 540
ggcagtggga ggataatctc tgcccggacc tttgagaagg atcaccgctt aacgataagg 600
acctgcggga cttgagagac agagaccnan anaaggactt caaggacaac gtttcangan 660
anaanttttg gagaaagtaa ncntgtcttt tggtgancgt anaaanaaat gattcttacn 720
cnaanaaga accggaatgg tt 742

```

&lt;210&gt; 476

&lt;211&gt; 1122

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 476

```

gnnnggggnn ttctaaaagc tgggnnnnnn nnngagggnnc ttctaatnct tctaatggtt 60
ggctctcggt ctttctncac gcagcnnngc gnnncgaatt cggcacgagc ctgcagccac 120
taatgcattg tgtatgataa caaaaactct ggtatgacac attttctgng atcattgnta 180
attagtgaca tagtaacatc tgtagcagct ggttagtaaa cctcatgtgg ggggtggggtg 240
ggggtgtatn cctngnggga nggnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 300
nnnnnnnnnn annnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 360
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 420
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 480
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 540
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 600
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 660
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 780
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 840
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 900
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 960
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1020
nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 1080
nnnnnnnnnn annnnnnnnn nnnnnnnnnn nnnnnnnnnn nc 1122

```

&lt;210&gt; 477

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 477

```

gnngtgcctt tgaaannccn tttgnnnnng nggcccttct aatgctnttn cgntcgnngg 60
gtcgaactcg cccacncng cnaggcgggg gctncaagcg attctaaacc acctatgagt 120
atttctttta gggctcactt aaatacatgt ntgngnntac tgggggctag ccngaataat 180
tttagatctg atcaggtngn ngctnaaatt ngaaaaanac cnnntngatg cttaaagaat 240
tngcntccat ttttgagtct aaatctttta aaatntactg ngatccacat ctagngaaat 300
gtcngtgtca anatattctn gatnatcgct naaatccnca ttaataactn ttnggggtnn 360
nnnatagngg aacttcntag nnntncnaaa agcacatngn ctctctgnet ccgctgctec 420
cacagnnggt nttgnaactg ggnaaatcag nnnnnngata gcgngngnnt ntnaganaaa 480

```

ntngatncac	acatncttnn	nnetcagnen	ncacatngat	tgaacactct	ggccaagatg	540
ctgngggngga	tgangttgga	gttcgannga	agaagccngc	gctggcctgg	cttgnaagac	600
ccnngncttt	cccntnccct	cncctngaaag	ctgcccngac	ngagggccnaa	ngnaaatggg	660
tganngnnen	gtcnngccen	cttcngncnc	ttngaaccnn	nnagngggnnc	tnnnngnacc	720
cnngnnntn	cgngnaaccg	nncncgc				747

&lt;210&gt; 478

&lt;211&gt; 746

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 478

gnnnnnnngcg	cgnccttcta	atgcttenta	attnnctnng	atactcgttc	tttctncagg	60
natenmntgc	gnntcgcaag	gagnagagt	atagnaattg	gcagtgaaat	atacgaacca	120
ccctcctgcc	ctctgggttc	acaatacgtg	tacacttgac	tgtgaagtgg	ctgtgagagt	180
gggtggagag	ttcttctttg	accctcagcc	tgcggtgcc	tctagaaaacc	tcgtgttgat	240
tgcaggagga	gtcggaatta	accctcgtct	ttccatcctg	cggcacgcag	cagatctcct	300
cagagagcag	gcaaacaaaa	gaaatggata	tgagatagga	acaataaaac	tattctacag	360
tgcaaaaaat	accagcgaac	tctgttttaa	gaaaaatata	cttgatttag	taaatagaatt	420
tcttgagaag	attgcatgca	gtttgcatgt	tacaaaacag	actacacaaa	tcaatgcgga	480
actcaagcca	tacatcacgg	aaggaagaat	aacggagaag	gagataagag	atcatatttc	540
aaaagagact	ttgttctata	tttgtggccc	acctccaatg	acagactttt	tctccaagca	600
actggaaaac	aaccatgtac	ccaaagaaca	catttgcttt	gagaagtggg	ggtaggaggg	660
aagaccaaaag	gcaggaaaaa	attaangagg	tgagatctac	tcaaggagag	ctcaaaaaaa	720
aaaaaaaaaa	actngggccc	tttaga				746

&lt;210&gt; 479

&lt;211&gt; 750

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 479

gnnnnnnnnn	nnngnnnnnn	ttctannntt	cntattnnct	nggagctcgt	tctttctnca	60
ggatcccntg	cgattcgaat	tcggcacgag	ggtagactgg	ctagggatcc	tggaaccagg	120
gttccacgta	gcaacacctg	ctgagttctc	tggtttttct	tcctgcctca	tgtagcccag	180
acttgagct	gaagaagctg	gaaacatgga	aacaccaaca	gctacagacc	aaaaaaagtc	240
ccaacaaagg	cctgtcagtc	tgccagcctg	ttctgtggat	ttccaactca	agattgcagc	300
atcaactcac	acctgaagtt	ctggcttccc	tacaaacttt	gaacttgcca	gtccccacaa	360
tggcataagc	caattcctta	aaatgaatgt	ctagtcttag	ataatgtgtg	tattctactg	420
gttctgtttc	tctggagaag	cctactaata	gatcatttgt	cttagtcaat	tcaagctact	480
ggtacagatt	accatagact	gggtgggtta	aactaccaat	cttattactc	acagtttttg	540
gagtctggaa	agtctgagat	cagggttcca	gcaggattga	gttctttggg	gaacatnctc	600
tttctggnc	acagaatact	gggttacttt	aagtnggaaa	aagtaggggtg	aagctgggtc	660
ntttggcctc	ttcttttaag	ggggactaat	tcatgaaggg	ttccaccctt	attgacctat	720
tttaccttnc	caaanggnnt	ccattttccn				750

&lt;210&gt; 480

&lt;211&gt; 714

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 480

gnnnnnnngnn	nngngggnnt	tcnaccgttc	ttntgacct	gnctcgnnt	nncnna	60
gctaggcttg	ngaattcggc	acgagataac	acacatcaca	gtatgctctc	agaaatttct	120
ttatttgaac	cctataccaa	tatctgntga	tcaatgacca	tttttgtca	gcatggagaa	180
acagtgcctt	gcatgaagg	tagtgagaat	aaaaaggatc	ttaccacctt	tatcatgagg	240
gtggctttgc	tctctccatt	ccaagttggt	ctctgttcta	gaaagcagat	gtagtagaca	300
tctactgttt	ttgcctaaac	agaatccctt	tttctttttt	ttgttaaaag	tactcatccc	360
taatattaca	ttgttctgga	aggactgaaa	ataacagaac	tcagcaccat	gatcggaacc	420
ggacaatcag	attatttcat	tcctcancaa	acggagatcg	atccgaaaag	tggaaatatg	480
agctcttctt	tggtgttggt	atatggaccc	tgagagaaa	aactttaatt	ttttctcttg	540
gactgcaata	aagtatagct	gcctaaaata	cgtttcctga	ccttggangt	ttgnccacaa	600
tcggtgaaat	aaangcaaga	cgtaaccttg	gatgaaaaaa	aaannnnnnn	naaaaaaaac	660
tcgaccttta	nactatnnga	gtcgatacnt	aatcngactg	atagatcatt	gnta	714

&lt;210&gt; 481

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 481

agccnttcta	aangccnttt	gnctnngnnc	cccnttcccta	anncntggct	aatncttggc	60
nactcgttct	ttctncacgc	acccatcgnn	ncgaattcgg	cacgaggcat	gaaaggagtc	120
ggaagcggaa	gcggtagccc	ggacgggtgct	gtgggtgcaag	ggcttgtgga	aaaattggag	180
aaaaccaagt	ccctggccca	gcagttgaca	agggaggcca	ctcaagcgga	aattgaagca	240
gatagggtct	atcagcacag	tctccgcctc	ctggattcag	tgtctcggct	tcagggagtc	300
agtgatcagt	ccttttcaggt	ggaagaagca	aagaggatca	aacaaaaagc	ggattcactc	360
tcaagcctgg	taaccaggca	tatggatgag	ttcaagcgta	cacagaagaa	tctgggaaac	420
tggaagaag	aagcacagca	gctcttacag	aatggaaaaa	gtgggagaga	gaaatcagat	480
cagctgcttt	cccggtccaa	tcttgctaaa	agcagancac	aagaagcact	gagtatgggc	540
aatgccactt	tttatgaagt	tgagagcatc	cttaaaaaacc	tcagagagtt	tgacctgcag	600
gtggacaaca	gaaaacagaa	ctgaagaacc	atgaagagac	tctnctacat	caccagaagg	660
ttcagancca	atgacaagac	ccancaagca	naagagccct	ggggagccct	ctgctgatcc	720
caaanggcaa	aaaatggggc	cn				742

&lt;210&gt; 482

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 482

gnnnngggag	nnttctaagt	ctttgntcta	gagtcnncnt	tctaanggct	tggnaatnct	60
ngctcttgtt	ctttntgcag	gatcccatcg	attcgaattc	ggcacgaggc	caagcctcgg	120
cctccactgc	acctgctgcg	gagtggcacc	tttgcttca	aggccctcta	ccccatggcc	180
cagtgtcatc	tcagcagggt	ctttggccac	tcaggaggcc	cttgtggtgg	gttgctcagt	240
ctgtccttcc	ctcatgagaa	gctactgctt	atgtccacag	accaggagga	gctgtcacgc	300
tggtaccaca	gtctgacttg	ggctatcagc	agccagaaaa	actagaggaa	tcttatagat	360
tccagaactc	aggatactc	agggataggt	cacagccaa	agtacaaaag	aatcttcagt	420
actgaacaaa	acagaaccct	tcatgatttg	acaaaggcta	ctttctgttt	gcctggacca	480
agctactcca	gatcatctga	ccaactctta	aaaatcacgg	ccaggcacag	tggtctatgc	540
ctgtaatccc	agcacttttg	gaagcaaang	tggcaggatc	attccagccc	aggagtttca	600
agancagcct	ggcaacacag	tgagttagac	cctgtctcta	tttaagaaaa	aaattattaa	660

gaaattttat taaaaaagga agaatcagga aaccaaagtc aaccccaact taaccctcaa 720  
tgaaccagcc ctaacacaga tgangggatt tg 752

<210> 483  
<211> 849  
<212> DNA  
<213> Homo sapiens

<400> 483  
gnnnnnnattt ccttttnaaa tncncngaa ancccttgga agcactaccn ctngacccc 60  
tttggaacgn cgactnctnn atatatcnng gatataatag gtgataagtt ctgncaatta 120  
gtaacatcng gaaaaaacag ctnnngcctg ggngaaaaag gatgccaaaa tngcctggaa 180  
aagagcagng gagaggagtc cgggagatgn gngatgcac gggacgcanc atngntnaac 240  
attcactggg tctgccccaa atgtggattt gngggctgct tagatngtta caaggcaaaa 300  
ggaaaggaaa gagttctaga gataaaagaa ctatatgctt ggatgaagtg tgtgaaggga 360  
cagcctcatg atcaccaaca tttaatgccc aaccccaaat tataccnggt tctgntttga 420  
cagacttcta gatgccatgc acactcttag ggaaaaaata ttgggattaa ancccatngg 480  
cattggacta acaaacagga atttacaagg tnggaaantt ttncnaccaa tgaaaggggg 540  
gatcncaagg ttttcagaa nggntcntaa tncaggnaa taaaaattnc tctngggcaa 600  
gccctgagtc ttaancagca aaaanactcc tcccgaaanc tgnagaaaaa agggggggca 660  
gccaggcccn naaanggaan gtnaggcccn agatnaacaa ngtnacctcc nccagnaaa 720  
ccccannccc caactggnac cngggnaacc cacaacnttt gcngaagncc aaaaaagncc 780  
nnnagangga aaaaaaaaaa naananaaaa aacctnnnag cccctaagaa accttagggg 840  
nggcccncc 849

<210> 484  
<211> 1098  
<212> DNA  
<213> Homo sapiens

<400> 484  
gnnnnnnnnt tttnnnnttt ttgnaaaanc ccccttttgc naaatngncc cttttnttgg 60  
cangggatcc ccatntttat ntccggacatt ttccggccac cggaaggggc cgggggcccc 120  
cgggccncca ggnccgggna aaggcccccc ttgggcggcc cccggncggc cccaatgggt 180  
tccaaaaagg gaaaaaaaaa aaagggggaa cctgggaagt tggcccanga aaangnaaaa 240  
aaaggnaagn aaaccttcg ccaatgggaa tggggaaaaa taattttttc ttgaaaaacc 300  
caaaaaagga atggttattt ttcaaattta aaaaaggaaac nttgggaaga aagaattggc 360  
ttcccacncg cagaaagggc attactggct atgtcaagta aaagaagtcc ttcaaagctt 420  
agttgatgat ggtatggttg actgtgagag gatcggaact tctaattatt attgggcttt 480  
tccaagtaaa gctcttcatg caagggaac ataagttgga ggttctggaa tctcaagttg 540  
tctgagggaa gtcaaaagca tgcaagccta cagaaaagca tttgagaaag ctaaaatttg 600  
ccgatgttga aacggaagag cgaaccaagg ctntgcaaaa agagcttttc tttcactttc 660  
gagaccaaag gggaaccagc tnnagggcn agaaaagttn gaaaaaaatt ccaaaggaaac 720  
tggtggaatc ccccaaaagg tttggttggg gaaagaaaaa tccccgccc aangccaaaa 780  
tttaaaaggt ttngccccca aagggaag ncttgnctt taaccagga attggggacc 840  
ctgggantta aaaccnataa ttttccgcc naattnnaaa aaattcnttt nggggncccc 900  
naaaanggna aaaaaatttt nggggggttt tggnaaggna aaaatttnaa atttgattt 960  
ngaaactttt ttngggaatt cccagaaag aacttttgac cttcctntng acctnaaaaa 1020  
ttttcccttg ggggggtgna anggatgttc ccaagctttg tggnatattg gtaaaatttt 1080  
naacctttt tnttacc 1098

<210> 485  
 <211> 798  
 <212> DNA  
 <213> Homo sapiens

<400> 485  
 gnnnnnnant nnnntttnaa atccttnntg aatcctttga antaccatcc cnttttnnca 60  
 attnggcacg aggaaagggtg gcgcgcttct cacggctgag ttgctgcgcc ttgcagacgg 120  
 aagctcccca caggcagagc tgcttggatg tgtgagtcac gaaccagaga agccccgctc 180  
 catgagcagt gactccccan gccctgtgac ctccctcctn cttgcagctc ctccctggcag 240  
 cagtcgccag ggctctcctg ttggtagtct ctgcttttct tcttggaat tccctcgtgga 300  
 cctcgagatc tttaccctaa aatagtctctg ttgaatttca ccctggcaat gtaaattgat 360  
 agcttatctt cacagatgcc agacaatgga caactcacca tcagtcctct gctcacctga 420  
 gacaaatgca tgtctgattg ctctctctgc cctattgntt atgtgaaaat gcagattcac 480  
 tgagccagac taaggcatca gtgactgttc ctctacctgc ctctcacatg gagattgtgt 540  
 attcagtgaaggctgatca aagaccctaa ggaatgcaac agtttatctc ttatctacct 600  
 atgacctgag aactggccaa caaccctagt gttgncgctc tttcagacag aaccagtgtc 660  
 atcttacacg tattnaaatg gatgtcctgg ngctcnccta atatgtattc aaaagcaagc 720  
 tggggcctng accacccttn ggcacatatt cctcanggac atcattcctg angctgtgtc 780  
 actggcatgt ccttaanc 798

<210> 486  
 <211> 785  
 <212> DNA  
 <213> Homo sapiens

<400> 486  
 gnnnnnnntt gaaanccctt tcnaatnctt ggcattgntc tctttgcagg atccctcgat 60  
 tcgctgacaa cttgattggg ttctccttca ggtttgaagc gccctcgaga agtgtctaaa 120  
 ggagacagtt gatagccaaa caacagtttt ggattcactg actgattatg aaagaagcag 180  
 tagactggta tcaagaatca gtcagcaagg aggccctcac cagacgccag tgccatgttc 240  
 ttggacttct cagcctccat attcatgaac taagtttttg gaatccttag gcttccacgt 300  
 gtggaaagcc tgagctaacc tactggagga tgagccatca cctggagcag attcaggcca 360  
 tcctagttag agcctcccta ggccaagcaa ccgtccaact accagacatt gaccattcag 420  
 ccttgaacat tcagcacaaa gacaaaacag accagaccag aagagtccca cagaataggg 480  
 gaaactattc agagaaaact taagccacta agttttatgg tgttttgttc ttagtcagaa 540  
 gcataggcat actgacaata caaacggaaa tccttctaac gtagtggacc ttttcangcc 600  
 agcatttttt ccttgaaaac ctggagcatg tatccatctt atagcagaga tcaatttcac 660  
 aatgggtggg ctcttggatt tgaattgatg atgtaatgag ccctctttnc ngattgnaac 720  
 ttaattactc tgggnatttg ntggattccc aaccttctaa tatttacttt tcctctttan 780  
 taanc 785

<210> 487  
 <211> 797  
 <212> DNA  
 <213> Homo sapiens

<400> 487  
 ttgtnnnncc cttttnaaat ncctttggct anttgntctn tttgctngat cccatcgatt 60  
 cgaattcggc acgagnnngg actaccttnc aaaaccnggt ngggaagcnt gttacagaan 120  
 tgatntctan tcccctgnat tctggatgct gcagaccaac acctgccnac aanacncana 180

cacacacann	caancantat	catgtaagac	agnnecgntna	ntnnnnnatt	ntnatncttn	240
nncatattacn	cantnttgta	nantggntca	tgngtctata	natnnttgta	antattntnt	300
gananangac	ganantctga	atcttaagca	tatgctccat	cnttnnatat	gctntgggtg	360
agaggctngc	cntnattcat	nttnncatgg	agncaagttt	aatgcctcta	gantacattc	420
tgggcttcaa	gcatncttat	tttnnaactcc	ctgagtgatg	ggtggataaa	tcnaacattg	480
nctnagtgg	ntcaagacaa	ctttgntggt	ggttttgntc	acaatcatga	aaatgggttn	540
gccagataaa	tattttgata	ttagnnttcn	tttttnatat	anncggttag	gtttgaattg	600
nacnttnaaa	tgntnggggt	tgtnaagaca	ntggnttnca	atnnaattta	tnacatgaat	660
tgngnctcc	cctttggnga	aaccttaaag	aantnttnga	tacttcttca	taaaaggggtg	720
tgngatttng	naantttcgg	gggttttnaa	tttttnntga	agcttatttc	ntganaatnt	780
acttggnntta	ccaagcc					797

&lt;210&gt; 488

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 488

caaatcnntt	gctctngttc	tttttgcagg	atcccatcga	ttcgcgacag	ctctccaata	60
ctcagggttaa	tgctgaaaaa	tcateccaaga	cagttattgc	aagagtttaa	tttttgaaaa	120
ctggctactg	ctctgtgttt	acagacgtgt	gcagttgtag	gcatgtagct	acaggacatt	180
tntannggcc	caggatcggt	ttttcccagg	gcaagcagaa	gagaaaaatgt	tgtatatgtc	240
ttttaccggg	cacattcccc	ttgcctaaat	acaagggctg	gagtcctgcac	gggacctatt	300
agagtatttt	ccacaatgat	gatgatttca	gcagggatga	cgtcatcatc	acattcaggg	360
ctattttttc	cccacaaaacc	caagggcagg	ggccactcct	agctaaatcc	ctccccgtga	420
ctgcaataga	accctctggg	gagctcagga	aggggtgtgc	tgagttctat	aatataagct	480
gccatatatt	ttgtagacaa	gtatggctcc	tccgtatctc	cctcttccct	aggagaggag	540
tgtgaagcaa	ggagcttaga	taagacaccc	cctcaaaccc	attccctctt	caggagacct	600
acccttcaca	ggcacangtc	ccccaaatga	gaagtcgtnt	accctcatt	tcttnatctt	660
tttacttaaa	ctcaagaggc	agtgacaggn	agtcaggggc	aagacattac	atttttcata	720
ctttcccaca	tctgaaaaga	tgacagggga	aactgcaaa	cc		762

&lt;210&gt; 489

&lt;211&gt; 822

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 489

ttnnnnnnct	nnnggnnttt	cnaatncttg	tttctcgnc	tttctgcagg	atcccatcga	60
ttcgaattcg	gcacgaggat	tttcgaaact	cttcagctac	ttgccctttt	ttatctgaaa	120
ccatcatacc	ttctgaaaga	aaaaagcata	tcttcattga	cataacagaa	gtgagatggc	180
ccagtcttga	tacagatggg	accatcntnt	atatggagag	tggcattgtg	aagataacat	240
ctttagatgg	tcatgcatac	ctctgcctgc	ccagatctca	gcatgaattt	acagtacatt	300
ttttgtgtaa	agttagccag	aagtcagact	catctgcagt	gttgtcagaa	acaaataata	360
aagccccaaa	agataaacta	gttgaaaaaa	ctggcaaaat	ctgtatacgt	ggaaatttac	420
cangacagag	actgaagaat	aaagaaaatg	agtttcattg	ccagatcatg	aaatccaaag	480
aaactttaaa	gaagatgagt	tgtgtaaatg	gaactgaagg	gagggagag	ctgccttcgc	540
ctggtacaaa	gcacacatgt	gtatacacat	gggtcaagca	gtgctgggtc	gtggctgcct	600
gtccagagga	atgggaaata	ttcctttgtc	tttagcactt	catttttcta	aataaaaaatc	660
anccaatatg	tctaaaaaaa	aantttnttn	ataataaacc	tngaagccct	nttanaacct	720
tntnntggag	gtcctnnttt	accntatgat	tcccggaaact	tggataagga	atcccnnttg	780

gattgganat tttgggcna aaaccncna nnccttgaat cc

822

&lt;210&gt; 490

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 490

ntgtaancct	tttcaaactc	cttggctact	tgntctttct	gcaggatccc	atcgattcga	60
attcggcacg	aggccggacn	gtgactctgg	nnacgcttgc	gnccntnacg	tagntngnng	120
acctgtcang	anggaanaan	ggctggccnn	cngntgtacn	ctnaccgtcc	taaccccgcg	180
aggtccaggn	ccgctccttt	cggngnggat	tctcgcgga	natccctccg	gcagctcttt	240
gcaaagctgn	ttagaaactt	ctccaaaact	cggcntggat	acgactgcta	tagggctcgc	300
tgctgctttt	gtggagctct	tgctcctcta	tccttggcct	ctcctgggat	acggcccaag	360
gccaagtntt	cacgcangtt	ggtacgctta	tttcgttctg	gactctgggg	gctntgaann	420
ttcaccacgt	ggactgctgg	ggancgggnt	nccgancact	ngnntacctt	acnccanaat	480
ctgacaactt	ttctggacaa	cctaccanc	ttcaattggc	tngngagcnc	ntcngntgct	540
ggggntntcn	gtgcaaatgg	agnncnaatt	ggtgggcaaa	tngttgatgg	ncaaaacggg	600
aaaaagcaac	nnncaangct	tttggctnaa	agccgatang	acncaaatta	nttnccttgg	660
accttganaa	tttctcaan	nnttttnagn	anncnctttt	ttnccttggan	aaanacttaa	720
aagtgaacga	ttnttgggaa	anaaacaac	tataataact	naaagctttt	ntaaaaaaaa	780
annaatnnt						789

&lt;210&gt; 491

&lt;211&gt; 790

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 491

tecaaaatnc	ccttggantn	atccccctt	ncaatacctt	tccttngnac	actcccngtt	60
tngntngatc	ccatcgattc	gaattcggca	cgaggnaaca	aagaaggaat	gtcttctctca	120
tgtttnggtc	tatagaagac	gttaaagaaa	acttcagaa	agtgggtttg	aggcatgagc	180
caccacgcct	ggccaaagga	tttaatgaat	taatggatgt	acagtgctgg	ggctgttatt	240
ctagggcctg	cattgagact	cacattttgc	catcaaaaagc	cttttaagag	gtggaggttg	300
cggtagctg	acatgggtgc	actgcactcc	ggcctgagtg	acagagtgg	actctgtctc	360
acaaaaaaaa	taatgccctt	taaataatga	ataatagtga	tagaaaatgt	catttcttgg	420
acaaatgaaa	aattgaaatt	aatgtatata	attagatatt	attagctact	cttaggtagc	480
ttcatttggt	gaaagtgtga	caagtgaatg	aagttcacat	ctggaaatcg	ttgaacattt	540
ttcgttcatg	gaactcaatg	gctacgttag	tcgtttatgc	ttttcactgt	tgtggtaggg	600
gctttggaaa	gtnaatgcca	tcaacaatgg	atacagaang	acctggattt	ggaataaggg	660
caaaaattta	ttttgatggg	gctgaattgc	tctgccaggg	agcattttgg	gtattgagat	720
gaaaatggcc	tctctttgag	actgagctgc	cacctggcaa	attattgnct	gcttaanggt	780
tctctttatn						790

&lt;210&gt; 492

&lt;211&gt; 804

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 492

tcnaaatccc	ttttggnagn	ttcncncttt	gtttcccttt	nctnggetnc	ttgttctttt	60
------------	------------	------------	------------	------------	------------	----

tgcaggaatc	ccatcgattc	gaattcggca	cgaggctcctt	ttgaaccacc	ccaaagaact	120
caacatggca	aagcaaattg	taaaagcttc	ccgactgttc	tactttgggt	ccgcgcgaag	180
cccactcacg	tgtgatctgt	gttgcccctg	ggaggcccgg	ggcgaccgga	aaagggctct	240
ctcaagttct	gaaaagagaa	tctgccacca	gacgaattt	cgaccctga	gcttggtcgg	300
acgtatggtc	caaattcaga	ttaagggtgt	cacccaaccc	gagatgtcag	gaaaggcctt	360
ctgcagagaa	aatgtccccc	caccgcctat	ctgcagccag	gtgtgtgcca	cacggcagcc	420
ttcccgaaac	atagtatgga	ttttaaaaat	gtgtttattt	ttgtttctca	accactttat	480
aacgtatttt	ttaattttat	ttgtaatgtc	ttgttttgaa	gtattgctgc	tatccttgnt	540
atccttccca	ctgtttttat	cactgattta	ttttgtgaaa	agttgtacac	taatgttcta	600
tgtcaaaatc	aaaaagtatt	taatgaaata	ctagttctat	ttaatgtggg	ntatggaacc	660
ancttggaag	cacaaaacaa	acaggggatt	gtacaagcan	gcttggggcc	caagnaaggt	720
caaggttcat	ttggttacca	tatgccnata	aaacctcanc	gaanttttaa	aaaaaaaaann	780
nnnnnnaaaa	aancttgng	ggct				804

&lt;210&gt; 493

&lt;211&gt; 800

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 493

ggnnncnnttt	ncccccttt	tgaaaacccc	ttttggngga	ancccncttc	tttnaaatcn	60
cttggctact	cgctcttnt	gcaggatccc	atcgattcga	attcggcacg	agtatataac	120
aacttttgct	ttcaaagttg	ggtgggacta	gaacacacaa	tggaaggatg	gagtcaggag	180
acctggattc	ttgtgcccgc	tctggctttt	acagtctgcc	taactctatg	cagtcacttc	240
ctgccagcct	gtttccctac	ctacaagagg	gagagacact	ccctggccag	cctagttctc	300
agggtgaacg	aaaggtcatt	atcactgcat	cctctagtca	tttgcttctt	cgctaattaa	360
cacatcttga	gcacctgcga	tgttccagga	acaggagatg	gcagcgtgca	agataaaaagt	420
ccctgacttc	tagagactgc	atgttagtgg	caatcggcgt	ctaccgggcc	ttcaataaac	480
tactgaatga	aggaaaattc	tacctagcac	cagacacaat	tactgggttt	ctaaaatgga	540
attattcccc	cggccccctg	catccagcag	cctgctgcag	ggaagctcct	ccgaagctgt	600
aggcaggagc	gggacaaatg	cttgctatca	gcttcacaga	atgttaccta	agtactattc	660
ctacacagcg	ccttacagaa	caaacagtaa	aaaccaaag	gnaagcatgc	acnggcttaa	720
aaactcaaac	ttcctaacta	ctcagtaatt	anganggtca	ttttaccca	aaatagaatt	780
ttcnatttat	ccaataanaa					800

&lt;210&gt; 494

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 494

nggnnttcnnt	ctaactnaaa	cngttnggna	actcnctct	ntctgtngat	cccatcgatt	60
cgctaacaag	cgattctaaa	ccacctatga	gtattttctt	tagggctcac	ttaaatacat	120
gtttgtatat	actgtattct	agccagaata	atttttagatc	tgatcaggta	gtagctaaaa	180
ttagaaaaaa	acaaaataga	tgcttaaaga	atttgcattc	atttttgagt	ctaaatcttt	240
taaaaatatac	tgagatccac	atctagtga	atgtcagtg	caaaatatta	tagattatag	300
ctaaaatcca	gattaatact	catttgggg	tttttatagt	ggaacttcat	agtaatacaa	360
aaagcagatt	gtcttcctgt	ctccgctgct	cccacagtag	gtattgaaac	tggtaaaatc	420
agttttttga	tagtgtgtgt	atataagaaa	aaatagatac	acacattctt	ttttctcagt	480
caacacattg	attgaacact	ctggcaaaga	tgctgtgggt	gatgangttg	gagttcgaaa	540
agaagaagca	agcgtggcc	tgcttgaaa	gaacccgaaa	gtctttccca	ttcacttctc	600

tagaaaagctg	ccaagacaga	ngcagaaagg	aaatggatga	tagttctgtc	aagcacactt	660
ctgntctcnt	agaacttaga	aatgggttcta	agagaacaga	agttatngag	aacagttcnt	720
gtggaattca	acatcttggg	tgggacncat	tggcttt			757

&lt;210&gt; 495

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 495

ggnnnnnnntc	ttttcnaatg	cttggctctc	gttctttntg	caggatccct	cgattogcaa	60
gagagagtga	tagaattggc	agtgaatat	acgaaccacc	ctcctgccct	ctgggttcac	120
aatacgtgta	cacttgactg	tgaagtggct	gtgagagtgg	gtggagagtt	cttctttgac	180
cctcagcctg	cggatgcctc	tagaaacctc	gtgttgattg	caggaggagt	cggaattaac	240
cctctgcttt	ccatcctgcg	gcacgcagca	gatctcctca	gagagcaggc	aaacaaaaga	300
aatggatatg	agataggaac	aataaaaacta	ttctacagtg	caaaaaatac	cagcgaactc	360
ctgtttaaga	aaaatatcct	tgatttagta	aatgaatttc	ctgagaagat	tgcatgcagt	420
ttgcatgtta	caaacacagac	tacacaaatc	aatgcggaac	tcaagccata	catnacggaa	480
ggaagaataa	cggagaagga	gataagagat	catatttcaa	aagagacttt	gttctatatt	540
tgtggccacc	ttcaatgaca	gactttttct	ccaagcaact	ggaaaacaac	catgtcccaa	600
agaacacatt	tgctttgaga	agtggtggtg	ggaggcagac	aaaggcagaa	aaaattaaga	660
ggtgagatct	actcaggaga	gctcaaaann	aaaaaaaaaa	aaactnggac	ctntagaact	720
atagtgagtc	gtnttccgta	gatccagaca	tgataa			756

&lt;210&gt; 496

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 496

ctttnaatcc	cttgactcgc	tcttntgnag	gaccttatcg	attcgaattc	ggcacgagat	60
aacacacatc	acagtatgct	ctcagaaatt	tctttatttg	aacctatac	caatatctgt	120
tgatcaatga	ccatttttgc	tcagcatgga	gaaacagtgc	cctgcatgaa	gggtagttag	180
aataaaaagg	atcttaccac	ctttatcatg	agggtggcct	tgctctctcc	attccaagtt	240
gttctctgtt	ctagaaagca	gatgtagtag	acatctactg	tttttgccta	aacagaatcc	300
ctttttcctt	tttttggtta	aagtactcat	ccctaataat	acattgttct	ggaaggactg	360
aaaataacag	aactcagcac	catgatcgga	ccgggacaat	cagattattt	cattcctcag	420
caaacggaga	tcgatccgaa	aagtggaaat	atgagctctt	ctttggtggt	ggcatatgga	480
ccctgagaga	aagaacttta	attttttctc	ttggactgca	ataaagtata	gctgcctaaa	540
ataccgtttc	ctgacacttg	gaggtttgcc	acaatcgggtg	aaataaaggc	aagacgtaac	600
actggatgaa	aaaaaaaaan	nnnnnnnaaa	aaactcgagc	ctntagaact	atgtgatcga	660
ttcgtagatc	cagaatgata	gatcattgtg	agtttggaca	accacactng	atgcagtgaa	720
aaaatcttat	tgngaattgn	gatn				744

&lt;210&gt; 497

&lt;211&gt; 772

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 497

gnttgngtn	taantttnta	aggatccctt	tntntgaanc	cctttctgca	ggatcccatc	60
-----------	------------	------------	------------	------------	------------	----

gattcgaatt	cggcagcagg	caggagnaat	cacttgaacc	ctggaggtn	cggttgcagt	120
gagcacagat	catgccactg	cactccagcc	tgggcaacaa	aacgagactt	cgtctcaaaa	180
aaaaaaaaaca	tagaatttgg	atcctttgg	cgggttctcc	caaattcttt	tgagggtgcc	240
atgggtcaact	gcttcagctt	tgttttggca	acccctgcc	cgaagtcgca	tataggctgt	300
tcttcacctt	gtttccaagg	ctgaggaaca	gaaagtagcc	tctgttttga	ggagggtggaa	360
gttaagtata	catttatatt	ttactgtgac	ttgttcagga	ccacatttta	caaaatgcct	420
tgtttccttc	attgtttctg	gaaaggaaag	ttctattaat	attgntttac	tttgaatata	480
gaatagtttt	tttaattagg	gcttatattg	aaaaattctg	agtttaattc	aaatgtatgc	540
caataccttc	caaagtaagg	taatattcag	agacagttgt	tggtagtcag	atggccttaga	600
gaaaattttct	ggaatattca	cattcgaaga	tccttattat	gaatgtcttt	gacttaaaatc	660
taacacaaaa	ctgcacatta	ttctttgnac	attttcatta	tatagngtta	acaagcttan	720
ttgcaaacca	ataaataact	aagctattta	aaaaaaaaaa	aaaaaaactc	nc	772

&lt;210&gt; 498

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 498

nttnagcanta	nnagccgttg	tantgaagcc	cntttgctac	ttgctctttt	tgcaggatcc	60
catcgattcg	aattcggcac	gaggacccag	gtagaccagc	tcaagagttc	atgttctttg	120
tcatectect	gtgagctctc	tgtaaagtctc	tnctcttgccc	atcaccacat	ccctagtact	180
gggtatcagt	ctggccactt	ggctttcttg	tttgccccaa	tgtggtctat	tcttgatgca	240
gctaccaaag	taattgtnta	aaaccattat	accaagttac	tatccttgtc	aaaaccccc	300
gtaactgcc	atctcactta	gaataaaaatc	cggactcctg	tgaagcacag	nataaaactgg	360
cactgcctat	gcagcaacct	catctttacc	gtttctgcct	tgctcactcc	cttcagcgcc	420
ggtattcttc	ctgatgcccc	tagtacacaa	caactccttc	ctgctccaag	agtaggaaaa	480
tnactgtctc	tctgccagt	agattcctct	tctggtatta	cctntgcttc	attgctgaat	540
cttctgcaat	atcatcttct	aaaaagagcc	tttnaaaatc	accttttcta	ttatgcccta	600
ctcantttcc	agtccttgaa	tggccattcc	ccactttcat	agccacttaa	ttgctatctg	660
aaattacact	taaaatggtc	accttcatga	tgggaaggca	attaattgcc	tttgtcactg	720
gtatgtctag	agaacaagca	gnttggctca	tagtaggcac	tcaacaaaaa	ttt	773

&lt;210&gt; 499

&lt;211&gt; 735

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 499

gcttcaatan	ctttttctaa	ngctcttttt	gcaggattcc	atcgattcga	attcggcacg	60
agagtaccca	nanttgcna	gagtnntn	actgatntag	ccagggtggca	atnatgagt	120
aatggatnaa	naaaggcccc	ttagaatggc	aagatnncat	ttacnnagag	gtccnagtgn	180
canccagtga	cangaatgag	tttnaaggga	tgggttttaa	ctacagaccc	agnctctgcc	240
aatatngacc	ttgtgaactt	ccttgaagat	ggcancatgt	ctgagaccgg	aattatggga	300
catgctgtgc	agactgttga	aactntgaat	gaagggggacc	atagagtga	ggataagctg	360
atgcattttg	ttcacgtctg	gagactgcaa	agcatacagc	ccacaggatc	tggagagag	420
aaagaacagc	ctanagnaaa	tggctngaga	ngaaccacat	tcccatcact	gaacagggan	480
acgcttcaag	gactctctgt	gtggctgggg	ncctgactat	ngaccaccca	tatggtcana	540
naaattncac	cagctctnat	gagantattn	tgtcgcgtgt	tcaggatctt	antgaaggac	600
atcttacant	ttnccaanna	naagncatga	aatgtgacat	tctgcttgaa	naagacnata	660
ttttatcttc	atnaatgttt	aaatgtaaaa	nnnnananaa	aanactcgag	ctntnaaatn	720



tngtgagttt anang

735

&lt;210&gt; 500

&lt;211&gt; 926

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 500

tttaagccct	ttctactnct	cttttgcagg	attccatcgn	ttcgaattcg	gcacgaggat	60
ctctatacta	gtgaacagtg	ccagttccac	actttggact	tagaactgtt	ctctagttat	120
tgtaacacag	aatactgtca	atccctaatt	tacttaatgt	tacttattgg	aagtggggct	180
gatgaaatac	gcacaggagg	gaaatctact	gtgttttagg	acaggcagnc	ccagtgtata	240
aggagatcat	attccaaang	gttgtcagtt	ggntgtttgc	aacctggaat	gtattttcct	300
ttagagacca	ngttatccat	ggtggttagg	cccctagagc	agctggaaaa	agatgatcaa	360
accaataggt	tngctgacat	cnaataatgt	aataagtttg	ctaaaggaat	ctaccatcaa	420
atntnatatt	gnttccaggg	aaggttgttn	nttaanntnc	cntcttngtg	ncatantgga	480
cnntccentn	ccagtcant	ncntnannnc	tngggcnngt	ntngnnttng	tntntttngn	540
cnntnanca	atatttcata	tcnccctng	ctaaaattct	ttnanannaa	nttctcantt	600
tctcccttta	ctanaanttt	ngtntttnt	ccntttanta	tttnnnccct	tntntntcgt	660
tcnnanant	cattnnntnn	ttntnngctn	ntnnatcacc	cttanctcnn	tctcanntat	720
cntntctnta	ttatctctnt	attntctnct	tntnatnct	nttccnnntt	gtntanncna	780
ttatntcttg	ttntntntct	cncatctctn	tctntttctc	ngetnannnn	actccnnnnn	840
tcnctctct	nnnnanant	atatnctnct	ttngntatat	annnnntnt	ntacntanct	900
cnntnatnca	tnncnatatn	nttngt				926

&lt;210&gt; 501

&lt;211&gt; 706

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 501

naatncttgg	ctcttgttct	ttntgcagga	tcccatcgat	tcgaattcgg	cacgagaatg	60
caaagggctg	cagttctcat	tcaggctact	ttcaggatgc	acagaacata	tattacattt	120
cagacttggg	aacatgcttc	aattctaatt	cagcaacatt	atcgaacata	tagagctgca	180
aaattgcaaa	gagaaaatta	tatcagacaa	tggcattctg	ctgtgggtat	tcaggctgca	240
tataaaggaa	tgaaagcaag	acaactttta	agggaaaaac	acaaagcttc	tattgtaata	300
caaggcacct	acagaatgta	taggcagtat	tgtttctacc	aaaagcttca	gtgggctaca	360
aaaatcatac	aagaaaaata	tagagcaaat	aaaaagaac	agaaagtatt	tcaacacaat	420
gaacttaaga	aagagacttg	tgttcaggca	ggttttcagg	acatgaacat	aaaaaaacag	480
attcaggaac	agcaccaggc	tgccattatt	attcagaagc	attgtaaagc	ctttaaaata	540
aggaagcatt	atctccacat	tagagcacag	tagtttctat	tcaaagaaga	tacagaaaac	600
taactgcagt	gcgtcccaag	cagttatttg	tatcagtctt	attacagagc	tttaagtcca	660
aagatatcaa	atatgcacgg	gctgcacact	aatcagtcct	ctatca		706

&lt;210&gt; 502

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 502

ttnttttttt	tggttaccct	ttgctctngg	nctttttgca	ggatccctcg	attcgaattc	60
------------	------------	------------	------------	------------	------------	----

ggcacgagcc	ttccacggtt	atttcacaga	tatggagagc	tggaagcagg	gagtgagtct	120
ctgagtgttg	gaattgtaag	ggatcagaag	cagggatcag	aagcagtggg	gaagttcatc	180
caccataaaa	cacacaggtg	actttgcctt	gaatctgcag	gactgaagcc	aactcttggg	240
cacagaccct	tagtcccttc	cttggccact	ctaagtcaga	tagtccagag	ccaggccctt	300
tgggatgtga	caccgagata	aatcagagaa	aagctgtgaa	gcttggggaa	cagagggact	360
tttgggtgaag	taggtggtct	gcagtttcta	tcttcttggg	aaaagcaagc	tggaaaagtg	420
aacagtgggt	ggtaggccat	agtgtcccca	gctgggtgac	ataatgacca	cacagcacag	480
tgatgttatt	agcaactgtg	tgggtggagta	gttgtgggct	ggacaaatca	atcgtgtgga	540
aattgttagg	agttttatta	cattaaactt	gttaacctaa	aataccatca	aaaaaaaaaa	600
ntncnnnnnn	ncnccccacc	nancntncna	aaaaaancct	cganccttta	aaaacnnntn	660
gnngaggccn	tattttacgtt	anattccaga	cnttgaatan	ggatnccatt	tgnattgaaa	720
ntttngggcc	aaacccccaa	ccttngaatt	gccattngaa	aaaaaaatgc	cttttatttt	780
gnnt						784

&lt;210&gt; 503

&lt;211&gt; 764

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 503

ttntntttcc	ttgaancctt	tttctacann	cncctttgca	gatcccnctg	tcgaattcgg	60
cacgagagac	aaagaaaagg	tggcaatcat	agaagagttt	ntagtagggt	atgaaacctc	120
tctaaaaagc	tgccggttat	ttaaccccaa	tgatgatgga	aaggaggaac	caccaaccac	180
attacttttg	gtccagtact	acttggcaca	acattatgac	aaaattgggt	agccatctat	240
tgctttggag	tacataaata	ctgctattga	aagtacacct	acattaatag	aactctttct	300
cgtgaaagct	aaaatctata	agcatgctgg	aaatattaaa	gaagctgcaa	ggtggatgga	360
tgaggcccag	gccttggaca	cagcagacag	atttatcaac	tccaaatgtg	caaaatacat	420
gctaaaagcc	aacctgatta	aagaagctga	agaaatgtgc	tcaaagttta	caaggggaagg	480
aacatcagcg	gtagagaatt	tgaatgaaat	gcagtgcatt	tggttccaaa	cagaatgtgc	540
ccaggccttat	aaagcaatga	attaaatttg	gtgaagcact	taagaaatgt	cattgagatt	600
gagagacttt	tataggaaat	cactgatgac	ccagtttgac	tttcatacat	actgtatgan	660
ggaanattac	ccttagnatc	ttatgggtgg	actttattta	aaaacttnca	nnaatgttcn	720
ttcgacagcc	ttccatttta	acttcnaagg	cnncaangaa	ttnt		764

&lt;210&gt; 504

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 504

ttgtacntct	tttttnaaac	cctnngctac	ttgttctctt	tgcanggata	cctcgattcg	60
ggaatctcct	agaaagtgtg	gatttttcgag	ccatatacctt	ctgtggtaga	tcctaattgat	120
cctcagatgt	tggccttcaa	ccccaggaaa	aagaactatg	atcgagtaat	gaaagcactg	180
gatagcataa	cttctatcag	agaaatgaca	caagcaccat	atctggaaat	caagaagcaa	240
atggataaac	aggaccccct	tgctcatccc	ttactgcaat	gggttatatc	aagtaataga	300
tcacatattg	tgaactgcc	agttaacagg	caattgaagt	ttatgcatac	tccacatcag	360
ttccttcttc	tcagcagtcc	accagccaaa	gaatccaatt	ttagagctgc	taaaaaactc	420
tttggagca	cctttgcatt	tcatggctca	cacattgaaa	actggcactc	ctcctganga	480
atggtctggt	ngttgcttct	aatacacgat	tgcagctnca	tgngngaagt	tatggaagtg	540
gaatctatct	tagtccaatg	tcaagcntat	cattttgntt	actcagggat	gaaccangaa	600
acagaaaagg	ntcagcccag	gacgagccac	cttcaagcng	ttaanaagcc	agcaattaca	660

ttcacagtcn ccaggaaana aaaggncagn cctatcccc ctttncttgg caaaaggccc	720
gtnaacctta aanaaactgc ctttagccct ttatnntgga aagtggattc ncncttnatt	780
cttggacccc tgnen	795

<210> 505  
 <211> 774  
 <212> DNA  
 <213> Homo sapiens

<400> 505	
tnntntnntt nantngaacc ctttntctctt gctctttttg caggatccct cgattcgaat	60
tcggcacgag cacaaggaga agaagttaat taacattgaa ngatgagaag acatcttgga	120
agaacttgaa ttgggccttg gaagaagaac agccattcaa atagatagaa ttgtggtagc	180
aaaggcatag aggtaggaaa gtatagatct ccagggacag tagtcatggg gttggggcac	240
tgttggaatt taaggttgga aggatatatt ggagccccct gaatacggta acaaggcaca	300
ccttgggcag tggagagtta tcagagtgtt tgaaaaggag ggttattgag taaataaata	360
gactgggtact ttagggaattt taaaatgtgg atcattgtac tactaataac tatttatttt	420
atatttacta tctactaagt aattttacatg tattttcttg tactgactgt aaaccttctg	480
ggtgtgggtg ttttaagtgc cattttactg atnaagaaac tgaggcttaa atagttgaaa	540
taagtcaccc tgttagtgag tggccagaat gacaagtcag atctanggtt tgtctaactn	600
ccaaagatna tataaaaata atggatctct ccttttcctt tatgcataaa atatggggag	660
cntttttaa tcattaccca tncgattgnc caaaaaata cctttnggga aaactgatta	720
ttantattcc anaataaatt tcaacggcct gentngnctn ctttacaact ttnt	774

<210> 506  
 <211> 796  
 <212> DNA  
 <213> Homo sapiens

<400> 506	
gccnccccnn tttngntctc aacttgtagc ctttttgcan nancncgnnc tncttgtagg	60
ntcccatcga ttogaattcg ccacgangtt atattaaatt attctttggt tttctttttc	120
ttttaataaa gcttgcaagt tactaaattg tagtttcata aattctgtag taaagtatca	180
tcttggcagt gtgccaaagg tgaaaatgat gctttctcta acagagaaat tcttagtgac	240
tccagtcgta gaaaaacgtc tttaacaacct gaataagatt gaagaattgt gaacatacca	300
tggcctattg gatgaatcat ttgccgtagg ctaaatacaga ctgtaggggt tgtgatggat	360
ttatggagta tgtgggtata gaaatcatga atctagcatt tgttttcaga gattcaagca	420
tagtcttaag ggtanatcag aaatgacaaa tgaattcaaa acctagcagg tgcattgtna	480
atgtgtgccc agtntgtttt tggaaatggc agttccttgg ggtcatgttt ctactggcaa	540
aatttgcaat antgtntctat tgtntgtaat ttcaaaattt ataagattat cccccgttcg	600
cccaagtaaa acctgtntctg cccaatanaa tcctggantc gnngagaaat cgcntccatt	660
cgnngntcaa ctcgggatnc ntgcncttaa naaaatnttn tccnggancc ccntcatnan	720
gaanaacacc anactattnn gggnacctgn aangctcaat ngcccnggcc ncnnangnnc	780
nttttccngg naannn	796

<210> 507  
 <211> 774  
 <212> DNA  
 <213> Homo sapiens

<400> 507

```

ctnntttntt ttngaancct tngctcttgt tctttttgcg gatcccatcg attcgtgaag      60
aggagacggt gacctgggct ccttatgtgc ctgaaagagt ttgagtttcc tgtaaactcc      120
aaatcaacag tattttcaac aagaaatgtg caattgaaat caagtgtctg ttaagtgcag      180
ctaggatttc cacaggaaga cacttgaggt gaacagagtt atggagcagc aaaaacacag      240
atctatttgg aaaaagagaa aacatatgcg ttgtattttg cttcaattat aaaataccat      300
cctctcaaag gtggttctaa attacaaagg actttgattt ctaggtagat tctgggtaga      360
gacttccttt catattgagg cattaatgac accttttaac ctgggaagca atatgactgg      420
agttgtactt tgagaagatt aatcaggttt ggttcagaa tgaaagagaa gatgaagtca      480
agagattggt ttagaggctc tagcagaagc ttagtcatat ttcaaatga tcaaatatca      540
agaaaaattc tgagctgcat aactgtata aagtaatttt cagtgtttt ttcattggtta      600
tgatnaaaga actggattta nccagaaacc tttacctgga ttcaagattt aatttttccct      660
ttgagcctca tccttaaagg attttcgga aaacattaag gggagccaaa nccnattggn      720
tggttgggcn tgccctnaa ttgcctttgg acttttttaa ccgggctttt gnnn          774

```

&lt;210&gt; 508

&lt;211&gt; 724

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 508

```

cttgcccttg aaaancgttg gctactngtt ctttttgtag gatcccatcg attcgaattc      60
ggcacgaggg ggcgtgacc cggccggccc cacaccgct ctccctcttc ttgcccggcg      120
actcccttcc ctgcctccaa gacctgggtg ctcccactgt gagcccagct gtcccacagg      180
cagtcctcat ggacctagac tcaccttccc ctgacctcta tgaacctctg ctggggccag      240
cccctgtccc agctcccgac ctgcacttcc tgctggactc aggcctccag ctccctgccc      300
agcagcggcg ctcagccacc gcctcccctt tcttccgggc cctgctgtca ggcagctttg      360
cagaagccca gatggacctg gtgcccctgc gaggtctgtc gcctgggtgca gcctggcctg      420
tcctgcatca tttgcatggt tgtcgggggt gtggggctgn nntggggccc gtgcccacac      480
cangcnancc cctgtatggg atcanaggcn cgaagangca ntgnangctg ntggcanntn      540
aantactgnc tgggctggaa nangaactnn taaaagtctc ngcccnatc caccttggn      600
cccnanntn nncctntant cnnngggntn angtggtnnn nctnggggac agntcnnnt      660
ggntgncna tngnncnnat gnanacttgg ggttcannaa ncntttccnn atgnaancng      720
ngtc          724

```

&lt;210&gt; 509

&lt;211&gt; 803

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 509

```

tnnnnnntta tttcnttctg tctngntttt attacatcag ctcttttctt tttgcggtcc      60
ctcgttcgca attcagagac acacataaga aactggaaga agagaaaggc aaaaaggaaa      120
aagaaagaca ggaaattgag aaagaacgga gagaaagaga gagggagcgt gaaagggaac      180
gagaaaggcg agaacgggaa cgagaaaggg aaagagaacg tgaacgagaa aaggagaaag      240
aacgggagcg ggaacgagaa cgggataggg accgtgaccg gacaaaagaa gagaccgaga      300
tcgggatcga gagagagatc gtgaccggga tagagaaagg agctcagatc gtaataaggga      360
tcgcagtcga tcaagagaaa aaagcagaga tcgtgaaagg gaacgagagc gggaaagaga      420
gagagagaga gaaccgagag cgagaacgag aacgggagcc gagagagaga gcgagagagg      480
gaaccgggag cgagaaagag aaaaagacaa aaaacgggac ccgagaagaa gatgaagaag      540
atgcatacga accgaaaaaa aaaaaaaaaa aactcgagcc tnttaactat agtgagtcgt      600
attacgtaga tccagacatg ataagataca ttgntgagtt tggacaaccc ccacttgaat      660

```

gcagtgaaaa	aaatgctttt	tttgtgaaat	tttgngatgc	tnttgctttt	tttgtaacca	720
tttttagctt	gcaataaaca	agtttnccac	caaccanttg	cnttcatttt	ntnttttcan	780
gttcaagggg	aagtttttgg	aag				803

<210> 510  
 <211> 789  
 <212> DNA  
 <213> Homo sapiens

<400> 510						
gnntttnnnnc	nnttttaatn	tacatacanc	tacttggtct	ttttgcaggg	atcccatcga	60
ttcgaattcg	gcacgagggg	acccccacca	ttaagctaaa	gtaaaaccct	tttgagggaa	120
gagggagact	ggggagaagg	gaaaagagag	aaggcagggg	gagtagggag	agaaaacctt	180
ccagcagccc	agtaaaactgc	gggcgaagag	atctaccctg	ctccctccct	cccacagtta	240
ccattggcct	tgtcatcgca	agcatttgac	aaagacttgc	ttgtttgggc	ctgtcacctc	300
ctgaaaaggc	gcttttagctg	tggatgccct	tgattaaggg	agagagcgcc	taggagctgc	360
ctgccccanc	tggggtgacg	gctgtagggc	tgggtctatg	ttgcaagccc	tatatcttan	420
catgcagtgg	aaagtgetta	gctctctccc	tcctgacctc	tgggcagcca	gtcatcaaag	480
cagagagacg	tggcgccatg	tgggcagcat	gccagggttc	cttgctgact	cagcacttat	540
ttctgtagtt	ttaaaaaaga	atttaatgtt	tttggttgta	tttttttggg	ggggtgaggg	600
tgggcaaaaa	catgggggta	gttctgagtt	gttagaaatg	tttctgaatc	aagtttgttt	660
gaaaacacgt	tgtgcctttg	taccatttat	aagatgggtc	taanacccaa	gaactgataa	720
gctttggggt	ttttttgggt	tggtttgggt	ttttgcttca	ttttacccat	tcatgcctag	780
gttttccat						789

<210> 511  
 <211> 776  
 <212> DNA  
 <213> Homo sapiens

<400> 511						
catanagntc	ttgccttttt	gnaggacnct	cgattcgaat	tcggcacgag	cccccatctt	60
cactgggttat	tccacttatt	taaaatgtcc	agaataagca	aatctccata	tagaggaagt	120
agattagtgg	ttgcttcggg	atgggaggaa	tgggaagatt	gaggtctttc	ttttgcagtg	180
ataaaaatgt	cctaaaattg	actgtagcga	tggtcacaca	actctgaata	tgcttaagac	240
cattgaatta	cacactttac	gttggtgaat	tgtatggatg	taaattatag	ttcaataaca	300
tagttacaaa	agataatcaa	aagcatgaaa	gcactgttga	tgtggnttgg	atctgtgtcc	360
tcaccgagtc	tnatggtgaa	atgtaagccc	cctggtggga	ggcgatggga	ttatggggca	420
gantcctcac	aaacgggtta	gcccaccgc	tcaggctgtt	ctcctgatat	tgagtctca	480
tcacatctgg	ttgcttcaaa	gtgtgtggng	ccttccctct	atctcctact	gctctggcca	540
tataagangt	gcctgcttct	ccttcgcctt	ntacatgatt	gtaaagtttc	ctgagcctcc	600
tagaacnaaa	gctgctgngc	tttctgtcca	tctacangan	cgtagagcca	attaaacctc	660
tttttttttt	ttngagggnn	ntttntnnnc	ntccnnnca	ntttnanann	cctngnanng	720
gttttnaaaa	anaanannn	naannnnnn	nnccccngc	ccttttaaaa	taaaaa	776

<210> 512  
 <211> 917  
 <212> DNA  
 <213> Homo sapiens

<400> 512

ttatttcata	aactattggt	ctttttgcag	gatccatcga	ttcgaattcg	gcacgagggc	60
tgcgaggttt	tgcgcttttg	ctcctgatat	gcagcgacag	aattttcggc	ccccaactcc	120
tccttaccct	ggtccgggtg	gaggaggttg	gggtagcggg	agcagcttcc	ggggaacccc	180
gggcgggggc	ggaccacggc	cgccctcccc	tcgagacggg	tacgggagtc	cgcaccacac	240
gccgcgtac	gggccccggg	ctaggccgta	cgggagcagt	cactctccgc	gacacggcgg	300
cagcttcccg	gggggcgggt	tgcggtctcc	gtccccctggc	ggctaccctg	gctcctactc	360
caggtccccc	gcggggtccc	agcagcaatt	cggctactcc	ccaaggcagg	annanaanca	420
nccncanggt	tntncaagga	catntacacc	atttggatca	nggcgtntta	naaaaaaaaa	480
aatgttaatg	anttggaaaa	ntatttnaaa	gcctttnaat	gnttnnnnna	atccttnggg	540
nttggcctta	naaanccaan	attntngtng	gngggntntt	aannccnnnc	aantncnnnn	600
nnattncntt	naaaacnttt	nnccanggn	cnnaaaaaaa	nggggnaann	aaaaaacttt	660
tttntttnaa	nnantttttt	tggaaaattt	naaancntng	gaaaancntt	tnnntngttn	720
ntnangggaa	annantnttt	tgggnncnaa	aaaacntttt	naannntnn	nggttnnnan	780
nnnttaaaaa	ntttnnnccc	ccaannnnnt	nnanngnanc	ttttnnantt	ngggantaaa	840
nttnnnnnna	nggggnnttt	tttnngnnna	atttnnnnnn	annnnnnnan	nnangggntt	900
ttngnnngna	annntnn					917

&lt;210&gt; 513

&lt;211&gt; 780

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 513

tnnnnnnttt	aaatccatta	gctacttggt	ctttttgcag	gatcccatcg	attcgtgcgg	60
gagcaccgga	gcctgcggct	ccagacggac	gcccgcaagg	tgagggtgcat	cctgacaggt	120
cacgagctgc	cctgcgcct	gccggagctc	caggtctaca	cccgcggcaa	aaagtaccag	180
cggctggtcc	gcgcctcccc	ggccttcgac	tatgcagagt	tcgagccgca	catcgtgcc	240
agcaccaana	acccgtagt	ggtcncggc	ggcgcgggga	ggcccagggc	aatnngacag	300
nccctccgnt	tgaactcgcc	agtgtgcag	nccctactct	ttcanagttg	ggagccctgg	360
gacccaggca	ccaattgttc	ttgcaaaact	accctgcggc	acatcaacaa	gtgcccanaa	420
cacgtgtgta	ngcacacca	aggcggcg	taccagcgag	cttttgtgta	aatatgaaga	480
atgtctnaag	caaggggtgg	agtacatgcc	tgtgcctgg	tgcacccgan	gangaagang	540
gaaggacaaa	tggacngtga	acggccttcg	cccgcgggaa	agcttctggg	agcccacatt	600
caatgatgaa	gggggagctg	caagtgatga	cagcatgaca	gacctgtnc	cctgactttt	660
caccagaagg	accttgaaca	cngaggatgg	ggatggactg	atgatttttg	acaacaaaga	720
ggttgaaagg	caaancccca	aaaaaaaggc	cttgtgaagg	cagganaaan	acaacctntc	780

&lt;210&gt; 514

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 514

tttnnnngnt	ttannncatt	ttgctactng	ttctttttgc	aggatcccat	cgattcggaa	60
ttatagtatt	gacgtgaatc	ccactgtggt	atagattcca	taatattgct	gaatattatg	120
atatagccat	ttaataacat	tgatttcatt	ctgtttaatg	aatttgga	tatgcactga	180
aagaaatgta	aaacatttag	aatagctcgt	gttatggaaa	aaagtgcact	gaatttatta	240
nacaaactta	cgaatgctta	actnttttac	acagcatagg	tgaaatcata	tttgggctat	300
tgtatactat	gaacaatttg	taaatgtctt	aatttgatgt	aaataactct	gaaacaagag	360
aaaaggtttt	taacttanag	tagccctaaa	atatggatgt	gcttatataa	tcgcttagtt	420
ttggaactgt	atctgagtaa	cagaggacag	ctgtttttta	accctcttct	gcaagtttgt	480

tgacctacat	gggctaatat	ggatactaaa	aatactacat	tgatctaaga	agaaactagc	540
cttgtggagt	atatagatgc	ttttcattat	acacacaaaa	atccctgagg	gacattttga	600
ggcatgaata	taaaacattt	ttatttcagt	aactttcccc	cctgtgtaaa	gttactatgg	660
tttgggggta	caacttcatt	ctatagaata	ttaagtggga	agtgggtgaa	ttctactttt	720
tatggttggg	gtggaccaat	ggctatcaag	agtgacaaat	naagggtaan	ggatgattcc	780
caaaaaaaaa	aaa					793

&lt;210&gt; 515

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 515

cttattncat	nnagctcttg	ttctttttgc	aggatcccat	cgattcgaat	tcggcacgag	60
gttgtattgg	aaagcagtag	tgtggacgaa	ttgcgagaga	agcttagtga	aatcagtgagg	120
attcctttgg	atgataattga	atttgctaag	ggtagaggaa	catttcctctg	tgatattttct	180
gtccttgata	ttcatcaaga	tttagactgg	aatcctaagg	tttctaccct	gaatgtctgg	240
cctctttata	tctgtgatga	tgggtcgggtc	atattttatag	ggataaaaaca	gaagaattaa	300
tggaaattgac	agatgagcaa	agaaatgaac	tgatgaaaaa	agaaagcagt	cgactccaga	360
agactggaca	tcgtgtaaca	tactcacctc	gtaaagagaa	agcactaaaa	atatactctgg	420
atggagcacc	aaataaagat	ctgactcaag	actgactctg	atagtgtagc	attttccctg	480
ggggagtttt	ggttttaatt	agatggttca	ctaccactgg	gtagtgccat	tttggccgga	540
catggttggg	gtaacccagt	gacaccacac	tgattggact	gccctacacc	aatcagaact	600
cagtgcccaa	tgggccactg	ttttgactcg	gaatcatggt	gtgcactata	gtcaaatgta	660
ctgtaaagtg	gaaanggatg	tgccaaaaaa	ttaaaaaaa	ccnccaaaaa	agcttccaaa	720
aaaaaacctt	taaactatag	tgagtctgnt	acntagatcc	aacatgataa		770

&lt;210&gt; 516

&lt;211&gt; 825

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 516

tttccagttt	tanttttttc	anctttttnga	tenntttgca	ggatccntct	tttcgaattc	60
ggcacgagat	tctccctaaa	ttgtngatcc	cactgtttac	naaactgttc	tnttgtgctg	120
gcntgctnan	tgctntgtag	nnccctttctg	nacnntaggc	attgctcttg	gagaaacnnga	180
tgtgctttnt	ntnaaanggc	anaccagnn	tggnctgnnt	ttaatgatgc	agancctnac	240
tttatccaca	cctggcccgt	ttnacatttn	agtaangnac	gatatttggc	tgatggctga	300
acantttctg	aaatacacnt	ttagtgtag	gaantacaag	accnntaaag	gnctgccagg	360
ttancatctc	atctngcatt	cnmntccttt	ggcnanaaag	gganatntca	gaattatatt	420
tcttgatggg	gtctttttcaa	tcantgtatc	tgctgaaann	tcttaganaa	anctatgtgn	480
tcnccggtgtt	gtctaaaaan	atnctttcaa	anatgacccc	tggaaatncc	tganananagc	540
ttaaactgta	gaagacnggt	nggcaaaaaca	ccctncnaag	gttnttggna	angcccnant	600
ntgtttttgtc	tggcccatat	aanccttngcn	ccattnaagc	cnccggngag	ctttgnatnt	660
atattngngg	ngttactttc	tttgnnccctt	tgccgggaac	ancttnnata	atgcttntcn	720
ncccnanntg	gacntttgct	ttttgnnncc	nnaccccccc	aaagggngcn	cacctccant	780
gaaaaagtct	tttttnaaaa	gggtctccttn	ctnaaaaaaa	nnnnnt		825

&lt;210&gt; 517

&lt;211&gt; 1444

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 517

ctctcncnnc	nnnnncnntc	tctnncnntn	nnnnntnntn	nnnctcnnnn	cnnnatctnn	60
nnncnctnn	nnnnncntnn	cntcentctc	ttntntngct	ctcntntctc	ntncatcttn	120
ccnctattnt	cntnntntc	nnntcncnn	antnctnnnt	tctnccnnc	canctntcca	180
tnntntactn	tcnntnntct	ggctntnta	tntggggggt	ctattnttn	ncttaaateg	240
actngttcca	agtctentan	cngctctnt	ctnnctntct	ntgcncnncn	ctggggcctt	300
aattncccn	gctnttatan	aagngngnaa	ttaaggtntc	nnntctann	ctntgcaagg	360
ctaagtntta	gatccngnta	gaanncgnta	catgttgga	acngacanct	tnctgcncaa	420
agngggctna	ggcanngnnn	tntgcaaann	ctcnnntntc	nnancttggn	tcncgtagan	480
cggnncccc	tgaatttttn	ancnngganc	nttaaantnt	ntngnggtac	ganncncnn	540
ncgnnnnnnc	gnntannccn	canngttaan	tgcncncna	nnnantcaac	tctntntec	600
tnntnnaacn	nnnttantct	annatnnta	cnnntnagnt	tttccctcct	nacnctctg	660
tnctntntnn	atctntntct	tctccttna	ttnttatctc	ntntntntnc	tnccctnate	720
tatctnctac	ncctntntcc	ncttctccct	nnctctctc	atcatatccc	acgcnactna	780
nccctctnn	ctcttacctn	nnntctctcn	tctatctctn	nnaccctctt	tctntntctt	840
atnnnccta	tcctctactt	attctctctc	tattntncca	ctcacccttc	ntntntctnc	900
nctnntcttn	tnctattnt	actntccta	ttctcncctc	tctnntgnct	cccacccct	960
cttctctcn	ctctcctnnn	nnnactactc	tcacntctc	nnctntcnc	ctacnnntnn	1020
ananntcctt	antttcctnc	tcacacant	actcttccct	ctcatntca	nanctaant	1080
ntnctctcac	tctaccactc	tntnctccac	tcataatana	cttctatant	nctaactcta	1140
tcttcttaaa	cntctcctct	tatcncctta	ancctctctt	cntcgctanc	tcenntncaa	1200
ctcgnaaatc	tctccaatnc	tnccccactc	taaaaatnnc	nctcngant	cccacttttc	1260
ngngcanaat	nnaacncnan	tcnctccct	ttagctatct	ctctanaaac	ccntttctc	1320
aacaggnacc	nccctntntc	tcnaaatcct	catnctncta	ctttatatnt	cnccaagcct	1380
cncctntgta	anagcatctc	nctntccncc	aatnmanate	tcctnctcc	natanatntn	1440
anat						1444

&lt;210&gt; 518

&lt;211&gt; 706

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 518

ctaattggtg	gnngctcggt	ctttccgcaa	cancncngcg	antcgaattc	ggcacgaggt	60
ccgaagaaaa	agactgtggt	ggcggagatg	ctctctccaa	tggcatcaag	aaacacagaa	120
caagtttgcc	ttctcctatg	ttttccagaa	atgacttcag	tatctggagc	atcctcagaa	180
aatgtattgg	aatggaacta	tccaagatca	cgatgccagt	tatatttaat	gagcctctga	240
gcttctctaca	gcgcctaact	gaatacatgg	agcatactta	cctcatccac	aaggccagtt	300
cactctctga	tcctgtggaa	aggatgcagt	gtgtagctgc	gtttgctgta	tctgctgttg	360
cttctcagtg	ggaacggact	ggaaaacctt	tcaacccact	gctgggagag	acttatgaat	420
tagtgcgaga	tgaccttgga	tttagactca	tctccgaaca	ggtcagccat	caccaccaa	480
tcagtgcatt	tcagtctgaa	ggattaaaca	atgacttcat	ctttcatggc	tctatctatc	540
ccaaactgaa	attctggggg	aagagtgtag	aagcagaacc	caaaggaacc	atcaccttgg	600
agctccttga	acacaatgag	gcatatacat	ggacaaatcc	cacctgctgt	gtgcataata	660
tcattgtggg	taaactgtgg	atcgaaacagt	atggcaatgt	ggaaat		706

&lt;210&gt; 519

&lt;211&gt; 734

&lt;212&gt; DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 519

tngtaccaat	tatctgctgg	ctanntagcc	taaanagntt	ggtcngggcg	aattcggcac	60
gagggnaaag	cagnaagtaa	tgagcttgtc	cgtcagctgg	tagctttcat	tcgtnaaaga	120
gataaaagag	tgaggcgca	tcgaaaactt	gtggaagaac	agaatgcaga	gaaggcgagg	180
aaagccgaan	agatgaggcg	gcagcagaag	ctaaagcagg	ccaaactggt	ggagcagtac	240
agagaacaga	gctggatgac	tatggccaat	ttggagaaag	agctccagga	gatggaggca	300
cggtagcaga	aggagtttgg	agatggatcg	gatgaaaatg	aaatggaaga	acatgaactc	360
aaagatgagg	aggatggtaa	agacagtgat	gaggccnagg	acgctgagct	ctatgatgac	420
ctttactgtc	cancatgtga	caaatcnttc	aagacanaaa	atggccatga	agaatcacga	480
gaagtctaan	aagcatcggt	aaatgggtggc	cttgctaaaa	caacagctng	angangaacg	540
aagaaaatth	ttcaagacct	caaattgatt	gaaaatccat	tagatgacaa	ttcttgagga	600
agaaatgnga	aagatgcacc	aaaaacaana	agctttctac	acantnaaat	ccnannaact	660
ccatccntct	anaactatnn	gtgagtcctt	nttacntcna	tccagacatg	antancnata	720
cnattgatgg	aacc					734

&lt;210&gt; 520

&lt;211&gt; 701

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 520

ctaagtctgg	ctnttgctct	ttttgcagga	tcccatcgat	tcgaattcgg	cacgagccca	60
catgtaccag	gttgagtttg	aagatggatc	ccagatagca	atgaagagag	aggacatcta	120
cacttttagat	gaagagttac	ccaagagagt	gaaagctcga	ttttccacag	cctctgacat	180
gcgatttgaa	gacacgtttt	atggagcaga	cattatccaa	ggggagagaa	agagacaaag	240
agtgtctgagc	tccaggttta	agaatgaata	tgtggccgac	cctgtatacc	gcactttttt	300
gaagagctct	ttccagaaga	agtgccagaa	gagacagtag	tctgcataca	tcgctgcagg	360
ccacagagca	gcttgggttg	gaagagagaa	gatgaaggga	catccttggg	gctgtgccgt	420
gagttttgct	ggcataggtg	acaggggtgtg	tctctgacag	tggtaaatcg	ggtttccaga	480
gtttgggtcac	caaaaataca	aaatacaccc	aatgaattgg	acgcagcaat	ctgaaatcat	540
ctctagtctt	gctttcactt	gtgagcagtt	gtcttctatg	atcccaaaga	agttttctaa	600
gtgaaaggaa	atactagtga	atcacccaca	aggaaaagcc	actgccacag	aggaggcggtg	660
tccccttggtg	cggtttangg	ccctgtcagg	aaacacacgg	g		701

&lt;210&gt; 521

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 521

naacacttng	ctacnngttc	tttttgacag	atcccatcga	ttcgaattcg	gcacgaggag	60
atctctggga	tgctcagtga	gctgggttgaa	gaccagaggt	aaactgcaga	ggtcaccacc	120
cccaccatgt	cccaggtgat	gtccagccca	ctgctggcag	gaggccatgc	tgctcagcttg	180
gcgccttggtg	atgagcccgag	gaggaccctg	caccacagc	ccagccccag	cctgccaccc	240
cagtgttctt	actacaccac	ggaaggctgg	ggagcccagg	ccctgatggc	ccccgtgcc	300
tgcatggggc	cccctggccg	actccagcaa	gccccacagg	tgagggccaa	agccacctgc	360
ttcttgccgt	cccctgggtga	gaaggccttg	gggaccccag	aggaccttga	ctcctacatt	420
gacttctcac	tgagagccct	caatcagatg	atcctggaac	tggaacccac	cttccagctg	480
cttccccccag	ggactggggg	ctcccaggct	gagctggccc	agagcaccat	gtcaatgaga	540

```

aagaaggagg aatctgaagc cttgggtaag gattttggggc acagtaccag gagggggggct 600
tggtgccaga cctcatgagg aagaaggatt ttcctatgta cagagaaggg gaccctgtc 660
ctgttgggan gtgctgtgca aacctaacca aagttactaa cccctctggt ttctgnggtt 720
acacaaangg ggataaatac aaagctttnc ctnaactagc caattctatt tgggtttcct 780
gagt 784

```

&lt;210&gt; 522

&lt;211&gt; 719

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 522

```

ttctaatttn aatccttnaa atnggttctt tntgcaggat cccatcgatt cgaattcggc 60
acgagagAAC acaggtgtcg tgaaaactac ccctaaaagc caaatggga aaggaaaaga 120
ctcatatcaa cattgtcgtc attggacacg tagattcggg caagtccacc actactggcc 180
atctgatcta taaatgcggt ggcacgcaca aaagaacat tgaaaaattt gagaaggagg 240
ctgctgagat gggaaagggc tccttcaagt atgcctgggt cttggataaa ctgaaagctg 300
agcgtgaacg tggatcacc attgatattc ccttgtggaa atttgagacc agcaagtact 360
atgtgactat cattgatgcc ccaggacaca gagactttat caaaaacatg attacaggga 420
catctcaggc tgactgtgct gtctgattg ttgctgtcgg tgttggtgaa tttgaagctg 480
gtatctccaa gaatgggcag acccgagagc atgcccctt ggcttacaca ctgggtgtga 540
aacaactaat tgcggtgtt aacaaaatgg attccactga gccaccctac agccagaaga 600
gatatgagga aattgttaag gaagtcagca cttacattaa gaaaattggc tacaaccccg 660
acacagtanc atttgtgcc aattctggtt tggaaatggtg acaacatgct ggagccaat 719

```

&lt;210&gt; 523

&lt;211&gt; 710

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 523

```

tnnncttcaa atcgnrngct cttgttcttt ttgcaggatc ccatcgattc gaattcggca 60
cgagagatta tgagcatgta gaagatgaaa cttttcctcc tttccacact ccagcctctc 120
cagagagaca agatggtgaa ggaactgagc ctgatgaaga gtcaggaaat ggagcacctg 180
ttcctgtacc tccaaagaga acagttaaaa gaaatatacc caagctggat gtcagagat 240
taatttcaga gagaggactt ccagccttaa ggcattgatt tgataaggca aaattcaaag 300
gtaaaggta tgaggctgaa gacttgaaga tgctaatacag acacatggag cactgggcac 360
ataggctatt ccctaaactg cagtttgagg attttattga cagagttgaa tacctgggaa 420
gtaaaaagga agttcagacc tgtttaaaac gaattcgact tgatctccct attttacatg 480
aagatthttg tagcaataat gatgaagttg cggagaataa tgaacatgat gtcacttcta 540
ctgaattaga tccctttctg acaaacttat ctgaaagtga gatgtttgct tctgagttaa 600
gtagaagcct aacagaagag caacaacaaa gaaattgaga gaaataaaca ctggccttgg 660
aaagaaggca ggcaaagctg ctgagtaata gtcagaccct aggaaatgat 710

```

&lt;210&gt; 524

&lt;211&gt; 730

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 524

```

ttnnnnnttt aancnttcaa atcnctaggc tacttgttct ttttgcagga tcccatcgat 60

```

tcgaattcgg	cacgagccca	cactcggaca	ctgtggaatt	ctaccagcgc	ctgtcgaccg	120
agacactctt	cttcactctt	tactatcttg	agggcactaa	ggcacagtat	ctggcagcca	180
agggccctaaa	gaagcagtca	tggecattcc	acaccaagta	catgatgtgg	ttccagaggg	240
acgaggagcc	caagaccatc	actgacgagt	ttgagcaggg	cacctacatc	tactttgact	300
acgagaagtg	gggccagcgg	aagaaggaa	gcttcacctt	tgagtaccgc	tacctggagg	360
accgggacct	ccagtgcac	cggccccctnc	ctctaccac	ccccctcccc	cgcatgctga	420
tccccctgcc	caggtaaggg	ccctgccctg	gaagactgga	gggaggcccc	aagccacggg	480
gcatccccct	ctcccaggaa	gcaggagggg	ggcgggagg	ttttcctctc	aagccccacc	540
ctggggggccc	ggggggcagg	gctgccccct	cctccccctc	ccagtgaggg	acattttttg	600
gtaaaacctta	ttttcatttt	ggaaaatatt	tatgaataaa	tagttttata	tgaaaaaaat	660
tntngnnntt	nnnatnnnan	aataaaancn	tcgnncctct	taaaactata	gtgaagtctg	720
attaccttag						730

&lt;210&gt; 525

&lt;211&gt; 711

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 525

gcngntnttn	antttcaa	cgctnggcta	cttggtcttt	ttgcaggatc	ccatcgattc	60
gaattcggca	cgaggataaa	tacctcagcc	cctcgccttc	ctcaaccac	ctggcaagtc	120
ttcttaggat	ctgatcccag	ttttctggaa	gcaatctac	cccagccaa	gcttcccaga	180
gtcgagcctt	aatccttctc	acttctcagt	gtcagagcag	aaatgaatcc	tggggttgac	240
tgtgtccatt	cgggttatta	gcagctaaga	agcccagacg	agtagtgtga	gctgccttgg	300
gagcctcagt	gagggcactg	ggactggcct	cactctcttg	ccccagcct	agtgggcttt	360
ctcctctgtc	tctccggtgg	ccccaggcaa	tcgactgcat	cacgcaggga	cgtgagttgg	420
agcgccacag	tgcccgccca	ccagaggtct	acgccatcat	gcggggctgc	tggcagcggg	480
agccccagca	acgccacagc	atcaaggatg	tgcacggccg	gctgcaagcc	ctggcccagg	540
cacctnctgt	ctacctggat	gtcctgggct	agggggccgg	ccaggggctg	ggagtggtta	600
gcccggaata	ctggggcctg	ccttagcatc	ccccatagct	tccacagccc	cagggtgatc	660
tcaaagtatc	taattcacct	taacatgtgg	gaagggacag	gtggggcttg	g	711

&lt;210&gt; 526

&lt;211&gt; 692

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 526

tacangctac	ttgttctttt	tgaggatcc	catcgattcg	aattcggcac	gagagaacag	60
ggagaagaga	ggaagagga	gctgcagggtg	ccagaagaga	acagggcgga	ctctcaggac	120
gaaaagagtc	aaaccttttt	gggaaaatca	gaggaagtaa	ctggaaagca	agaagatcat	180
ggtataaagg	agaaaggggt	cccagtcagc	gggcaggagg	cgaaagagcc	agagagttgg	240
gatgggggca	ggctgggggc	agtgggaaga	gcgaggagca	gggaagagga	gaatgagcat	300
catgggcctt	caatgcccgc	tctgatagcc	cctgaggact	ctcctcactg	tgacctgttt	360
ccaggtgcct	catatctcgt	gactcagatt	cccgggactc	agacagagtc	cagggctgag	420
gaactgtccc	ccgcagctct	gtctcccctg	ctagagccca	tcagatgctc	tcaccagccc	480
atttctctac	tgggtctcct	tttgactgag	gagtcacctg	acaaggaaaa	acttctatca	540
gtactttgat	atgtcacagt	ttcatgttta	tccagttcaa	tgtattttta	aatttttctt	600
tgagacttct	ttgactgata	gattattgtg	aatgtgtttt	taaattttcca	aatgtttang	660
gattttcata	tctttcttat	gctgatttcc	aa			692

<210> 527  
 <211> 769  
 <212> DNA  
 <213> Homo sapiens

<400> 527  
 gttctnngttc tttttgcagg atccctcgat tcgaattcgg cacgaggcca agcctcggcc 60  
 tccactgcac ctgctgcgga gtgggcacct ttgcctgcaa ggccctttnc ccantgncca 120  
 atggtanttt aaccaggggt tttgncnntt aaggaggcct tngtgggtggg tngttaatct 180  
 ggccnttccn tattgaaaag ctccctgttat tgtccacaga ccagaaggac ttgtaacctt 240  
 ggtcccacag tctgacttng gcttttcaag caccagaaa acttagaggg aatcttatag 300  
 attccagaac ttaaggatac ctcaagggat agggtcacag ccaagaagtn caaaggaatc 360  
 ttcagtctgg aacaaaaaca gaaccctttc atgattgaca aangtcactt tctgtttgcc 420  
 tggaccaagc tactncagat catctgacca actcttaaaa atcacggcca ggcacagtgg 480  
 ctcatgcctg taatcccagc actttgggaa gcaaaagtgg caggatcatt ncagcccaag 540  
 agttcaagac cagcctgggc aacacagtga gtgagaccct gctctattta agaaaaatna 600  
 ttaagaaatt tattaaaaaa gaagaatcag gaaaccaagt ncaacccaac ttaacctcaa 660  
 tgaaccagcc cctaacacag atgangggat ttgggactga taagctctgt gctgngtcca 720  
 tggcccgta nttatcaagg ttgcactttt aaatgnggta tttttatgn 769

<210> 528  
 <211> 757  
 <212> DNA  
 <213> Homo sapiens

<400> 528  
 tnaatatcag ctcttgttct ttttgcagga tcctctgatt cgcangaggg tgttcgactg 60  
 ctngagccna gcgaancgat gcctaaatca anggaacttg nttcttcaag ctcttctggc 120  
 nngnattctg acagtggagt tgacananag ntaancagga aaaacaagtn gctccagaaa 180  
 anccgtgtaca gaaacataag acagggtgana ctctgagagc cctgtcatct tctaaacaga 240  
 gcagcatcng cagagatnat nacatgtntc atattgggaa aatgaggcac gttantgttc 300  
 gcnattttaa aggcaaagtg ctaattgata ttanagaata ttgnatggat cctgaagggtg 360  
 aaatgaaacc aggaagaaaa ggtatttctt taaatccana acantggagc cagctgaang 420  
 aacagattct gacattgatg atgcagtaag aaactgtgaa attcgagcca tataaataaa 480  
 acctgtactg tctagttgnt ntaatctgtc tttttacatt ggcttttgtt nnctnaatgt 540  
 tctccangct attgtatggt tggattgcag angaatttgn angatgaata cttnttttta 600  
 atgngcatta ttaaaaatat tgagtgaagc tnatngtcaa ctttattaag gattactttg 660  
 ctgccaccac ctagtgtcaa ataaaatcaa gtaatacaat ctttaataaac ntttaaacta 720  
 taaaaactcg acccttagac ctatantnag tcggttt 757

<210> 529  
 <211> 821  
 <212> DNA  
 <213> Homo sapiens

<400> 529  
 tnannnnannc annnnnnnnn nnnnnntttga agccattgct acttgttctt tttgcaggat 60  
 cccatcgatt cgaattcggc acgagagcaa ttccactcct agctccaccc acaggaaatt 120  
 gaaagcaaag acgcaaacag atgcctgtgc accaaagtgc acgggcaagc atccttcggc 180  
 cttaatgggc agcattccgt cgtcacaagc gggcattcat cctttcatca atagcgggca 240  
 gcattccgtc gtcacaagcg ggcagcattc ctttcgccac aagcgggcag catcttgtcc 300

gtcacaagcg	ggcagcatcc	ttcgccaaag	cgggcaagca	tccttcgtca	tagcggcagc	360
atcctttgcc	atagcgggca	aggtggaaac	cctgtccatc	cactgaggcg	tgcatagact	420
aaacatggcc	agtccaggca	ctggaatcca	ggcccgtaga	acggcgccca	cgggtcaaaag	480
gaatgagacc	ctgatgcact	gggcgacaca	gacgggagac	acagacttgg	agacatcatg	540
ctaagtgaag	agccaggcac	acggagcgga	cggcgtgac	ctgctcacgt	gatgtgtccc	600
gaatgggcac	gttcagaggg	aagaagggag	atggcgcttg	cgggtgcccg	gggacnnggg	660
ttgggagcga	cggttgctgg	tttgggggtt	ctttctgggg	tgangaantg	gttttgatat	720
ttggnccgtt	ggtgatgttt	gcatacctct	gaatatgctt	aaganccaca	gaattgacca	780
ctttaaatgg	atgaattgna	tggatattgg	aattacccaa	n		821

&lt;210&gt; 530

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 530

gnntttnnnn	nnnnnnnttt	tatnnntaca	gctacttggt	ctttttgcag	gatcccatcg	60
attcgaattc	ggcagagac	taccccggt	acggttcccc	catgcctggc	agcttgcca	120
tgggcccgtg	cacgaacaaa	acgggcttgg	acgcctcgcc	cttgcccga	gatacctcct	180
actaccangg	ggtgtactcc	ggccattat	gaactccttt	aagaaagacg	acggcttcag	240
cccgttaact	ctggcaccac	ggatcgagga	caagtgcag	agcaagtggg	ggtcgagact	300
ttggggagac	ggtgtgcag	agacgcaagg	gagaagaaat	ccataacacc	cccaccccaa	360
cacccccaag	acagcagtc	tcttaccgc	tgacgcccgt	ccgtccaaac	agaggccac	420
acagataccc	cacgttctat	ataaggagga	aaacgggaaa	gaatataaag	ttaaaaaaaa	480
gcctccggtt	tccactactg	tgtagactcc	tgcttcttca	agcacctgca	gattctgatt	540
ttttggtggt	gtgtctcctn	cattgctggt	gttgacggga	agtcttactt	aaaaaaaaaa	600
aaattttgtg	agtgcactcg	tgtaaaacca	tgtagttaa	cagaaccaga	nggttgacta	660
ttgttaaaaa	caggaaaaaa	ataatgtaag	gtctgttgta	aatgaccaan	aaaaaaaaaa	720
aaactcngcc	tntaaactnt	tntgagtcgt	nttcgtaaat	ccaan		765

&lt;210&gt; 531

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 531

gnntttnnnn	nnnnnnnttt	taagntactg	ctacttggtc	tttttgcagg	atcccatcga	60
ttcgaattcg	gcacgaggtt	cttcaaagcc	aaccaagaca	ggcttagcag	tttttagagct	120
tcagaacaaa	ttgcacaaa	ccagagttgt	ttatgctagt	gcaactgggt	gcttctgaac	180
cacgcaacat	ggcctatatg	aaccgcttgg	catatggggg	gaggggtact	ccatttagag	240
aattcaagtg	attttattca	agcagtagaa	cggagaggag	ttggtgccat	ggaaatagtt	300
gctatggata	tgaagcttag	aggaatgtac	attgctcgac	aactgagctt	tactggagtg	360
accttcaaan	ttgaggaagt	tcttctttct	cagagctacg	ttaaaatgta	taacaaagct	420
gtcaagctgt	nggtcattgn	cagagagccg	gntcagcaag	ctgcagatct	gattgatgct	480
gancaacgaa	tgaagaagtn	catgtggggg	cagttctggc	tgccaccaga	ggttcttcaa	540
atacttatgc	atagcatcca	aagttaaaag	ggttggtgcac	tagctcgaga	ggaaatcang	600
aatggaaaa	gtgtngtaat	tggctgcagt	ctcaggagaa	gctnnaacat	tagaactttt	660
gaagaaggcn	ggggagaatt	gatganttgg	ttcaactgcc	aaagtgtgtg	cantcactca	720
ttggaaaaa	tttctgtctc	cagcngggaa	aacttatggt	tacttggn		768

&lt;210&gt; 532

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 532

```

cgtntttttnn nncnannga aagcccttgg ctacttgntc tttttgcagg atcccatcga      60
ttcgaattcg gcacgaggat cagcccacct cggcctcaca aagtgntggg attacaggcg      120
tgagccacct tgcccaccca catcatacag ttgaaatgaa actttgccac aaccagcctt      180
tgctgtacac acacatatat cactgaacct ggttgaaata aagntttttt tctttttcct      240
ctggtattct gggttctgaa gtctggtatt ctggtattct gggttcaaaa gtatgacttg      300
agagtgttgc tctggtattc tgagagttgc tctgtattct gggttctgaa gattatttga      360
aaaataactc ctactacatt gaaatgcaga cttaaaaatt taaacattgg attaggcagt      420
caaaaaaacc aagcaagcat aaaaggtcaa taagttgtaa tcttgatagt aaaggtggaa      480
aacttattat aaatggaaag aaagtttatt tccttttttg gttgatgggc agtatgccat      540
attataccca aagttctttt aaaaaatatt tccatcacca tttttattta aaataaacat      600
ttgaggggaag taccaaggca gcttttttcc tcaaaagtac ctggtcctct ttgggaatag      660
cacattttan gggcattggg taatcctgag attttactca ntaaatcctg atggtactgg      720
gtgtaaaata tctttagtng gattgaaggc cttngggggg a                          761

```

&lt;210&gt; 533

&lt;211&gt; 735

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 533

```

taaacatcng gctacttggt ctttttgcag ggatcccatc gattcgaatt cggcacgaga      60
cactgtccca ctccatcacc caggctggag tccagtggtg tgatcatagc tcgctgcac      120
ctccagttcc tgggttcaag ccacccctcc tgcctcagcc tccccagtag ctggaactac      180
aggtgtgtgc catcacacct ggctttacat tttctgtggg ggtcttacta tgttgccag      240
gccggtctca aactcctgag ctcaagtgat cctctgcctc agcctccaga gtatctggga      300
ttacatatgt cggctaccgt gtctggcctg tcacatcttt ggccactatt tgcttgtaa      360
aaggtataat gaggtggtac ttatcatttt tactgngtct catgttttgt atatttttgt      420
ttcatcaact aagatgcact gtaacatctc tgaaatctgg atatattatc aatggtttat      480
catagttttg ttagcaatac actgtctttt agtgggtgct aaaataatgg tatagtttgt      540
aggtgatctt agatttgatg aagcacagta tgcaggtagg cctaattggg gaagatggta      600
atataaaaagc aagaagtatt ttttttttgt aatgactgaa agctgtctgt ggatgacct      660
cccttttctt taaacacgat tntntcactt ncaactncaa acttgctcaa ctaatnctt      720
aaaaataact tgagc                          735

```

&lt;210&gt; 534

&lt;211&gt; 735

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 534

```

natngnttgc tctngttct ttttgcagga tcccatcgat tcgagacaac ccagaaacaa      60
attcatacat ctatggtgac cacttttgac aaaggaatga agaacataca ctggggggaa      120
agataatgtc ttttaataaat ggtgctggga aaactggntn tccantntgc agaagaatga      180
aactagaccc ccatctctta gcatatacaa aaatcaaaat taattaaaaa gttaaactta      240
agacctcaaa ctatgaaaca gctaaaagaa aacatcgggg aatctctcca ggacattgga      300
gtggggcaaag atttcttgtg taatacctga caaacaggca accaaagcaa aagtggacaa      360

```

atgggatcac	atcaagttaa	aaatcttctg	cattgcaaag	gaaataacaa	agtgaagaga	420
cacccataga	atgtgagata	atatttgcaa	actatccatc	tgtattaggc	catttttgaa	480
gtctacaaag	aaatacttga	gactgagtaa	tttataaaga	agaggtttaa	ttggctcacg	540
gttttgcagg	ctgtcaggaa	gcatggtgct	aacatctgat	cagcttgtag	ggaggcatca	600
ggaagtttcc	acccatggtg	gangcaaaag	gggaataagt	ttctccatgg	cagggtgcagg	660
gcaaaaanan	gggggaaggg	aagtgcncna	caaccagatc	ttgtgagtnc	tcagatttgn	720
ggngggngct	tgngg					735

&lt;210&gt; 535

&lt;211&gt; 735

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 535

tnaannanag	ctacttggtc	tttttgcagg	atcccatcga	ttcgaattcg	gcacgaggtc	60
catacatgga	gctccctgga	cccgtgtgct	ctcgtgtgac	tgaacgtttt	gtgatgaaag	120
gaggagaggc	tgtctgcctt	tatgaggagc	cagtgtctga	attgctgagg	agatgtggga	180
attgcacacg	ggaaagctgt	gtggtttcct	tttaccttcc	agctgacct	gaactcctga	240
gcccagacaa	ctaccacttc	ctgtcctcac	cgaaggaggc	cgtggggctc	tgcaaggcgc	300
agatcactgc	catcatctct	cagcaagggtg	acatatttgt	ttttgacctg	gagacctcag	360
ctgtcgtctc	ctttgttttg	ttggatgtag	gaagcatccc	agggagattt	agtgacaatg	420
gtttcctcat	gactgagaag	acacgaacta	tattatttta	cccttgggag	cccaccagca	480
agaatgagtt	ggagcaatct	tttcatgtga	cctccttaac	agatatttac	tgaaggaatc	540
taggttgtat	tttcagtggg	caatgggaat	aaagcatttc	taaagcaccg	actggagagg	600
aaggcaacag	aaacaaggag	agaagcccga	gagacatgtc	tgcgtgctgc	cacgcactctg	660
ancgattgct	cttgtgaaga	gtttgtcact	gaacattttc	aggggaggct	gtttaccag	720
cnatgtntcn	aacan					735

&lt;210&gt; 536

&lt;211&gt; 785

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 536

gcccccnnn	nnnnnnnttt	tcaaanncn	ttnnnnnnnn	nngnnnnnttt	tannnnnttn	60
ttannnnaca	gctcttggtc	tttttgcagg	atccctcgat	tcgattcggc	acgagctacc	120
ttgggctggc	cctctatnat	gctntgaggg	gagctgggac	agatgacnt	nccctcntca	180
gngtcatggn	tnccangngt	gagnttnatc	tgccnnacat	ngtgacggag	tttaggaaga	240
atgntgccnc	ctctntttat	tccatgatta	aggganatcc	atnnggggac	tataagaaaa	300
gcnnntttnc	tgctntgngg	ncaanangan	tnacnngncc	cgggnnanag	ctcctatgct	360
gtntgcctgc	accacccct	gccttccttc	atacctttcc	ntggatatgn	atgccagggc	420
ttnnacatt	gcctnattna	tactnacntg	ctnatgacca	anacatncac	gtgataacac	480
aaacantggg	tgettgnntc	tgatcnctag	aggnganctn	ttggnnngnt	ggagnactna	540
antnttctna	gtgtgnacttn	agttcaatgc	ctggccatnt	gcnatnacct	tatatcntnc	600
aaagaggcta	ctgtgctttt	ancctttttt	aaaacctcca	tctgtattac	attgnnaacc	660
angtttcttt	aatnaggagc	ttgacctcta	nantgggaac	tcttggaat	ggnccttagtg	720
aagttcgena	ctaacttaac	ctgaaaatta	tnatgnnctg	tttnacctat	catgttnata	780
actnt						785

&lt;210&gt; 537

&lt;211&gt; 967

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 537

```

agtangggcgn ttcctaattnn annnggctaa ggcactttna aagangagge tngcgtgntg      60
aataccgunc gaggggggat nacaatagta nacnnggtnc caatncatgc ttaacaccgc      120
atntctttac ccccnannnn ncacanatgc agacncacac atngcanncg nacacncaga      180
cacacacang caagcactnn catgcatggc ccatgctcac acacntgnan nnaacatgcn      240
gtagacatnt nagacacgtc atgtnacaca tgnnacacan gnnnaanaca ctgctttnc      300
ngcanacnca gacggcacnn ngagacanac atgcnnaaac aacatgctcn ctcacntnna      360
nncgntgggc cngtagtagt gtactgtggg tgnnactggg tgccatcnac nnngtatttt      420
acgnnctttt aactaaaaan cttggagcct tnanttnntn tggtgantnc aatncctana      480
antnncttga gngggatgaa cctaanannc ctggccctnn tnccnctttc aaggccnagn      540
aattganatt attncntant ngnnacagaa gcttntggta ncangngncc cgagnctnt      600
tnaaanttnn ctnttttnan aatnaaacat tttancgggt ctnaggancc gngcctncng      660
ggtanggann naattgtnc tgggnatagt tctcacaant natnttnaag gggnaaagn      720
atnngngngg nccntntatg nggcnngcca annaangggg tcgnggttaa natattccaa      780
gntaacanan gnacnatggn accnatccct ntngaagna aggaactncc tgnncgacta      840
nnnactatgn naaatattct cacatntaca naaaaagnag gnnccnnggt ncttnaagnt      900
tntgcatagn nactatncnt gggacnggtt aacnnanatt ntatgcttta nnngatnggg      960
gcttnnn
967

```

&lt;210&gt; 538

&lt;211&gt; 892

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 538

```

gctagttnga agaggtgttt ctaangnntn ggaatcgaca tctnnnnagg cngncntgc      60
gattcgcttt gctctctcca ttccaagttg ttctctgttc tagaaagcng atgnmgggnt      120
acatctactg tttttgccta aacagaatcc cttnttcctt tttttgttaa aaggctcatn      180
cctaataatta cattgctctg gaacgantga caataccana actcagcacc ntgatcggac      240
cgggacaatc agattatcta attcctcagc aaacggagat cgatccgaaa agtggaaata      300
tganctcntn ctttgtgntg gcatatggac cctgagagaa agaaacttta atcttttact      360
cttggactgc aatnaagtnt agctgcctaa aaatcnnttt cntgacactt ngnaggtttg      420
tccacaatcg ggngaaatta nngggttnnga cntaancact ggatgaaaaa aaatnccgnt      480
tantntatt ncnnttccan ncttntnaaa tanananttt ntanccttn nntaatacta      540
ttanntatat ntntnnncc cnatnnncc ttcttntctc tacnncnntn cnatntnnnn      600
nnangntcnn cnannnttc tnttatttct annatatntc ntancnttna ctaaaacctc      660
cnctcgtnna nattncnnta taatattntc tctaganttt ntntntnttt gnnncttaaa      720
anctcntcta tccctantat nantnattct taccatnaaa tacactanaa gtnntntcac      780
gagacncgnt atgttantnc anactataat cgcttncatn tanntatatn taaaantgct      840
atncagnnag nngntnttat atntttanct ngnnaggnta tctcnatan cc      892

```

&lt;210&gt; 539

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 539

```

gnnnaggttn tagancagct cttgttcntt gngcaggatc cctcgattcg aattcggcac      60

```



```

gagagtgtca gttttcctaa tctcagtcca ggtaggaatt aagaaatata tcaagtgttg 120
atgctatcca agcatgttg ggtggaagg aattggtgcc cagaaaaatgg gactggagtg 180
aggaatatct tttcttttga gagtaccccc agtttatttc tactgtgctt tattgctact 240
gttctttatt gtgaatgttg taacatttta aaaatgtttt gccatagctt tttaggactt 300
ggtgttaaag gagccagtgg tctctctggg tgggtactat aatgagttat tgtgaccac 360
agctgtgtgg gaccacatca cttgttaata acacaacctt taaagtaacc catcttccag 420
gggggttcct tcatgttgcc actccttttt aaggacaaac tcaggcaagg agcatgtttt 480
tttgntattt acaaaatcta gcagactgtg ggtatccata ttttaattgt cgggtgacac 540
atgttcttgg taactaaact caaatatgtc ttttctcata tatgttgctg atggttttaa 600
taaagtcaa agttctcctg ttaaaaaaaaa aaaaaaaaaa actcgancct ntanactata 660
gtgagtcctt attacgtaga tccagacatg atnagatcat tgatgaattt ggaccaaccc 720
aactagaatg cagtgaaaaa aatgcttttn t 751

```

&lt;210&gt; 540

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 540

```

gntnngntcn agancagcta cttgttcttt tgcaggatcc ctcgattcga attcggcacg 60
agcctgcagc cactaatgca ttgtgtatga taacaaaaac tctggtatga cacattttct 120
gtgatcattg ttaattagtg acatagtaac atctgtagca gctggttagt aaacctcatg 180
tgggggtggg gtgggggtgt attccttggg ggatggtttg ggccgaatgg ggagtggaa 240
atttgacatt tttcctgttt taaattctag gatagatttt aacatccttt gcggtcccag 300
tccaaggtag gctggtgtca tagtcttctc actcctaate catgaccact gtttttttcc 360
tatttatatc accaggtagc cactgagtt aatatttaag ttgtcaatag ataagtgtcc 420
ctgttttctg gcataatata actgaatttc atgagaagat ttattccacc aggggtattt 480
cagctttgaa accaaaatctg tgtatctaata actaaccaat ctgttggtatg tgggttttaa 540
aaaatgtttg ctaactaccc aagtnagatt tactggatta aatggccctt cgggtctgaa 600
aaagcttttt taactttctn gcttaaaatg ccgtttaatt ttgataagat ncttnaaatn 660
gcctccaaaa gtgttananc caatcatttn aaataaacn ggntgtatat tgcattnatgt 720
gtacatgcnt atncccttct ggttaaaact naaaaaaaaa t 761

```

&lt;210&gt; 541

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 541

```

ggtttanttt aaatccntnc ncagctactt gttctttttg caggatccca tcgattcgaa 60
ttcggcacga gcggacccat cggagcgtaa cctggatctc cgcaggcctg gcggaggccg 120
gccacctgga ggggcattgc ttggttcgcg tgggtancaga ggagcttgag aatgttcgca 180
tcttaccaca tacagttctt tacatggctg attcagaaac tttcattagt ctggaagagt 240
gtcgtggcca taagagagca aggaaaagaa ctagtatgga aacagcactt gcccttgaga 300
agctattccc caaacaatgc caagtccttg ggattgtgac cccaggaatt gtagtgactc 360
caatgggatc angtagcaat cgacctcagg aaatagaaat tggagaatct ggttttgctt 420
tattattccc ttcaaattga aggaataaaa atncaacctt ttcattttat taaggatcca 480
aagaatttaa cattagaaag acatnaactt actgaagtag gtctttttaga taccctgaac 540
ttcgtgtggt cttgnctttg gttataattg ctgtaagggt ggagccagta attatctgca 600
gcaagtagtc acncttttca gtgatatgaa tatcatcttt ggcttggang ccantngaca 660
acctgncatt actgactttt tgaaaaaac cctctggata ttgatgcctc ggggtgtggt 720

```

ggactgncat ttagtggacc ccgaatcc

748

&lt;210&gt; 542

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 542

gtnnnnntng	tgtaatcgct	tggtgcagg	atccctcgat	ggcgaattcg	gcacgaggtg	60
ttgctcaang	agcagacccg	actccntaag	gtcatcattg	aatgggcatn	atangtttga	120
anactgtcca	ananantang	ngtcaataca	tcaacnnctt	tanntgcttg	atattggnat	180
tgaanaacac	angnetcngn	ctagttcgcc	tganatgatg	tttaagatac	tccggaagga	240
gacanantgt	tntgantgcg	gattaganac	cacngaagnn	acactnaagg	ancancatct	300
ccacctngna	actgnattnn	cngaccanaa	aagngaactg	gaccaaagtc	tctcaaaggt	360
gctggcagct	taanagcgtg	ttangactct	gcacgaagan	gacaggtntt	ntgagagcct	420
ggnnannaca	ctctcccaaa	ctaaactgna	nctttcaaca	nangggancc	ccannttggg	480
ggagaaatca	ggtganctgt	tggcccttcc	acaaagangc	aaattctntg	agggcnagac	540
ttnanctttt	ttgcngaacc	agtncttgac	tgactaaatg	aaagcttttt	aagccaggtg	600
gcccancctt	aangaagcna	ctttttaatc	cancggaacc	ngcttgagan	aaaaccnttt	660
ttgacccaaa	accnggagaa	ccagctggcc	taccaaaggg	aaatgggccc	ccatttgaac	720
ttgggggtnc	ccangaacaa	nccttgnccg	ggncaaagcc	cnttgttgga	aaggacctca	780
acct						784

&lt;210&gt; 543

&lt;211&gt; 764

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 543

ntantaaatc	ccttgctctt	gttctttntg	caggatccca	tcgattcgaa	tnccggcacga	60
ggacccggcg	gcgcggacag	gcttgctgct	tcctcctcct	nngactcacc	attncaganc	120
agaanntgaa	aaaatggng	anctcaccca	ggtaanggat	gatgaagtnt	tnatggctnn	180
tgcatactat	gcannanttn	tncttntgna	aatgatgcnt	atgagtactg	taanngnntt	240
ctatncattg	ncaagaangg	ntnttgnaaa	tncatangac	tgtgtagcat	tcggcanagg	300
agaaaatgnc	aagaactatc	ttcgaaacaga	tgacanagtg	taacgggtac	gcagagncca	360
cctgaatgac	cttgaaaata	tnattccatt	ncttgnaatt	ggcatnctgt	attccttgag	420
tggtcccgac	ccctctacag	cnntcctgta	ctttagacta	tntgtcggag	cncggnteta	480
ccacaccatg	tgcataattg	acaccctttt	cnnatccaaa	tatagctatg	actttttttt	540
gtaggatatg	gannactctt	tccatggctt	acacgntgcn	gtaaagtaaa	ttggccctgt	600
gcagaaaaac	attccactca	gtnttccaan	tggcttntta	aggaattctn	gaccttgcaa	660
ttnatantgg	agnnctttcc	ttaagattta	aaggtttgan	ggngagccnn	aggaattntn	720
aaccnggggt	aaaccctttt	tggaattttt	agcnttgnaa	anaa		764

&lt;210&gt; 544

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 544

gatgtggnt	ncnnatgctt	gnngatccct	cgattcgaa	tcggcacgag	gaaatgtgta	60
tttcagtgac	aatttcgtgg	tctttttaga	ggtatattcc	aaaatttcc	tgtattttta	120

ggttatgcaa	ctaataaaaa	ctaccttaca	ttaattaatt	acagttttct	acacatggta	180
atacaggata	tgctactgat	ttaggaagtt	tttaagttca	tggtattctc	ttgattccaa	240
caaagtttga	ttttctcttg	tattacattt	tttatttttc	aaattggatg	ataattttct	300
ggaaacattt	tttatgtttt	agtaaacagt	atttttttgn	tgtttcaaac	tgaagtttac	360
tgagagatcc	atcaaattga	acaatctggt	gtaatttaaa	attttggcca	cttttttcag	420
attttacatc	attcttgctg	aacttcaact	tgaattgtn	ttttnttttc	tttttggatg	480
tgaagggtgaa	cattcctgat	ttttgctgat	gtgaaaaagc	cttggtattt	tacattttga	540
aaattcaaag	aagcttaata	taaaagggtg	cattctctca	ggaaaaagcc	atcttcttgn	600
atatgtcnta	aatgtatttt	tgncctcata	taccggaaag	ttcttaattg	gattttacca	660
gctgnaatgc	tttganggtt	ttaaaaataa	taacattttt	aataattttt	taaaaggaca	720
aactttcata	atnatcccg	ngntcctttt	ccnnn			755

&lt;210&gt; 545

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 545

agntttttnaa	tcctttggcc	antcgcncctt	tntgcangat	cccatcgatt	cgaattcggc	60
acgagaaaaa	gtnaagcttt	tcatgagcac	anntnccttg	cattgttnga	tgttactgat	120
attcgtaaaa	tgaatatttt	ctgttttggt	ctgttnnatt	tttttgagac	aagtcttgct	180
ttgttgccca	ggctggagt	caatggcatg	atcttggtct	actgnaaccc	ctgccttgcg	240
agttcaagt	attcttctgc	ctnagncctc	tgagtagctg	ggattacagg	cgctcaccac	300
cacacccagc	taatttctgt	cttttnagtn	gacacaggtt	tttaccatgn	tggccaggct	360
ggtctcaaac	tctgacctg	aaactnctca	caccngtnat	ctcagcactt	tgggaggctg	420
angtggaag	gatcacttga	agccatgagt	ttgagaccag	cctgngcnac	acagcngaga	480
cccngtgnt	gtacaaaagc	ttncnacatt	tancgtgctg	aggagtnnct	caccntaac	540
ttccancnan	tcnnttaagc	nnanncatnt	tgaacacntg	agcccannta	nggtcgatgc	600
tnntagtnaa	ccgtgactgg	accacttaca	gtccaagccc	gggtngcctt	ataaaagaan	660
cggaaaacat	ttcnttaatt	cgggttnnag	cnttanctat	ttcggaatnc	cttgngtttt	720
naaaaacttg	aatctccaan	aaacagggtt	ttttcttttg	gnccann		767

&lt;210&gt; 546

&lt;211&gt; 989

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 546

tncccttggt	gaaanccctt	tgctcctttt	tncnccggt	tgncatncna	ttegctcagc	60
tgaggcaatt	aaactggaaa	agaaatagat	tgaaaagata	ctntngaaga	agcagtacag	120
aagttggggg	actgaaggag	agggagccac	tgcaggtgct	agctgcttaa	ggggatacca	180
gtccttttac	agatataata	gatacagctt	ctgaggtgga	gggtgatagg	agtgtgtatg	240
agaaanttgc	agnttnacaa	ctgctcntgc	ctectnggca	anaggannan	cntttcncn	300
nttncnnccc	ttatnqnaca	cacattgncc	tgattggncn	tnccncngct	agcttncagt	360
cttnantnta	ctcannagnn	nnnnggggaa	cncnctntcn	nantatgntc	ccttttcctc	420
tnncntnncc	nnatancacc	ccnctcnctt	tcctttctaa	acttncacan	ntccctgana	480
atgncttccg	aatggantct	tngaatttct	ncgcccctnc	ntentcataa	tenttttgc	540
netcngctc	nccctcattt	tncctagctc	cnccttctnn	ttnactgnct	ttaaatntta	600
ttanncnct	ntnctntcn	atctncaant	ttcnnnccn	acnnntttt	netnntnca	660
aatcgcgna	aataagtntt	gncactcnn	ntnctancnt	attntccctc	gcnntntcn	720
tcctctcccg	cnnactcac	ntnnncnnnt	caattntntn	nnacnncnc	tgctctacnn	780

ncnatntctn tncctncaca cccntnancn tntcnctcan aatgcctttt ctnccttann	840
nctntcnttc ncnnatctan ccaantttnc tttnacatcc cctncnnntc tnncccgacn	900
atatntnacc tcttnnaten cagngcntan natcncccn ttntcnctnt cnetctcann	960
cttntnttna tcttcatnna tcanncncc	989

&lt;210&gt; 547

&lt;211&gt; 781

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 547

tgtnnctttt cnnccctcnnc cgaaatcnct ttgntttetaa ctttccctaat tacctgggct	60
acttgacata tcccntcgat ncgcatagat ggccnngtta ctaanggtga ntttccagcg	120
cggggggacac gtggagtcac tggaaacattt gngcaatgct ggtgggaatg tcaacccgng	180
cnggcctctg gaatangcct ggcnnntcct gcnagagtta cntgtgacc cagcaattcc	240
actcctagct ccacccacag gantngaaag cnaagacgca nacagatgcc tngncncaa	300
anttcacggc agcatectnc gccatantgg cancatcgt cgtnacagcg gcatcatcct	360
tcatcattac ggcanatcc gtcgtaacag cggtacatc acttcgccac agnggcagca	420
tctgtngtca cagnggcngc anccttngcc aaagcggcag cntccttctg catagcggna	480
ncatnctttg ccatancngc naggtggaaa ccctgnccat cactgaggg ntncatanac	540
tanncatggc cagtccaggg cactggaanc cangccgtng aacggcgccn acggtnanna	600
ggaatganac cntgatgcnc tggggccana catactggct anacanactt ggagacatca	660
tgcttanttg nannnccant cacacttgc nncggcgtna tcctgctcac gtgatnccgac	720
ccgaatgggc acttcaaag ggaanaagg ngatggcact nccggtnncc tnganagggg	780
n	781

&lt;210&gt; 548

&lt;211&gt; 735

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 548

tctaaacgct tggnncttgc tctttctnca ngnanccnnt gcgntncgaa ttcggcacga	60
tctagatatt gcccaatgc tgcccacagt gcacatacct ttccaccagt cacatgtgag	120
agggcagatt ttccaaatgc tcatcaccac ttggcactgt gtggactata attttggcca	180
gttaggaaat ggcattctcat tgttttctac ttaatttgcg tcagcctgat tactcattga	240
aacttgtgag gttgagaaac ttttcttaag cttattggcc attcaagttt cctcctttat	300
gaaatggttg tcatgtcat ttgctcattt ttatattaga ttgtttttct ttttccagc	360
tgactttag gaactctaca tcttatcaat attaatacatt tatcgaaaac tatttgggtg	420
ccattatctt ctcctagtca atgttttttg tttgtgatat cttttataat atataagttt	480
ttaatgttgg cagaagtaaa gttaatcttt ttggctgtgt tgtgtgtctt gttttagtga	540
aagatagttt ctgtaatagt tttgcagttt gattgntcat ctttaggtct tcaattcaac	600
ctgcacatcc atcccctcta tcctctttct tactctgttt ttctccatac cacttatcat	660
ccaataatat ggtcatgcc tttattnacc ngntttgcat atataatttg gcttgnnccc	720
ggttccctcc ctana	735

&lt;210&gt; 549

&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 549

ttctaatact	tggctctngt	tctttcngca	ggatcccatc	gattcgaatt	cggcacgagg	60
ggaaggagcg	ggcgtgaggc	cagctgaggc	atggtgacct	ctgggaagga	gcgggcgtga	120
ggccagctga	ggcatggcga	cccctgggaa	ggancgggcg	tgaggccagc	ttgaggcatg	180
gtgacccttg	ggaaggancg	gncgtgaggc	cagctgaggc	atggtgacct	ctgggtacgg	240
gggacttggg	ggccgacctt	ggtttgccca	gggcccctnc	tgcaccacgg	ccacatgcgg	300
aggacggcgt	tgggatangc	tccctgggtc	cacagcttct	gcccgtgtat	tggggaaccc	360
tncttggcca	aggcttcang	ctcttggcag	atggggcaag	gaaccctgag	gcttccgcgc	420
ccttccatgg	ncctctgatg	gggacacttg	aacgangcac	gattctgaag	gactccatgg	480
atcttgggan	gattangccc	accttcngtt	ggtggncnaa	agccgtcctt	ncggggcccg	540
gcttgtttaa	cnggacaact	tttcnggtcg	ggcttggttg	gccccaatcn	ttgggttggg	600
naanttcncc	ttaaactctg	ggcccgncct	tttaaccttt	tttcccaatc	ttttgacctt	660
tttccaaaaa	ggggtncccc	tgggcttttt	ngggncnaat	ggttccgggg	gccaaaggtt	720
gggaaaaaat	gccttncatt	gggnaaaacc	ctggatccct	tgttaancct	ttgggagntt	780
aaaatggaat	gaattttccc	cccgggcttt	tt			812

&lt;210&gt; 550

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 550

ggnnantcna	tgetggtctt	gtctctntct	aaaagtggc	nattcgaatt	cggcacgagg	60
ttcttggtgt	ggcatggtct	gcctgtact	ggagagatct	cctgagantt	cagttttgga	120
ttggtgctgt	catcttcctg	ggaatgcttg	anaaagetgt	cttctntgcg	gaatttcaga	180
ntntccgntc	caaaggagaa	tntgtccagg	gtgctttgat	ccttgcaaag	ctgctttcan	240
cagtgaacacg	ctnactggct	cgaaccctgg	catcatagtc	agtctgggat	atggcatcgt	300
caagccacgc	cttgagtgca	ctcttcataa	ggttgtagta	ncaggagccc	tctatctttt	360
gtntcttgca	tggaaagggg	cctcagagta	ctgggtatatt	tncttatccc	ttgactctga	420
tagtaaacct	ggccctntca	gcagtttgac	gcctgggtat	ttatggatat	taattagcct	480
gactcaaaca	atgaagcttt	taaaacttcg	gaggaacatt	gtaaaactct	ctttgtatcg	540
gcatttcacc	aacacgctta	tttggcagtg	gcagcatcca	ttgggttaat	catctggaca	600
acccatgaag	tcaanaatag	tgacatgtca	ntcggactgg	ccggnagctn	ttgggtagac	660
catgccaatn	ggcgcccttg	tggctctcca	tganccctt	tggcaatcat	gggtcttntg	720
gcgaaccatt	ttgcaaacaa	ct				742

&lt;210&gt; 551

&lt;211&gt; 736

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 551

agtctaatagc	tggctttgtc	ttttotaatg	ctngggcatt	cgtcctgggtg	tcaaactacta	60
taaacctttg	accagctgag	ctgtgactgg	ctgtcacntn	tctgagtcct	gtgtgcacag	120
tantntcctg	ggtcaggtaa	aatccaggtn	ttcaagtttt	aaggnttttt	tgaanaattc	180
gggcttnttt	aanacgatcc	ntgcccnaant	ccacaagctt	gttgacagtg	gnttacagtt	240
ngngtggcaa	agtccaagtt	gttacactgn	gctttaaaaa	aaatcttatc	tgcattgtatt	300
gttaacttag	agaccatgag	atctatattt	caggaccagg	aagatncaca	cttcagggtcc	360
attgcaactg	acttttttct	tgttttttct	aaaaccctgg	tggagcctgg	gaagggggcc	420
tccacaattc	tgtggctttg	atattagccc	caatttttaca	agcacatata	agccccataa	480
ttgccgcagg	aaaacacaag	atggaaaatg	caataaccca	tgcactgaga	cttagaaaaat	540

catccttact	aggcaaaatg	tattatgatg	caataagtgc	cactgggnat	tttnacgttg	600
ggactggnc	ggaactgctg	caaagaaaaa	taacagctcc	ttctccatta	tttacattta	660
agatggtggt	ggggggaagg	ttgggagaaa	ttagtctga	gggtatcata	tgcctttttt	720
aaagaaaatg	ggaata					736

&lt;210&gt; 552

&lt;211&gt; 733

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 552

nagtttaann	gtatgtcttg	tcttttccaa	gacccatcc	gattcgaatt	cggcacgaga	60
agtgtcagtt	ttcctaact	cagtccaggt	aggattttaa	aantntctca	agtgttgatg	120
ctntccaagc	ntggtgggg	ggaagggaat	tggtgccag	aaaatgggac	tggagtggag	180
aatatctttt	cttttgagag	tnccccagt	taattntnc	tgtgcttnat	tgctnctgtn	240
ctttattgtg	aatgttgtaa	cattttaaaa	atgttttgcc	ntagcttttt	aggacttggn	300
gttaaaggag	ccagtgggtc	ctctgggtgg	gtntataat	gagttattgt	gacccacagc	360
ttgtgtggga	ccacatcact	tgtaataaac	acaaccttta	aagtaacca	tcttccaggg	420
gggttccttc	atgttgccac	tcctttttta	nggacaaact	caggcaagga	gcatgttttt	480
tngtnattta	caaaatctan	cagactgtgg	gtatccatat	ttnaattgtc	gggtgacaca	540
tggtcttggt	aactaaactc	aaatatgtct	ttctcatata	tgtgctgatg	gttttaataa	600
atgtcaaagt	tctcctgtta	aaaaaaaaaa	aaaaaaaaac	tcgagccttt	anaactntnt	660
gagtcgtnta	cntagatccn	gacatgataa	gatcatgatg	agtttgga	accnactng	720
aagcagtga	aaa					733

&lt;210&gt; 553

&lt;211&gt; 870

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 553

nagttaanag	taggtcttgt	cttttgcaag	atcntancga	ttcgaattcg	gcacgagtat	60
ataacaactt	ttgctttcaa	agttgggtgg	gactagancn	cncantggaa	ggntggagtc	120
agganacctg	gattnttgng	cccgnnttgg	nttttacagt	ntgcctaant	ttntgcagtn	180
acttontgcc	ancctgtttc	nttacntnca	anagggaaag	acantccttg	gccagcctag	240
ttttnaggg	gaacgaaagg	tcntntncac	tgntcctct	agtcatttgc	ttcttcgnta	300
attaacacat	cttgagcacc	tgcnatgttc	caggaaacagg	agatggcanc	gtgcaagata	360
aagtccttga	cttctagaga	ctgcatgtta	gtggcaatcg	gcgtntaccc	ggccttnaat	420
aaactactga	atgaaggaaa	attctaccta	caccagacac	aattactggg	gtttctaaaa	480
tggaaattatt	cccccgccc	cntgcatcca	gcagcctgnt	gcagggaaac	tcctccnaaa	540
ggcttgtaag	gcaaggaanc	cgggacaatg	gcntggctat	ttaagcttnc	aacaagatgg	600
ttacccttaa	gtncctaatt	ccctaacacc	aagggggccc	tttaccagga	aacccaaacc	660
aggttaaaaa	accccaaagt	tggnnaaaaa	gccatttggc	anccggggcc	nttttaaaaa	720
aaacctttna	aaaacctttc	ccttttaaaa	ctttaccttc	aagntaaan	tttaagggga	780
atgggnccaa	nttttttaac	cancccaaaa	aaaaantng	gnaatttttt	ttccnnaaat	840
tttttnaant	tcccaaat	tnggaaaang				870

&lt;210&gt; 554

&lt;211&gt; 766

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 554

tatcaatgnt	atgtntgggc	tnttcgaaag	anctagnccg	ntcgaattcg	gcacgagcca	60
acacccagtt	ctnactctgt	catccaggct	ggtgtgcagt	ggtgcaatgt	gggcttactg	120
cagccttgac	ctccaggaca	agtgatctcc	cacctnagcc	tccggaatag	ctgggactac	180
agntcaacaa	cgccccctctg	aaagtaggac	tcttggaat	gaaccttggt	gggagtaaag	240
ctgaaccttc	acctctcctt	tccaggattc	tactccattc	atacggcctc	acactgaatt	300
aatgtttnta	gcagccacat	cacttngtta	cccaattgat	ctagtagtaa	agtcttccca	360
tctnttcagt	taaaaaaaaa	aannnaaaan	gggnnaggaa	ccntnangnt	nnnaaaaaa	420
aaaaaaanca	gngngngngc	nttttttaac	ctataacctg	ntttnaggcc	tttccccang	480
ttntntccna	ncnngggtan	tagggggccna	aagctaaccg	natttttgnt	cccntnagg	540
tagggcngaa	attaaccngg	gtttaaagaa	cncattgant	aaagccttgc	ctngggccaa	600
tccgggaaaa	gggaanagcc	tccttggttt	acanattggg	aaaaattggc	cccaangggg	660
gttaaccang	tttgcccntt	aataactnaa	anggatTTTT	gncaaaacct	ggttccaagg	720
ntttaanccc	aanccttttn	aaanntnggn	cnctttggat	gnaann		766

&lt;210&gt; 555

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 555

gttatccnat	gngegtntgt	ngnnnnncnt	aanantttg	gctngncgct	gggccttgct	60
tctctgagaa	aacttttggtc	acacntccaa	agccaggggtg	ggtgcctccn	tnaggagggtg	120
ggctttcctg	gttggtggcn	cagnaggagt	ccaggctttg	taccgtggac	accatgggct	180
atggcaacac	cttccctaacc	atccttccat	gaggacctcg	gnaganagt	gacatgaaac	240
cctttgtgct	ctgaancatt	caacagaagc	ttcttggttc	tgtgcctatt	tctttggcac	300
ttgancgtgt	ttgcaggttc	attacncaca	tgatgaaagc	tctggcccat	agcactagaa	360
ttcatgtttt	naggggtttg	gagtgtgaca	ggtgctatgg	tttggtatgtg	gtttgtttcc	420
acaaaaactc	ttgcttgaag	tttaactgcc	agcatggcaa	ttgttggnag	gtggggccta	480
cggggagggtg	attgggtcat	gggggcttga	accctccgga	atagattacn	gctgcctcct	540
ganaaagttc	tacctgtcat	gggggctgga	tcagtcaaca	ttgannantg	gggttggtat	600
aaagcaagac	tnactcctta	tgcaccgttt	ntttgcatat	gccccctctg	gggnancttc	660
tttggtgctg	aacatttttg	gacccaaccc	aatgggcctt	nacccagaaa	nccggaacaa	720
aatgcnnnnn	gccattcctt	tnngganctt	tccaacttnc	canaaataat		770

&lt;210&gt; 556

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 556

gtngtcnatg	anatgtcttg	cctnnccaag	aacnaggcgn	ntcggtagaa	cagaaaaatga	60
gcatccgatt	tcttacttaa	aggagaccaa	actggttcct	tgcggcctag	tnntnaagan	120
ctggancttg	aaagtccctc	ttntaccaac	tccacntcca	ccccntnatt	cccntntncc	180
caaagtncta	ctgntgttgc	ntgacanccc	caaanttgtn	ctgtcaacac	aaacctgcct	240
ttggngtata	aacagggcnt	tacagaatgg	tnacccttat	atatttctgt	tcagtatcca	300
ttcactagtt	cttcattaat	aaatatcatc	ttccccattc	tgctgttgaa	tgccacacat	360
ccatccagtc	tgagaaagt	agagaggcaa	tcagtccaag	aacaagccag	caaagctctt	420
tcaccagatg	tagactgtag	ccctgctgcc	ttccctccag	cgagtctgcc	agcatgcttc	480
ttcatccttt	taatatgtcc	tttgcttcc	acttccctgn	cttccaacat	actgtcactt	540
actctggcag	tcttctgctt	ttcatthaag	ctcaaaatct	cctctgtcta	cttggcacca	600

caagctatgt cctatatatg natttctgga cttggcangg atagttcaag gggctcttggc	660
aagttttttat ttaccttcoat tatttaaaan gggccttttg gggatgttgg cctntttaag	720
gagccttttt ggggaaatca atacttctct taanaa	756

&lt;210&gt; 557

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 557

tcgtcnaaan nnatgtcctg gctatccgca ggatccaggc ggntcgaatt cggcacgagt	60
gatttttttg gttttttttt ttgntnttgn caaaagctta ntentttcan ttaaaantgc	120
cactantttg actttttaag taaaaantgt aggggggtttt aaanctactt tcctnctncc	180
aaaaantcag aaagtttcta nctttntaaa ttgggaaagc aagcantgtt ttaaaancac	240
tgaaggaatc tctttnttcg ngnccttttg ttaaactcgg ttaagctgt agacctntt	300
taaantaaaa tttaccacag aacaggaaat agaantctgt gaagactcga aatacacctt	360
tgtncttctc tgttcttcac ctgctctctc gctgtctcta cacacacaca cacaaacaca	420
cacacaccta tatttgcatt aaaaatgggt agtaaaagca gtgaagggca aacagaaggt	480
ccattncatc aagtaagagg ttgaatataa actggaccaa gtcttaattt tttatttctc	540
tcatcggat ncgtttacta atttctttgc tagctttaag acttttataa cattcttttg	600
ccctgggagg gagttgttta cccctaaact tggagaatcc tggccctaga ataatgttc	660
cttttaaac ccanggccg gaaaattgaa tncngctgtg ccaaaaagga aaaaannnaa	720
aaaaaaactc gnggcctnta na	742

&lt;210&gt; 558

&lt;211&gt; 730

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 558

gggtcnntaa tntnnagcnt gtnaaacccc tgagncttnc gggncgttca caaagaaaca	60
tttaataggg acttncaanc aaataattnt cggtttntca ggtggcagca agacaagatg	120
gtggatcccc atgccattac ctgctagact cagggttnat atactgtagt ggaaagggtga	180
ttccgaagga atgttgtaag acaattgaag tgcagtanca tcaaagttat ttgacctaa	240
ggcaggagtt ncagtaagta tccactttta tncaagaaac antagataaa ctggaaatct	300
tggagccctt cctggaactg gggttaatga gaagtcaaca tgggtggatta ncatggaaga	360
tggagttgct tagtctccca ttcaagatgg agtttcttta gcctccattg ataggagtn	420
tttaacaaaa ncangaaata agtctttgat ccattgaatc tctaagagtg agcccttgat	480
gactcagggt taaacagtnc tgagacaatt taggagatag ttttgaagnt caatttgaat	540
tgtaaaaggt caggattttt taactttttc acatctttga anaaaagccc atagagcgca	600
agttttcagc aaganctgga aancnatatt nctatggaat taaatagctc ctcagggcaa	660
tcaattnggc ctggganaac ataatgcttc aanggctgan gnaatctgga atttctatgg	720
gatttcttca	730

&lt;210&gt; 559

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 559

gttagtctat aangtnngnt atgtactngc cctttccggn ggatcccntc gnttcgaatt	60
---	----



cggcaccgaga	ggaaacacccc	ccttataaaaa	ccatcatntc	aggctgggtg	atctgacaga	120
gctagacact	gtcaaacaaa	caaacaacaa	aacaaaaaaa	ccccatcaca	tctcatgaga	180
cttatttact	atcatgagag	cagctcagga	aacacccact	cccgtgattc	agttacatcc	240
cactgggtct	gtcccacaaa	ttgtgggagc	tacaattcaa	gatgaggttt	gggtggggac	300
acagccaaac	cctatcacca	tgtaaaataa	tatctaattt	gtagagatta	aagaacaaga	360
taacttaaat	cttggatgta	agttaagaga	gtgggtgtca	gagttaaatc	attttaaggt	420
tcattttattg	tctggacaag	aataaaaattt	tgattatcag	gaaatacaag	taaaaccaca	480
gggagacatt	gnttatatcc	aaattgtcaa	aaattacaaa	gtcttataat	accaagtttt	540
gctganggtg	tggagcaaca	gaaacttttg	ttcactgggtg	ggtatataaa	ttgaataatt	600
tcagcttgga	cattacctag	caaaattgaa	ggctgtatac	gtacatacct	accaatctag	660
caattcactt	ctagatatta	agtcttgaaa	aactcacatg	tttccagaga	cgtgttaaaa	720
ggtggttaaa	tcattntgng	aat				743

&lt;210&gt; 560

&lt;211&gt; 833

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 560

atccngttct	ntannnnngtc	tngttctttc	tnacagatcn	nntgcgattc	gaattcggca	60
cgaggggtcc	tgggtgggagt	tccatccagc	agtgagtgca	ttttttcccc	agagcagtta	120
agggtcttat	taaaagccac	cactttgctg	aggcctgtac	aggccttggg	ggtttgggga	180
agagaantaa	ggcaggcact	tgtcccttca	gggagggact	tgtccntact	gggaggtttg	240
gggttgacct	tggctccagc	agagataccc	agcctggcnt	ggaagggcag	gtcttgagct	300
tacgcttgac	tgaaggggca	agctgcaggc	ctcttctgcc	ttccccctgca	ttcaccaagg	360
acaagtagga	ccaagaagtc	aagggaaaag	tgccaagata	gatctattcc	catttctttc	420
ttccacctgg	agaattcctg	agctatgctt	caaacctctt	ttggggccagg	gaaagactgg	480
gggacatttt	ttagtcaagg	atgctttaag	aaagtaaatt	cctgcttggg	ggcccaggcc	540
ttcttttttca	agggttgct	tgtgaatgcc	caacccaaaa	aaagggggccc	ccaaggccca	600
atcccttact	tcctnggtcc	ccccaaaaag	ggatnccaan	ttgggggaatt	gggaaaactt	660
gggcanncac	ccnaanccca	ctttggtagg	anttnaccaa	cccaaccaac	ccaaaaccan	720
cccacccaaa	tnnaaaaaaa	ggccaaaacc	accaaccaac	cnaaacccnn	annnnnnnnn	780
nannnnnnnn	nnnaaaaaaa	ctttgangcc	ttttaaaaac	tntttngngn	ggn	833

&lt;210&gt; 561

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 561

tagtctaattg	tnnnaaantn	ngcncngtt	ctttctgcag	gatcccatcg	attcgaattc	60
ggcacgagga	agaggaggct	gtgtatgagg	aacctccaga	gcaggagacc	ttctacgagc	120
agccccact	ggtgcagcag	caaggtgctg	gctctgagca	cattgaccac	cacattcagg	180
gccaggggct	cagtgggcaa	gggctctgtg	cccgtgccct	gtacgactac	caggcagccg	240
acgacacaga	gatctccttt	gaccccgaga	acctcatcac	gggcatcgag	gtgatcgacg	300
aagctgggtg	cgtggctatg	gccggatggc	catttttgca	tgttccttgc	caactacgtt	360
ggagctcatt	gagtgangct	ganggcacat	cttgcccttc	cctctnaaca	tggttcctt	420
attgctggaa	gaagaagcct	gggaattgac	attcagcact	cttncaggaa	taggaccccc	480
agtgangatg	aagcctcagg	gcttccttcc	ggcttggcag	actaacctgt	caccccaaat	540
gcagcaatgg	cctggtgatt	nccacacatn	ctttcttgca	ttcccccgac	cttcagaca	600
gctttggctc	ttgcccctga	caggatactt	gagccnagcc	cttgccctgn	ggccaaaccc	660

tgaattgggc cacttgccaa acttgcnggg gaaaggggttc cttgaaacaa gggggccatt	720
tttggggaag gcttcttggc ttggcctttt ggcatttnaa tttggccttt ttt	773

<210> 562  
 <211> 655  
 <212> DNA  
 <213> Homo sapiens

<400> 562	
nnatanacat taangnnaga ngntgagnan ttncntcgc tctntganna naaggcgncg	60
cgaattcggc acgaggccac cggctctcttc ctaatctgca cattntatct tgggtatttc	120
tgggcgggca gttcctttgc atgtttcggg agaggtttgt tgatttgggg cttatatgtc	180
aggcctttgg tttgcgtctt attttagggg ttgtttgggg gcctgggtgg tcggcctcac	240
atgggaaggg gatgggtagt ggatgggggt tctgtcgnat cttgnggccg gtgattttgc	300
tnncgnnctg tttcacattc ttccccctcc acaagccaaa tcgttcattt ggntnactg	360
tgtggactgt ctgagcttgc cctgccagaa aaatttgggg ctaggcaccc aggtgcanac	420
tttgaagaa gcantccacc tgtgggtacc gcctctcgtg ngctccactg gcaggctgaa	480
cctacttgaa catggaaaca gcatgcccat atggcaaagg ggccnnnacn nnnngnnaaa	540
tnnnannnn ncnagacann ncnnaatca ngannntcna cannnatcnn annnnancnn	600
nncaantacn ncnaaaacac accnnccana annnnnaann nnnnnncann nnnac	655

<210> 563  
 <211> 738  
 <212> DNA  
 <213> Homo sapiens

<400> 563	
tnntaatgct ggaattcctn atncttgggc tactcgttct ttctncagga tcccntgcga	60
ttcgcagaaa agagtatagt aggggatgac caagggtcaaa gtgggtaaaag aagactcatc	120
atccactgag tttgtagaaa aacggagagc agctcttgaa aggtatcttc aaagaacagt	180
aaaacatcca actttactac aggatcctga ttttaaggcag ttcttggaag gtccagagct	240
gcctagagca gttataacac aggtctctgag tggagcagga atattgagga tgggtgaacaa	300
ggctgccgac gctgtcaaca aaatgacaat caagatgaat gaatcggatg catggtttga	360
agaaaagcag cagcaatttg agaactctgga tcagcaactt aggaaacttc atgtcagtg	420
tgaagccttg gtctgtcata gaaaagaact ttcagccaac acagctgcct ttgctaaaag	480
tgctgccatg ttaggttaatt ctgaggatca tactgcttta tctagagctt tgtctcaact	540
tgcagagggt gaggagaaga tagaccagc tccatcaaga acaagctttt gctgactttt	600
atatgttttc agaactactt aatgactaca ttctgttatt gctgcagtga aaagngtggt	660
tgccatcgat gaatgctgca gaaatgggaa gatctcaaat tctttgctca aaaacgtgaa	720
cttaaccaaa atgatggt	738

<210> 564  
 <211> 798  
 <212> DNA  
 <213> Homo sapiens

<400> 564	
ngggngtct aatgctgcnc nnatcnannc anggnnctcg ctctngctcn acnnanaagg	60
cgntgngtgt gccaccacac ccagctcatt attattatta ttattattat tatttttgaga	120
cgaagtttca ctcttatccc ccaggctgga gtgcaatggt gcgatactgg ctactgcaa	180
cctctgcctc ctgggttcaa gcggttctcc tgccttggca ggcacctgta gtgtcagcta	240

ctcgaagctg	aggtgggaga	atcgcttgaa	cctggggggc	ggagattgca	atggtgtggt	300
ctcggtcac	tgactcgag	cctggcgaca	gagcaagact	ctgtctcaaa	aaaaaaaaaa	360
aaaaaaactc	gagccntnna	actattngng	aggctgtatt	acgtagatcc	agacattgat	420
aagatccatt	gatgaagttt	gggccaaacc	ncaacttgaa	tgcnnngaaa	aaaagcttaa	480
ttgggaaaat	ttgggaatgc	ctatngcttt	atttgaacc	ctttntaagc	tgcaantaaa	540
acaagttaan	caccncccaa	ttggcntcca	ttttaatgtt	tncagggttn	agggggggaag	600
gttttgggaa	ggtttttttna	aattcncggg	ccnnggggnc	ccaatgcttt	ggggccccgg	660
gtncccaann	ttttgggncc	cttttaangg	gngggnttan	attggcccc	cttgggggna	720
aaancgnggn	anatacctng	gtcccctgtg	nanaaatngg	nttcccntta	caaaatttcc	780
cacnnaatt	tnngnncc					798

&lt;210&gt; 565

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 565

ttntnngttt	naatnntcnn	ggntcgnct	tnnctcnaa	nanaataggt	ttggcgaatt	60
cggcacgagc	atgctggcca	gcacccctgc	ctgtgcaagc	tctggatgag	ctgtgtgccc	120
ctgccacnca	caccncgcac	tccctgccag	cctggcctca	gggcctctga	tccatgtgca	180
ctggagtggg	gatgactgac	agggccactg	gggcatttnc	acgttaacag	cagctgccac	240
tggcaaaaga	agtactcgc	caatggtggc	atctcagatg	tgggccccagg	agtctgggga	300
gctactttga	acagggttat	ccattcattg	tcccacaaaa	ggctatggag	cccacccacc	360
atgtgctgga	gtagtcaagg	gaaataagac	actctccttg	tccttggttaa	ctcaatcaac	420
aagcatttgc	agagcacgcg	ctatatgccg	gcgctgtccg	aagtgtctgaa	gatacagcaa	480
tgagctaagt	aagcactgac	ttcgtagaaa	accataacat	cggccatctt	tggaaaagag	540
aaaaacaatg	gagttactta	tttaaaaaaa	aaagaaagaa	agttatctct	tccanganag	600
gctagaagta	cttttctgct	ttttggccag	tgcccantgg	aatgcctggg	ttggggggaag	660
aagaagggac	tgggttaact	gtggtgcttt	tgttgtaaaa	aggcanctgg	cctttgtact	720
tgaggagaaa	natggagcct	tggg				744

&lt;210&gt; 566

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 566

gnagtnttat	tgatttntct	ccgtgaatcg	ttctnnctnn	annanaagtg	ngttngccg	60
ctggctatgt	ggacgctggg	gcagagccag	gccggagtcg	aatgatcagc	caggaagagt	120
ttgccaggca	gctacagctc	tctgatccctc	agacgggtggc	tgggtgccttt	ggctacttcc	180
agcaggatac	caagggtttg	gtggacttcc	gagatgtggc	ccttgcaacta	gcagctctgg	240
atggggggcag	gagcctggaa	gagctaactc	gtctggcctt	tgaggtaatg	gggggtggcg	300
gtggtggggg	gtgcttantg	gctatgctca	ccccgctnca	ttangcctat	tttgggtctgc	360
tgtttccaaa	tgcttctana	tctaggcatt	tggtatccaa	cctattgcca	cantgcctan	420
aactncanac	ccccngccnc	tatgntnana	cctacttggc	acaagaacaa	nngnanacnt	480
tgnnnatatn	ccanaangnn	naanattaca	nantnttata	ataccaattn	ntnttgangg	540
tgtnnnnnnc	anaaacnttt	gntnacngnn	nnnnntatna	atnnataatt	nnnnntttgn	600
nancannanc	tatgnnnaat	taaangnntn	tnnncnnnc	nnnacnnnna	nnnnntttan	660
nnanttnenn	ttnnntnnnn	nnnnnnnnnt	tnaanaannt	nnnnnttnat	nnnannnnnc	720
nctnnaangt	ntntttnnnn	nnatnnnnnn	nnnnccg			756

<210> 567  
 <211> 746  
 <212> DNA  
 <213> Homo sapiens

<400> 567  
 gnntgtnttt nncnnnnnnn anganagagn tactcgctct ntctctacga tanantgngt 60  
 tncgaattcg gcacgagatt tcctccagtc ctgggccccca tccttnaggg ccttcccagc 120  
 cagccagcag gagaggcaag aactggggga acacaggaaac ctaggggagg aggggagcgc 180  
 tgggcatcct caggctggcg gccaaagcctg cccctggagg cactagagga gggcatctgt 240  
 ctgtgggagc ccagagctgc agggaggagg agggaggagg tatctggtgt gagcgttgcc 300  
 cctgcgacat ttgggaccac acaggtgggc ttccttatto cctgacaaaag cctctgtttc 360  
 cagctcttcc gccctctctg gatgaggga cagaagtga ggaaacaaa gaagcagcag 420  
 cagcacagt cctgtcgctg ggtgcggaga cagcctggca aagtcctact cagccatggc 480  
 ctgatgcang cccagccct nctttcttgg gtgtcaaag actgtgtcct ggacatctga 540  
 tgcaccacct gccctgcctg ttgcaaacgt gatgctcccg gatggaatgg agaaactagg 600  
 agactgggac aagcaaaang ctgcaaaaca cccagaaccc attcttagaa nactggagaa 660  
 atgattgagg aatcattggc accgtggncc tgtgcttcat nacaacacc ttnagaaca 720  
 acttgggatt gaaaaaccaa gacant 746

<210> 568  
 <211> 738  
 <212> DNA  
 <213> Homo sapiens

<400> 568  
 gnnntnngtn gttcttanng ttnggatctc gttctttctn cacgatcn cn tcgattcggt 60  
 ctgggcagcc tacgctttcc ggataaaaaat ggagaaatga aagaaattat gaggggaact 120  
 agagaatagg aaagacatga accaacgccc aaaatgagaa agaaggacat ataaagaaaa 180  
 agacaaatac aagtgaaaaa aatagactaa tggattaacg tccctgtcgt gtgacatttt 240  
 ctgctatgga aatgatatta gacaaaaagc acttcaagtg gttttcttat ttgagttcaa 300  
 aatgggtcat aacgcagcag agataacttg aaacatgaac agcgcatttg gccaggaac 360  
 tactaacgaa catacagggc agctgtgatt caagaagttt tgcaaagcag actagagcct 420  
 tgaatatgag gaacacagtg gccagccatt ggatgcttca cttcttgaag catcttgaca 480  
 gctttttgca ggtgaaatgc ttncacacca gcaggatgca gaaaaatgct ttccaagagt 540  
 ttgttgaatn cagaacatgg atgtttatgc tgcaggaatt aacaaattta tttctcgttg 600  
 gcaaaaaagt gttgattgna atgggtccta tttgattaat aaagatgtgt ttgagcctaa 660  
 aaaaaaaan nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720  
 nnnnnnnnnn nnnnnnat 738

<210> 569  
 <211> 753  
 <212> DNA  
 <213> Homo sapiens

<400> 569  
 gttnttgant ntgattctta tgcttngnct aatgctttnt cttnnangatc ccnncgattc 60  
 gctggaggag aggagctcag agttctacag agtctttntc gaacaatatc agaaagctgc 120  
 tgaagagggt gaagcaaatg tcaagcgata tgagtctcat ccagtctgtg ctgatctgca 180  
 ggccaaaatt cttcagtgtt accgtgagaa caccacccag accctcaa at gctccgctct 240  
 ggccaccag tatatgcact gtgtcaatca tgccaaacag agcatgcttg agaaggagg 300

ataaaaaactt	tcagaatgag	caaaacacca	tcaacgttaa	ttccagagat	ggaacatttt	360
ttttcctagt	gagaaaaaca	cccatTTgaa	gagaagaccc	taatgagaag	accctaaaga	420
gagacatcaa	gaatggattc	agcagaatca	tttcacgttt	tgaacagcag	cagtttgaan	480
ggccaaagcc	tttgatcagg	gatcccgta	ttaaaggaca	ctcttgagta	ttagtaaacc	540
ctcttatgat	gattaaaaga	gaagggcagc	cctnttcacc	tttttggctc	ttctattcaa	600
cttgccctgac	cataaaatgg	ttctcttctg	nacaaagccc	catcatttgg	tgaacctcac	660
ccttaacaaa	gtaggattgg	ggttgggggg	cttaattaat	tggaatgggg	ccaaggagaa	720
gagcccgaaa	ccttagatnc	canggggnana	agt			753

&lt;210&gt; 570

&lt;211&gt; 832

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 570

tnatnaataa	ggtttgantt	cttatgcttn	ccaanngctt	ggacctannt	anccangcgg	60
tgcgaattcg	gcacgagcca	ggccccaata	atctgggntt	naaaactttga	ggaaatgcca	120
gtgacttatt	ccagagtgcc	tcagtttaggg	gaactttctc	gtaaagaacc	ctgggtattg	180
agcaaaaacc	ttattatcgt	taatgaccta	taattggaag	cttcctgcct	ttttctttgg	240
ttgtcctcgt	ggaaaatact	gaaaagatta	ctttgtttta	ttttgttgct	tttttataaa	300
aggggaggtg	gagagacccc	ttcagagcag	ggattgtgcc	gggagagtgc	ctctgacttt	360
gggacatttc	atccacagaa	attncaagc	caatggtttc	ttttgggttt	tgggttttta	420
tgtttgnttt	ttgggggttt	ggaaaaacat	gcatttttac	cgtgcacgta	aaattgggtca	480
nagaaaaagg	gagcccagaa	aangcagcan	atgggccatg	cccctttgct	gggttttcct	540
ttctttttgg	gactgtnaag	gggaaatggg	tttttanaag	gtgaagggtt	ggtcctgttg	600
gaaggaaaaag	aantgtctct	gttngggggg	acaanaaggn	acccttgggg	gaggtccatt	660
cgcaatggtg	cctacaaaaa	cnnggntctt	taanaacacc	ngggcctttg	nccaggnaa	720
aaaaccctgg	gcccctttaa	naaaactttg	nangggaacc	ccggaaaaacc	cccttggggcc	780
ttnccaaatac	ttttttccca	aagncncccc	cggggggggccc	aaaaaaaaaac	ct	832

&lt;210&gt; 571

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 571

agtnttaatn	ntggacttct	aanganttn	gctnntcgt	tggaannnnn	cagtnctcta	60
nnagcccatc	gatgcgaatt	cggcacgagg	ctaggattac	aggtgtgagc	caccatgccc	120
agccacttat	ctttaaagga	ttaagtatt	gtttcctact	atgggaaacc	atcccacccc	180
aaacttgatg	accgcattat	gtgcttttat	agaacatggc	acttctccag	gatagcattt	240
attctgtttt	gtaagtgtga	atgtaattac	cctacacaca	gcatacacat	aatcttcata	300
ttcttttgct	tgtcttgta	aggcaagggc	catgtctatc	ttattcgtca	ttagattccc	360
acatccaaca	tagtcctggg	gacagcacca	atgcactttt	ggtgcataag	caaatagtgc	420
atttatagct	cttacctaca	atatctgata	gactaatcaa	atatagtagg	ttatctgggc	480
cttttttgatt	catgtctcta	gcttaacttt	catttttttc	ttatttggta	tctctcactt	540
tgccttttga	tatactctta	cagtttctgct	cactgagtaa	aagaaaatnt	aaacagcaag	600
aagtaaactt	gtgttttatg	gatttngata	acatcttcta	aaagaccccc	caagattggt	660
gatgtctaaa	aaaattaaag	ggccttcaac	tcataataat	acttaatagt	tcttaaaaata	720
ttacaaaactg	attggaacat	tgccctaac				748

&lt;210&gt; 572

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 572

```

agtcttatta nnnngttcta atcctttctt aangagnnta ggctactcgt nctttctgca      60
ggtatcccnt gcgatncgaa ttcggcacga ggctgagcac ctttggaac aacatttaag      120
ggaatgtgag cacaatgcat aatgtcttta aaaagcatgt tgtgatgtac acattttgta      180
attacctttt ttgttgtttt gtagcaacca tttgtaaaac attccaaata attccacagt      240
cctgaagcag caatcgaatc cctttctcac ttttggaagg tgacttttca ccttaatgca      300
tattcccctc tccatagagg agaggaaaag gtgtaggcct gccttaccga gagccaaaca      360
gagcccaggg agactccgct gtgggaaacc tcattgttct gtacaaagta ctagctaaac      420
cagaaagggtg attccaggag gagttagcca aacaacanca aaaacaaaaa atgtgctgtt      480
caagttttca gctttaagat atccttggat aatgttattt ctatctttat ttttttcatt      540
anaagttacc anattaagat ggtaagacct ctgagaccaa aattttgtcc catctctacc      600
ccctnacaac tgcttacaga atggatcatg tcccccttat gttgaggtga ccacttaatt      660
gcttttctgc ctccctgaaa gaaagaaaag aaagaagact gtgtttttgc cactgattta      720
accatgtgaa actcatctna ttaccctttt ctngg                                     755

```

&lt;210&gt; 573

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 573

```

cangtetaat gctggctctn atcggttctt nnnantnaag ntactcgttc tttctncang      60
natecnntgc gntnecetca cacagcatgt gtcagatcca tggggtagga gtcggccaga      120
gacttggtaa cagacagatt gctggatccc acccctagac tctctgattc agttagtgtg      180
gggtaaggcg caagactgaa tttttcacia gtttcccagt ggtgctgata cttctggtcc      240
aggaacttag tggggagaga acgactaatc tagaccattt cacttcacat tctgagcttc      300
ttgtcactgt cacactgcat ccttttaaca atgcattccc tatectattg caatactgac      360
atctcatcaa tattttaaaa catgcgtttt cagaaacaat attttatatc aaatactcac      420
ttttagtaat atttctgcaa ttttgcccta tggatctgag atctaacaaa tactattctg      480
gacatgggct acaacagttg aggctggaag taaaaatgtt aaaccctgct gaccacgtta      540
ttttaaagtg tatttttagtt aagaataata tggcttagga gcagggctaa acagtagcag      600
tcacatgggg aatgatactt tgcttttgca cataaaatgt cctgaaggga aaaaataaag      660
cagaaaattn ncagatgaac tgaaaatctg taaaaatgtt gggctgaata ctgccagcgt      720
tgangtgtag gaaaatgaac cnt                                              743

```

&lt;210&gt; 574

&lt;211&gt; 737

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 574

```

ccgtctaatt ctggnnttcta atcgctttct taangctcnn gggctcgntc tcnctncacg      60
cagcccgccg gtgcgaattc ggcacgaggg gattacaggc atgaccacc gcgccagcc      120
tgtatcttct tatactntgt attttgnct tgtattatgc ttctgatacg ctataattat      180
ttatgtccat gtncttttct tcaatagact gtgaactctt cgaatgtngg actcctagag      240
ctagatnctc nattattnnn tattaaattg aatgacttgn aactacagat cttttattta      300
aacttcccaa atttctgctt tatctagcgn actctttaa ttcttttata tcatgtagat      360

```

ttcanaggct	gaaataattg	agatttttag	tttgaagaaa	agagaactgn	ggatttaatg	420
gcntttattat	tatatTTTTA	atggctgttt	gggagtnagg	ttgcagacat	tggtcacttt	480
cctcctaaat	ncttaaatat	ttcctaaaaa	caggncattc	tttntttnt	tatggagtct	540
ggctctggcn	tccaggctgg	antgccnggg	cccatcttgg	cttactgcag	ctccccctcc	600
cgattcncgc	tgggtctcctg	nctngetgct	cgggaggetn	aggccnggga	atcgttgacc	660
cggaggcg	aggttnncan	agcctnnacg	ggccctnggn	ctccccggetg	ggtacnngac	720
cggacctccg	nctgnat					737

&lt;210&gt; 575

&lt;211&gt; 766

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 575

gnagttnaaa	agcggnTTTT	antcctctcn	aatcngnttg	ggctactngc	tctttctgna	60
ggnatcccat	cgattcgaat	tcggcacgag	ctttctccct	ctgtgcctcc	tgtctccttt	120
ctctctcctg	cctctcctct	gtccccatc	ccactttctc	atctgcctcc	ttttctcact	180
tctgtcagtc	tgtaaagcttt	gataacctgc	ttataactcc	aaagtgtgag	ttcctctgat	240
ctcttgatgc	cttagtttcta	atctcacggt	ttgtttttta	gagatggagt	ctctcactct	300
gtggcccagg	ctggagtgc	gtggcatgat	catagctcat	tgcacccctg	aaatcctggg	360
ctcaggtgat	cctnccgcct	gagcctcctg	agtatctggg	actacagatg	cgtgccacca	420
agcctggcta	atTTTgtctc	atgtcttcta	aaaattatTT	tgtgaagccc	cttcacaaaa	480
aaccttaang	gaaatctgat	ggtgctcagg	aatctaactc	tccttaaacc	atcctctttt	540
aactgcttct	aaaatatctc	tgggtggcctt	tcttagcctt	tttctgggtc	attcaatgct	600
tcaaagcgct	ttttgnttct	aagttgagtn	ctttgggggt	ttgacaggta	gtgacgtgta	660
gttttgacac	tgttaacttg	ttnaatacac	tgaaaangtt	tgtgaagtga	aaaatgcttg	720
anaaagaatg	gnaatgcctt	tntacaaata	aaagtnttgt	taaaat		766

&lt;210&gt; 576

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 576

ggggtnnnna	gngnnttgan	cccccttctt	attatcaagg	ngctngcnct	nnctnnannn	60
ancacaggcg	ntgngaattc	ggcacgagaa	gataacctct	taatgcattc	atgttgtata	120
tgaaggaaat	gagagcaaag	gtcgtagctg	agtgcacgtt	gaaagaaagc	gcggccatca	180
accagatcct	tgggcnaggg	tggcatgcac	tgtccagtag	tatttattgc	tttagagatt	240
gcttgctgta	cctgtatgtc	gtcccccttt	aaatatgttt	tcctttttct	tgaaactgta	300
taaagtTTTT	ttccccctta	gcataagcat	cttatatata	acaactcatt	tgtacaagggt	360
ttttaagtTT	atatataaaa	tgtgtatata	tatttttgnt	tcctcttttt	gacttttttt	420
ttctgtatga	aaccagatg	tcaccaaagt	gacattaata	gttgcatata	ggatcagtag	480
cattaacaaa	agttgcttta	aaagccatta	tgtaaaacaa	gacttgaaaa	tgagtgaggg	540
aatttttagcg	acactgtctg	agcacagtgg	gaaccatctt	cgtttccctt	ttgaactcca	600
antgggatgc	cctaccctgg	cgcccccttag	gaccccgagc	tggcccgngt	acaaaacttt	660
accgtgccaa	aattcttaag	tgaatttacc	tttctncctc	tttttgaaagc	tngaaatttt	720
tggatcatcan	gnTTTgcttg	tgatngtaca	tanggtngaa	n		761

&lt;210&gt; 577

&lt;211&gt; 803

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 577

gggtngttnn	nnngtggnt	tnttnnnngt	ttctaantnt	cgngngntc	ganctnnctc	60
nananagaat	aggtttgnga	attcggcacg	aggtctcccg	ccggcgccc	ccagtgtttt	120
ctgagggcgg	aaatggccaa	ttcgggcctg	cagttgctgg	gcttctccat	ggccctgctg	180
ggctgggtgg	ggtctggtgg	cctgcaccgn	catcccgag	tggcagatga	gctcctatgc	240
gggtgacaac	atcatcacgg	tccagccatg	tacaangggc	tgtggatgga	ctgcgtcacg	300
cagcctctag	aactatagtg	agtcgtatta	cgtagatcca	gacatgataa	gatcattgat	360
gagtttgga	aaaccacaac	tagaatgcag	tgaaaaaat	gctttatttg	tgaaatttgt	420
gatgctattg	ctttatttgt	aaccattata	agctgcaata	aacaaagtta	acaacaacaa	480
ttgcattcat	tttatgttca	agttcagggg	gaggtgttgg	aggtttttta	aatnnncggc	540
cncngcgcca	atgcattggg	ccccgtaccc	acttttggtg	cctttaantg	aaggggttaa	600
tttgccccnc	tntgccgtaa	ttcatgggnc	atanncttgn	tttcttgng	ttgaaaattg	660
gntaatcccc	ttcnacaaat	ttcncacca	atcatttacc	aaacccnng	gaggcctttn	720
aaagnngtna	aaanccctgg	gggtggccct	taatttaaagt	ggnnccctaa	ctcncnttta	780
antgccttgg	cccttcactg	cct				803

&lt;210&gt; 578

&lt;211&gt; 738

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 578

tcgtcccntn	gateggggta	acgtccttnc	ctatnaaant	tctttcggga	aagcagaaac	60
caagctggca	gaagcacaga	tagaagagct	ntcgtcagaa	aacacaggag	gaaggggagg	120
agcgggctga	gtcggagcag	gaggcctacc	tgctgagga	ttgagggcct	gagcacactg	180
ccctgtctcc	ccactcagtg	gggaaagcag	gggcagatgc	caccctgccc	agggttggca	240
tgactgtctg	tgcaccgaga	agaggcggca	gatcctgccc	tggccaatca	ggcgagacgc	300
ctttgtgagc	tgtgagtgcc	tctgtgtgtc	tcaggcttgc	gctggacctg	gttcttagcc	360
cttgggcact	gcaccctgtt	taacatttca	ccccactctg	tacagctgct	cttaccattt	420
ttttttacct	cacaccaaa	gcattttgcc	tacctgggtc	agagagagga	gtcctttttg	480
tcattgcctt	aagttagcga	actgtttaac	ctgttttcag	tcttatttac	gtcgtcaaaa	540
atgatttagt	actgtttccc	tctgttggga	tgccagttgt	ggcaagggga	ggggaacctg	600
tccagtttgt	accatttctt	tgnatgtatt	tctgatgtgn	tctcttgatc	tgccccact	660
gtcctgtgaa	ggacagctna	ngncaaggag	tgaaaaactt	tacttcttaa	aaaaaaaaan	720
nnnnnnnnnn	nnnnnnnaa					738

&lt;210&gt; 579

&lt;211&gt; 758

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 579

gnngtgncta	nctaaatnnt	tggnntnaaa	cgtnctttct	gcatnatccc	tnnttgacga	60
attnggcacg	agacagagtc	ctgaaatatg	caaatgaagt	aaattctgat	gctggcgccct	120
tcaagaaaca	gcctaaagga	cctgcctgat	gtgcaagagc	tcatcactca	agtcgggtca	180
gagaagtgtc	ccctgcaggc	cgaagccatc	cttgatgcaa	acgacgtcca	tcaaacagag	240
accttctcct	cccaagtcaa	agggacaaat	aagcctctgg	gttgaacggg	ttgagacatt	300
ctgccttgga	ccttcccttg	tcaccaaaca	agccaacctt	gtgcacttcc	accaggcttt	360
caccatttcc	ctgcaagcct	tgtctttttg	acctggccct	caaccatgtg	gctttccacc	420



```

ccttgaggac aagtgggaac agaagaccaa gaggggcctc actggataca tcaanggcac      480
ctttggattc aggaagctaac caggctcttn ctcgggggscg ggggagattc tgactcttaa      540
tctggattgt gagaaaaatc cagcaagttc catgatattt aaatccaggt ctgcattggc      600
ccggggcaag agtttaacat cttcggggccc tgcatcttct acatcttggg gtctgtacac      660
gttcttaagc aagcgtgtca ngagagcacc ctgttggcctt cttggtaaaa tgtgtgcaag      720
gtcatnctgt cttctgnacc ttctggggaa aagggncc                                758

```

&lt;210&gt; 580

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 580

```

tttctaaatn gcttgggttt cnaaatccct tgggtgacgc cctgcgctaa nntggcgtn      60
nantgccnc gattcgctgn caagtctgga antcatattg gagcctgngt ngactgaaaa      120
ctcagcanga gttgatgtta aagtcttggg tctgaaattn gtngggcagg agattaggct      180
ggaaactcag gcagaatttc tgtgttacaa tcttgaggca taattcttct ccaaaaaaat      240
ctccattttt ttctcttaaa gccttggatg agccttggat gattggatga ggactacca      300
cattatctag ggtaatctcc tttgcttaaa gtaaaactcac tgtgttaatc acatcaacaa      360
aataccttca cagctacatg tagtgtttga ccaaacaact aggcaccata gcctagccac      420
ataaaattac tatcattata ctttgtctta tcacatactt ctaccttggg agggatattt      480
cccagttggt atagctacaa aacagaggca gatcatttag cctgcattng attngtantg      540
aaaaataagc ctttgggtng ttttaaccact gaaaatgttt gcggcctatt agtantngca      600
caacttatcc tatnctggcc aaacatagaa tgctttcggg ttgcaaggta acangatccc      660
ctttacagnt gtacnaaaaa tnancnntaa aaaaactnga gccctntaga acntnntagt      720
ggagtcggan ttaacgttng ancccagacc ntggattang gatncattgg atggagtttg      780
gacataccac cancttggaa tggcnantga aaaaaa                                816

```

&lt;210&gt; 581

&lt;211&gt; 868

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 581

```

ccnnganncn nncnnnnnc nnacaaaanc nnnnnnnann nnnnnnancn nnnnnnctct      60
tcnaannctg ctnacgccc aagcatgacc cagcatcgaa tcggcacgag gttgcaagca      120
gccttggaaat agtaactctt ctcatttggt tgggatctgg ccaccaagtn ccagaatgat      180
acacggatca gngcanaagn tcatcaggct ctcggacctt agggctgntg gagaagcttc      240
agcagcagaa ctgatggtga aggcctcgtg tctccatcct caactttctt tgcttcgata      300
atacacaaga atacattngg aagggcacaa aaatgaacac tgcggnncat tgcagcccgn      360
gtttngtgac acagatgcac agtctgcttg tgaagacctt ctctcaagtg gcatttggga      420
gtccatgcca gancatggtg cttcatgaga gactgacagc tatcaggggt tngggcactt      480
agngaggact ctctccccc agtgtgtgct gatgacacat cacacctgac aatagctnga      540
agnctnctct gaccntntt actctgtagc caacatacca catganttta aaaccnttc      600
taaaatatcc aancaatggg gtcatacntg gcccaaatgc cagaantcna gagcctaata      660
ggacttccaa tnattaactt tnccaaannc gaaaaaagna gggcnttccn ntatggcaa      720
aaaaatnaan nnaaaaggan atntggnatn gttngccnaa aaaaaagcc cnntnngaaa      780
cctaatanga ggaggtccca ctttaaccgn cgnancccca gaacantgga atacaggant      840
accnatngga ntgaanattt ggggancc                                868

```

&lt;210&gt; 582

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 582

ttctgaatac	cttnttaacn	gccttcttca	ggantttcaa	gacctaatte	ggcacgagac	60
cctttctgcc	ttctgtttgg	gacccagctg	gtgttctttg	gtttgctttc	ttcaggtctc	120
agggctgtgc	tatccaatac	agtaaccaca	tgcggctgtt	taaagttaag	ccaattaaaa	180
tcacataaga	ttaaaaattc	cttcctcagt	tgcactaacc	acgtttctag	aggcgtcact	240
gtatgtagtt	catggctact	gtactgacag	cgagagcatg	tccatctgtt	ggacagcact	300
attctagaga	actaaactgg	cttaacgagt	cacagcctca	gctgtgctgg	gacgaccctt	360
gtctccctgg	gtaggagggg	ggggaatggg	ggaagggtct	atgagacccc	agctggggcc	420
tgttgctggg	gacccttctc	ctnctganaa	gggaggcctg	gtggcttaac	ctgggcangt	480
cnngtcttct	ctgaccccan	tggctgcngt	gaagggggaa	cacccttctc	tgcttgacca	540
ntggccatta	nctnccntna	ccacttgnaa	cccanggtcc	canctggctg	ggaccctntt	600
ntncccccaa	ngncctttcc	cttgggctnt	nttggantga	gcaccttctn	tgtnngcacc	660
ttttanaant	gnnnnnntgn	tactgatttt	tttgntaaaa	agannttaaa	anctgggnant	720
ttntnaaaaa	aaannannaa	aannnn				745

&lt;210&gt; 583

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 583

gnttctaant	cttggcctac	tgcctntctc	ncaggatctt	atcgatncna	attcggcacg	60
agatatggta	tagttggaaa	taggttattg	tgagttattt	gtagtcatgt	ctttaatggc	120
ccttgcatgg	tgtctaactt	ctgcaataaa	tgatctgcca	gtcctagtgt	ctgggcttta	180
tgcaatttgt	tttcctttgt	ggatgaagtg	ggagtaagac	ttgttgctgt	gaggatcaga	240
tgaagtggct	aggatatgga	cacactttac	ttgaattgga	aaacaagcca	tgtatcccta	300
atctgcaaaa	tgtggcatgt	cacacgtgta	atctctgagg	tttagttttt	gctcaagatt	360
gcaaagggtga	cttgcttgat	gctttctttg	cttgagcaca	catctcatte	attaaatggt	420
gtctcccttt	ttgcacacag	gatgcagaac	ataattgacc	ttttccaagt	ctacttagca	480
gaaatgaaaa	tggaaatcata	taaatacagt	attatacttt	aaaataaaaa	ggctgtacaa	540
aagtttggct	gacatagctt	gcttctagta	atctgaatgg	cttattttaa	taaagttgga	600
tctatggact	cttcacagnc	tagatattat	cctactggaa	gatgtgcctc	gaaagctggt	660
gaaccacngc	aaaaaaaccc	ttcagtcagc	acgtgagaaa	acctgcgagc	ccacatttcc	720
cccgggacca	ttctgaacat	cctactgg				748

&lt;210&gt; 584

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 584

tttaatgctt	gttacacgcc	ttctgcagga	tttatcgatt	cnaattcggc	acgaggctat	60
gtattgtgtc	ctaccatgaa	ttcactccat	gctagccaca	ttggcctgta	tggtatttcc	120
ttggacacac	ctaggatgtt	cttgccctctt	agcttgcccta	cctttctctc	atcatttggg	180
cctcancgag	gatatcatct	cctcagagaa	gccttctgtg	accatgctat	ctaaaatact	240
ccagcacttc	agtcaccctt	tatcccatta	ctctgctttt	tcagaaacat	tggtgctccc	300
tgaacatat	ttgtttactt	gcttagtgct	ttttctcccg	cactaccatg	taagcttctt	360

gaggggtaag	ggaccttggt	agggataacc	actgtatcct	tagagtgtga	cacatagtag	420
gttctcaata	catatctttg	aaactctacc	ctgatgcaaa	agagatatca	aataattata	480
gtttttgcat	tataaatggc	tttggtgaaa	tccctggcac	aaaactaata	ataaaagaaa	540
taaacagata	atgttgaagt	tctgggcctg	caaaacctaa	ctctttttaa	gcagtcaccag	600
taaatgtgtc	attgggatcc	ataagacttt	gtgggaaagt	caacataatt	ttatnnggga	660
aaaagcattg	aaccttcaaa	agtnaaaact	ttatnngncc	aaaatctcaa	ttactggggg	720
gccgttcttt	aagtcatttt	aaaccctttg	angccnacag	ttttacacca	aat	773

&lt;210&gt; 585

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 585

ttcaatacnt	ntttcnngcc	ttttgcagga	tcnctcgatt	cgatggaaca	tgagtgggaag	60
tgggcagctc	ttttctttcc	ctatcagctg	agtgaatgaa	gatttagagg	gcagcagagt	120
catgacatgg	atgacgttgg	gtctctggat	ggctaaatgg	aagacccgcc	ccccaacgcc	180
actctacccc	cctgctttga	actatgcttt	gagaaatgag	cttatgagac	cactgagact	240
tgggggctgt	ttgttcagca	gttcacctac	acttattagg	aaagggtgac	ttcttgtact	300
acgcctttcc	ttaaatcatc	ttttgtataa	ttctcagaac	actgctgggt	tgggtggtct	360
cacacatttc	tcacatccaa	attttaaga	tttcatgaat	gttcattaca	gtggatttat	420
ttttctcttt	ctgcttctcg	gcatgccctc	tcaatttggg	agaaatctct	aattggatga	480
ctttggtggg	accacaggag	tgtaaggatc	gtaattccct	cacttcatcc	cctgcaaatt	540
aaagcctggg	cacttaagac	tcactcaact	gaatcttgat	atgtgggact	ttanatctta	600
agcaaatgan	gcaaaagaag	gaaaagacag	ttgagaaaat	caatctctga	agttcagcac	660
ttgatttcca	cgtggaccg	gactcctgca	nctttgcatt	ngccttgggt	cctggccatt	720
ttccnaaccc	gggttccttt	ttgan				745

&lt;210&gt; 586

&lt;211&gt; 749

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 586

tgttctaata	ctaggtntac	tcgccttttg	caggatctna	tcgattcnaa	ttcggcacga	60
ggggtcctgg	tgggagtnnc	atncagcagn	ganngcatte	tttcncaca	ncagtnaacg	120
gtcttattaa	nagccaccac	tttctgang	cctgtacagg	ccttgnggt	tngngaaca	180
gaaatnncgc	aggcacttgt	accttcaagn	anggacttgt	gcctnactgn	nagggttggc	240
gttgaccttg	gctcnacnga	cataccant	ctgacttnna	acngcncgt	ctnagcttac	300
gctagactgc	acnnccaagn	ttgcangcct	ntntgnctt	ccctgcattn	accaatgaca	360
gtacgaccaa	cagtcaanga	aaagtgccaa	gatatatcta	tccattttct	tctacacctg	420
tanattcctn	actatgctca	aactatgtgg	ngcaangaan	actggngac	atttttagtc	480
aatgatgctg	acaattaatt	actggtgngg	ccaggcatat	nttcacggct	gcttgtgatg	540
ccaacnaaga	acgggcccc	gccatcctt	actcctngnc	cccaaanaga	tccagtngna	600
atgggaagct	gnnannacca	acccaactnn	tgatttacca	ccaacncaa	anatcacgca	660
tgnnnacagc	aaaacaacaa	cncnatgcac	ttaacaagna	nccnaaaant	naactcgngc	720
ctctaaaact	attngggant	cctttanct				749

&lt;210&gt; 587

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 587

gttctaata	ttggcctact	cgccntcttg	caggatcttn	tcgaccttat	tcggcacgag	60
cccaaggcaa	gctgttaaca	aaatcaacct	gggccaatca	tcaaaggggt	ggacctaaag	120
ttgctatact	caatagaaca	agcattttta	ataaatttct	cgtaagttgt	tgctttcttt	180
atgtgggtgg	tgtggcttta	aagagcacia	aaccacaaca	aatcaaagag	tagctcgggc	240
ttgtcttttg	ctttatggct	gagggtttga	aggatgattc	atggacttgt	gaatgccagc	300
cccagtcceg	gcttaggtct	atctgccaat	accaccaggg	ccaacaaatt	cacgcaacaa	360
attctctcat	tttttacagt	ttatcagttg	cactcatagt	tattgtcata	atcactcccc	420
acagtaacct	gtaaggcata	taaagtagct	attttagtaa	gataaatgat	attttatata	480
tgttatgata	agataaatct	tatcatttta	agaagaaact	gagctcggag	agatgaaatg	540
acttcctcag	ttgctgctgt	aataaaaagtc	tactttttgc	taaaaaaaaa	aaannnaaat	600
atnntntann	attnnantaa	naanaaaaac	ttcgagccnt	tttnaaactt	tnantggagt	660
cnntttntcc	cgtaaaatcc	nnnacttttg	atnaaananc	catttngatn	aagtttttgg	720
gacaaacccc	ccaacttaga	aattgcnntn	ggaaaaaaa	ntgcntttta	ttttgnggaa	780
aan						783

&lt;210&gt; 588

&lt;211&gt; 771

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 588

tcttctaata	ctgggtacan	gccttctgcn	gatccctcga	ttcgaattcg	gcacgagata	60
cttttttaaa	cttttttggc	agctcagatg	gtgtaaattt	taaaattttg	tataggtatt	120
tcataacaaa	aatatgtatt	tcttttttgt	tattttatct	tgaaaacggg	acatatatta	180
gtattttgtc	agaaaaacaa	gtcctaaagt	atttgttttt	atgtgtacca	tccacttgtg	240
ccttactgta	tctgtgtca	tgtccaatca	gttgtaaaaca	atggcatctt	tgaacagtgt	300
gatgagaata	ggaatgtggt	gttttaaaagc	agtgttgcat	tttaatcagt	aatctacctg	360
gtggatttgt	ttttaaccaa	aaagatgaat	tatcaatgat	ttgtaattat	atcggttgat	420
tntttttgaa	aagatgaacc	aaaggatttg	actgctaata	ttttattcct	tacacttttt	480
tctgaataag	tctctcataa	tgagtgcagt	gtcagactgt	gcctactctg	atgggtatngt	540
gccatttgta	aaatnanaat	aagagcagaa	aaaacacaaa	nangagaaca	ctggnttcag	600
acattcantg	gggcaagtta	aattatggga	ctgcaaaaat	aatggatttt	ttattcaaag	660
aaaagcttta	aaaagtttta	ttatccanat	ttacaaccca	ctanttaagc	taaataancc	720
tactttnaaa	aatngnaaat	ggttnctatc	tttataangt	gccaanntna	n	771

&lt;210&gt; 589

&lt;211&gt; 844

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 589

tnactnnaa	tcctntnta	aaaagccttc	tgcntgatcc	catcgattcg	aattcggcac	60
gaggccagag	cctagaggag	agatcaaaga	cnttngccga	agtgaagccc	attctgcaag	120
caactgggtt	cccatggcat	gtggtggcct	tagaggaggt	gttcagcctg	ccaccgtcgg	180
tgctttggtg	ctctgccag	gagctggtgg	gatccgaggg	ggcctacaag	gcgccgtggtg	240
acagcttcct	ccagcagcag	catgtgctgg	gggcccggggg	tggtcctggc	ccgactcaag	300
gggaggaaca	gccacccag	cccccgctgg	acccccagaa	cctggcaaga	ccgcctgccc	360
ctgccagac	tgaggtctct	tcccaactgt	tctgctcaat	gaggacactg	actgccaaag	420

aggagcttct	gcagaccctg	eggacccacc	tgatccctnca	cgtggcccca	gccccaggct	480
actccaaggt	catgactggg	gacagntgca	cacgcttggc	tatcaagctc	atgaccaacc	540
tgcnctgggt	ccaaagggcc	ttcctggcct	gggatacngg	ctttcttggg	tgaaccngna	600
ccgggngaac	gtnggtggtn	ggtgccggnn	cattgacctg	gaaccaccac	ccccttnaaa	660
angaangntc	gnttatttct	aacaaaaacc	ggnccttgnt	tcntaccntn	ttccctntct	720
tggnnnnntt	tnaanacnnc	annncccaat	tnagnaanaac	ccnaaaangg	gnccctttgn	780
aaaaaaangg	ggccnatatn	ntntntcana	cccngggnc	ttgaatnngg	aaaangccnc	840
tnct						844

&lt;210&gt; 590

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 590

tctaattgctt	ggntctngcc	ttttgcggat	ctttcgatcc	gnattcggca	cgagagaacg	60
ttctcaggtt	gaccagctgc	tgaatatctt	tttaaggagg	gaagaactta	gtanntcatt	120
gcagtgcagt	gataacaatc	ttctgcaagc	ccgtgcagcc	cttcagacag	cttatgtgga	180
agttcagagg	ctacttatgc	tcaagcagca	gataactatg	gagatgagtg	cactgaggac	240
ccatagaata	cagattctac	agggattaca	agaaacatat	gaaccttctg	agcaccagg	300
tttggcatag	aaatggtacc	ccttggtcaa	aatgaacaag	aagccttaga	tttggatggg	360
gaacctgac	tgtccagtct	agaaggattc	cagtgggaag	gtgtttccat	ttcctcgtcc	420
cctggcttgg	caagaaagcg	aagcctttct	gagagcagcg	tgatcatgga	cagagctcct	480
tctgtgtata	gcttcttcag	tgaggaangt	acaggcaaag	aaaatgagcc	ccagcagatg	540
gtttcaccta	gtaactcatt	ganggctgga	cagaaccaga	aagcaaccat	gcacctcaa	600
acaaggaagt	nacacctcng	gctggccttc	ccttcgaac	aggtgaaagg	ggcttgaaaa	660
atgttgctac	cccaaaggcg	acattnttgg	caccaaatta	tcctcttga	ccnntttaat	720
accttttgat	tncatttngg	caaaagactt	tnnaccagcc	nnggaga		767

&lt;210&gt; 591

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 591

tctttgaatc	cttttgtaaa	agccttttgc	atgatccctc	gattcgaatt	cggcacgaga	60
cttcttggtt	gcctttttta	taaggaaatg	ttggagagtt	acatcattgc	taatgtagaa	120
atgttaagtg	gaaaaatata	cagtttggtg	aaataaacta	gattctacat	ttatttggg	180
gtttttttcc	cctcctttct	ttccacagca	cttttgatat	caagcaagtg	gcttcctttt	240
tgagatatta	aaaaaaaaaa	gaaaaggaaa	aaagtaaatg	aagcccaact	acctaaccct	300
ttcttatttg	tatttgtttt	agtattgtga	agttgtgtta	aatagtacta	gctagaaata	360
caaatttctg	gttatcattt	ctcttcctg	tggcacttga	cattttaatt	gtcttaaagt	420
ttttgaagtc	atcttctggc	cccttgagta	ctgccagagg	caaaagatgt	ttgtttctta	480
ttcattccac	ttttgtctcc	tgggatccct	tctgtagcct	aaagtatggc	tgggaaatgg	540
acttgagaag	attggcttga	attangatca	taatcatgtg	tgatcccatc	atgaattcat	600
tggaatntgg	ggtncatgta	angcaatcnt	tctgggtgta	atcttccttt	ttttaatgna	660
catatanntt	tggaaaaaat	tttgaattaa	ccctgaaaat	ttttaaaaaa	gccctcttan	720
aactattann	ggaggtcnca	ttaccctaga	atccanacat	tnant		765

&lt;210&gt; 592

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 592

tnttcnaana	ctngttctng	ncTTTTgcag	gatcccatcg	attcgccaaa	tctgcctaga	60
gattgagttc	acagtgtatg	ttctgggggc	gctgggtgcag	tcagcgggtcc	agtctccagc	120
ctgcaggcgt	gcacactggg	gtggacgatg	ggTggccccc	caggTgtaca	cattTgggtg	180
gccccggccc	ctatacccca	gtgttctctt	tgatccagtc	ccgaaacaga	gggagccttg	240
tgtacacgcc	tncaaagtgg	agctgggagg	tagaagggga	ggacactggT	ggTtctactg	300
acccaactgg	gggcaaaggT	ttgaagacac	agcctccccc	gccagcccca	agctggggccg	360
aggcgcgTtt	gtgcatatct	gcctcccctg	tctctaagga	gcagcgggaa	cggagcTtcg	420
gggcctcctc	agtgaaggTg	gtggggctgc	cggatctggg	ctgtggggcc	cttggggccac	480
gctcttgagg	aacccaggct	cggaggaccc	tggaaaacag	acgggtctga	gactgaaatt	540
gttttaccag	ctcccaaggT	ggacttcant	gtgtgtattt	gtgtaaatga	gtaaaacatt	600
ttatttcttt	ttaaaaaaaa	aaaaaaaaaa	actcgancct	ntanaactat	tagtgagtcc	660
tattttacctt	agatncagac	atgataagaa	tncattgatg	aattttggac	aaaccacaac	720
ttggaatgca	ntgaaaaaaaa	atgcttttatt	tgtgnat			757

&lt;210&gt; 593

&lt;211&gt; 766

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 593

tcttgaatnc	tngttnntgc	ctttttcgga	tccctcgatt	cgaattcggc	acgagagaac	60
attggTgtgt	gagTgtttt	tgatggTgca	ggacccggag	gtgctttcct	tgccaagaat	120
agaaacatcc	agaatgctcc	tcccatcccc	ccaatcccag	acagcaatta	tgTcagccct	180
gtaaggcatt	gcctgctctt	gaccctttgg	cccatctttt	tattttttaa	aaattcccat	240
gtcacagatg	ccctgtctat	gcagagggTg	gcgtgggatg	ggTgaccact	aagTttaggc	300
tggtgaaggT	ggTgagccct	tctgaggccc	tgatagaact	ttccaggagt	tcatggTccg	360
cggctccagc	ttctcactgt	aaagTtgtca	tcttggcaga	ggcagccaat	gcttttcatt	420
ctagggggTa	gagatttatg	ctaattgagTg	aatattgcac	cactagtga	tttctgttta	480
aagTtcagct	cttagaaaat	ggaatcttac	ctgaccctca	gtgaattatg	tacataagca	540
gggaatgttt	ccaactagat	ctccttcaga	agagTccctg	tgctggaata	ggTcactgaa	600
tcttattttg	ntttgtnaaa	caaaagcttt	tgggtctctg	ggggTgtgtg	TgtgnTttgg	660
ngTgtgtTgc	cccntntgcc	gtttcaaata	aaaggTttgg	taccaccttt	tcaaaaaaaaa	720
aaaatantnt	anntnanant	nnTntanent	tnntnnent	tanant		766

&lt;210&gt; 594

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 594

ttgnTtagga	tcccatcgat	tcgaaTtcgg	cacgagggaa	ggcagTggga	ggagaggacc	60
aagTctcaaa	ctccagaagc	cccacctccc	tgagctcagc	tcctctgcca	agccccctca	120
gcgcgaagTc	ctcgtccaga	gaaggcaacg	gcgagaaaaca	aatccaacat	cctggggctgc	180
tttttctctc	ccccactttt	taaaagTttg	gtgtccaagt	cacttgacaa	acccagaccc	240
taacaatgat	atTttgtgta	gaattctggg	atcaaaatat	aatttcaaaa	ataatatatt	300
ttctgacatc	ccccaaaaaa	aaaaanaaaa	aaaactcgag	cctctagaac	tatagtgaTg	360
cgtattacgt	agatccagac	atgataagat	acattgatga	gtttggacaa	accacaacta	420

gaatgcantg	aaaaaaatgc	tttatttgtg	aaattttgtg	atgctattgc	tttattttna	480
accattataa	agctgcaata	aacaagttaa	caacaacaat	tgcatccatt	ttatgtttca	540
aggttcangg	ggaggtntgg	gangtttttt	taattcngcn	ggcgcnngcn	caatgcattg	600
gggccccggg	nncccanctt	ttggntccct	ttaagnngan	gggtaaaantg	ncgcncctgg	660
cntaatcttt	gnncatnggt	tggnttntctg	nggnngnaaat	tggttttccn	ggnnanaatt	720
tccccncatn	ttangatccc	nggnngntnt	aang			754

&lt;210&gt; 595

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 595

gggtttaatgc	tgtnnaanc	cttcttnanc	ctttgtacag	catccctcga	ttcgaattcg	60
gcacgaggaa	cgcttccatt	ttatacctgt	gtctagttag	tttctgccta	tctatccaag	120
aagcttttat	caagggtcca	ccatgtgcca	gccactgaag	tagatataaa	tacaaggatg	180
tgtaagggtat	ggatgatggg	atacgaactg	tcactctact	ggatttgtcc	gctctgttaa	240
agatacgggt	ccgaaaactt	tttaaagccc	tagagagggc	tttaaggcaa	tgtagcatca	300
tatatagagg	catnaacctg	ttcatatctt	tctatttaac	agaactgtgc	acctgggcac	360
aagggtgtgc	acaacaggat	gtgtacagca	gcactgttaa	agtgtancac	atccatacta	420
cangatctta	tgcaactgtt	ggaaagaatg	aagcgatgct	gcactgtggg	catgcagtga	480
tctctaagac	atattaactc	gaaagcaaaa	ggtttaacaa	tgtatnacaa	actgggctgc	540
aattgactcg	cgctgtaat	cccagcnctt	tgggaggctt	gantaaggcg	gatcacctga	600
ngtcangagt	ttgagaccaa	acctggccaa	tggtggccna	aaccnctgct	tctactnaaa	660
ctacnaaaaa	ttaacctnng	gcntgggttg	ctccgtgcct	tntaatcccn	gcttactcgg	720
caatgcttga	gngaangnan	aattngcttt	gaacctnggg	gaggnng		767

&lt;210&gt; 596

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 596

tnttnaatnc	tnttttaatn	cttgcgtgcan	gatcttttoga	tgatcccatc	gattcnctgg	60
tctcgaacac	ctgacctcag	gtgatccatt	cgncttggcc	tctcgaagtg	ttgggattcc	120
aggcggtgagc	cactgcggcc	agcacatttc	cacttntaga	tcctactcca	taccacaggt	180
ttcattttaag	angaaaganc	tanataaatg	tgctcttntg	gataccccac	cctgacagan	240
tgcatgttta	cacagntanc	atgggttgac	actgcaanct	ggcctgtcag	ccatnggagg	300
ngtttannga	aaggcanatn	atgtnactct	gtgncagggg	gccatntgct	taccntnac	360
ctagcatang	gggnttctac	gggtgacccc	nagcatattt	ctaggttact	tatgggcaga	420
tttghtaagt	acaaaaactc	agctgatgct	gggaatgggg	agagggccct	tganggactt	480
tgtggntttg	tgcttctggg	ttcctggcca	accccagggg	cacttgtctg	gagcccagct	540
gggcactaat	gtctgccanc	gactatntta	cagtgtataa	atgattcctc	tatttgggga	600
gagatcttcc	aatccagaag	agcccctntt	ggactgcctg	ggttaaatct	gcatagcana	660
agtggttgat	gagtcactct	aagaaattca	gccccactt	nncaacctgc	ccttcctgnt	720
tcctttttta	tgngggcctn	tgg				743

&lt;210&gt; 597

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 597

ngttttnnncc	ngttttttaat	ncnttgctac	tngetctttt	tgcaggatcc	catcgattcg	60
aattcggcac	gaggacanac	cgttgagagg	acgtggaggc	ccnttagggg	gtntgcncng	120
nanaggcaga	ngtggccctg	ggaacagagt	tttatgacnc	tttnnaccat	anangaangn	180
gagaatttna	aagatatggt	gggaatgaca	aaatagcagn	cataactgaa	gacaacatgg	240
gtggatgtgg	agtttgggnac	ctngggatcg	ngnaaagata	ccagtgatgt	ggagccaact	300
gctccgatgg	aggaaccac	agtgggtggag	gagttccant	gcancngga	agaggagtat	360
ccagcctaag	ttntgactg	gatgtcaaga	agaaacccaa	nttataanag	atgactntan	420
ntgantggnn	aaatctttca	gatcanncca	gaccatanen	tgagttaaac	atccgnaanc	480
cacaatccan	tgnnccttac	taagccgtgg	tgattnacaa	gtcataaatc	cattanatga	540
tgtggtnaaa	gatgcctatn	atgaccnatt	ctccatngtt	ntccngaaac	ccgtcaattg	600
acatcacatn	tcctnttgga	gattaaattt	tnggtananc	tnccttcgtc	cttgggcatt	660
ngaancata	agaatgcacc	cccnggntag	gccngtnna	aaggttnatg	aaggccntta	720
taanttttgn	nncccaanc	attaaantgg	ctngattccc	ttaatntttt	cctccnaac	780
ccagnt						786

&lt;210&gt; 598

&lt;211&gt; 809

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 598

ngttttnnnnn	cnnnttttct	aatgcttget	tctcgttctt	ttgcaggatc	ccatcgattc	60
gaattcggca	cgaggacaga	cgttgagag	gacgtggagg	cccagagagg	ggtatncncg	120
gcagaggcag	aggtggccct	gggaacagag	tttttgacgc	ttttgaccag	agaggaaagc	180
gagaatttga	aagatatggt	gggaatgaca	aaatagcagt	cagaactgaa	gacaacatgg	240
gtggatgtgg	agttcgaacc	tgnggatcgg	gtaaagatac	cagtgatgtg	gagccaactg	300
caccgatgga	ggaaccacaca	gtggtggagg	agtcccaggg	caccccgga	gaggagtctc	360
cagccaaagt	tcctgagttg	gaggtagaag	aagaaaccca	agttcaagag	atgactttag	420
atgagtggaa	aaatcttcaa	gaacagacca	gaccaaagcc	tgagttaaac	atccggaaac	480
cagaatccac	tgttcttcca	aagccgtggt	gattcacaag	tcaaaataca	tagatgatat	540
ggtaaaaaga	tgactatgag	gaccattccc	atgttttccg	gaaaaccccc	cattgacatc	600
acattccaac	ttggagatta	aattttgggt	aacccttcc	ttgtntcttg	gccttngaac	660
ccntgaagga	aggcacccon	ggtgaagggc	ccngggggaa	agggattcan	ggnaaggggc	720
cantaanaaa	ccttttggga	cccccttaa	nccaataaaa	tttggtngaa	ttgcnangga	780
atggtttgnc	ccccnaaac	ccnaaaant				809

&lt;210&gt; 599

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 599

ttntaatnc	ttttcnaat	gctngcttca	ggannntntg	cangatccct	cgattcgaat	60
tcggcacgag	ccaggtttagc	tgctgaatca	aagcttcaaa	cagaagttaa	agaaggaaaa	120
gaaacttcaa	gcaaattgga	aaaagaaact	tgtaagaaat	cacaccctat	tctatatgtg	180
tcttctaata	ctactccaga	gacccagtgc	cctcaacagt	aaagactttt	ctttaataag	240
agtacggtgc	cacttgccctc	aaaagttact	atggtgctta	agattgtctt	gatctgacat	300
atatcacctt	ctgggttatt	tactcattgt	gccaggacct	ggcattttca	tgtgcctttg	360
accaagtgtt	cagaatttgc	ttgactctaa	cctggagagc	ttcttaagtg	atgcccttc	420
atggagcttc	tatgacagtg	aataaactat	taattgaagg	aaaatgttat	aattaatgta	480



tctatttgc	gcattgtata	tggattaaat	gataaaaaac	aagtaatcta	ccctcagagc	540
catgtatttg	agaatgcttc	aatcatat	tcctatgtac	ctttttttta	taaacttagt	600
tttagactat	gttgtaaaaa	tggggaaagg	ttgtaaacta	tgtngtaaaa	aatnngggaaa	660
tgtggcttta	aaatatatnc	attatat	gttcaaggat	tttggcaggg	gntaaaggaa	720
ncnatgggtc	aatcctttna	tttatatacc	ntgat	ttta		759

&lt;210&gt; 600

&lt;211&gt; 769

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 600

ttttaatacn	tttttnaatn	cttgcctncc	ntccttttga	ggatcccatc	gattcgaatt	60
cggcagcaga	gcaattccac	tcctagctcc	acccacaggt	aattgaaagc	aaagacgcaa	120
acagatgcct	gtgcacccaa	gttcacggca	gcaccccttc	ccatagtggc	agcatccgtc	180
gtcacagcgg	natcatcctt	catcatagcg	gcagcatccg	tcgtcacagc	ggcagcatcc	240
ttcgccacag	cggcagcatc	tgtcgtcaca	gnngcagcat	ccttcgccaa	agcggcagca	300
tccttcgtca	tagcggcagc	atccttttgc	atagcggcaa	ggtggaaacc	ctgtccatcc	360
actgagggcg	gcatagacta	aacatggcca	gtccaggcac	tggaaatccag	gccgtanaac	420
ggngcccacn	gtcaaaagga	atgagaccct	gatgcactgg	gcgacacaga	cgggcgacac	480
agacttgagg	acatcatgct	aagtgaagag	ccaggcacac	ggagcggacg	gggtgatcct	540
gctcacgtga	tgtgtcccga	atgggcacnt	tcagagggga	agaanggaga	tggcgcttga	600
cngtgnccgg	gacnggggtt	gggagcgacc	ggttggttgg	ttnggggttc	tttctnnggt	660
gaaggaaatg	tttttgatat	tggggccgtt	tgggtgatnt	ttgcattacc	ctttgaatat	720
gcttanaacc	cnctagaaat	tggnacactt	tttaaatngn	ttggaaatt		769

&lt;210&gt; 601

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 601

ntgtttaata	ctattttcta	atacttgcct	tcgttctntt	tgcangatcc	catcgattcn	60
aattcggcac	gaggagacag	cagccccag	ggaatgaagc	tgatgccaga	gtcagacccg	120
aggaggaaga	ggagccactg	atggagatgc	ggctccggga	tgcgcctcag	cacttntatg	180
cagcaactgc	tgcagctggn	cctcaagtac	ctctttatcc	ttggtattca	gattctggcc	240
tgtgccttgg	cannctncat	ccttngnagg	catctcatgg	tctggaaagt	gtttgccctt	300
aagttcatat	ttgangctgt	gggttccatt	gnnagcancg	nnggacttnt	nctgggcata	360
gctttggtga	tnagagtggg	tgggtgctgn	ancnctgggt	tcangcanct	atttctggcc	420
agcagatgta	nnctatatct	gtgattactg	gcacttggct	acagagagtg	ctggataaca	480
gtgtagcctg	cctgtacagg	tactggatga	tctgnaanac	aggctcagcn	atactcttac	540
tatcatgcaa	ccagggggccg	gttgacatct	aagacttgnt	tattctatag	ttcnagganc	600
acaatggaat	atgatccctt	aactcctgat	ttgggatcat	ctgaaggacc	aaggngggca	660
gtcttcgaag	tgggaataaaa	tagccccggc	ngtngtgact	tgcacctata	ttcccagact	720
tttggggaggc	naannttnga	aggattgntt	gcct			755

&lt;210&gt; 602

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 602

nttghtaatag	ctgggtttcta	aannntngnt	ttcaaccctt	ttgcatgatn	ccatcgattc	60
gagcaaatca	agatcttcag	gtacagtgg	accaggcact	ccagcaagcc	ttggatccca	120
atagtttaagg	caactctttg	tttgacaggg	tggagatcg	aagggcagca	atggaacgtc	180
agcttatcag	tatgaaagtc	aagtatcagt	cactaaagaa	gcaaaatgta	tttaacagag	240
aacanatgca	gagaatgaag	ttacaaattg	ccacgttgct	acagatgaaa	gggtctcaaa	300
ctgaatttga	gcagcaggaa	cgggtgcttg	ccatgttgga	gcanaagaat	ggtgaaataa	360
aacatctttt	aagtgaatt	ngaaatctgg	anaaaattta	gaatttatat	gacagnatgg	420
aatctaagcc	tttagtcgac	tctggtactc	tgganataa	cacctattat	acagatttac	480
ttcatatgaa	gctggataac	tnaaaacaat	agaaattgaa	ngcactaaan	gtgaattgtc	540
atacaagcga	aatgaaancn	ttatttgana	gccngcgggc	ttctaacata	ttgagcgata	600
actttttgca	aatgaaagat	gcccttcngc	ttnttgaatt	gnaaaatatt	gaaacctgan	660
agntnancct	agntgaattg	aaacttaaat	ttgaaccctg	nacnanaccg	gttaantgcc	720
tgttcctgat	aaaaanaagc	cntnangtgc	ttncctgntn	gatttanccc	ccg	773

&lt;210&gt; 603

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 603

tgctttntaa	tagctgtttt	taaatnctn	gctttgcgct	cnntttgcag	gcatcccatc	60
gattcgaatt	cggcacgagg	gggacatcag	tgatcgtaag	tctcctgggn	ccgttattct	120
canattaggt	gacggagcta	agacttcgag	accatctcgt	cctttntgta	tcgcggaac	180
ctgangaacg	agccggcggc	ggtgacctgc	acgagaagcc	aggctaactg	ggtgaagtac	240
catgcaagca	tttcttaaag	gtacatccat	cagnactaaa	cccccgctga	ccaaggatcg	300
aggagtagct	gccagtgcng	gaagtagcgg	agagaacaag	aaagccaaac	ccgttcctctg	360
ggtggaaaaa	tatcgcccaa	aatgtgtgga	tgaagttgct	ttccaggaan	aagtggttgc	420
antgcttgaa	aaaatcttta	gaaggngnca	natcttccta	atctcttgct	ttacggacca	480
cctggaactg	gaaaaacntc	cactattttg	gcagcaaact	tgagaactct	ttgggcctga	540
acttttccga	ttaagaattc	ttgagttaaa	tgcatctgat	gaacctggaa	tacaanttag	600
nttcganaag	aaagtgaaaa	atttttgctc	aattaanctn	gtgtcaagga	aaatngnttc	660
anatgggaaa	gccgttttcc	ncctttttaa	gantgggaat	tcttngatga	ngncnaattc	720
ntnttganc	taactgnntt	angcagcttt	taaaaaanta	ccattggata	aangagtcen	780
aant						784

&lt;210&gt; 604

&lt;211&gt; 801

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 604

gttnnctn	aacctttttt	tgaaatcnnt	ngcttctact	ctttggcatn	catnccatcg	60
atnccggccc	gtgtggggag	acngacagca	ccctttttnt	ctggcatttg	cccttgangc	120
tatagcgct	ccctctctcc	ctcagagggc	acagctgcag	gcctgaccaa	ggccacgccc	180
ggctctcgtg	ctctaggacc	tgacacggac	ttgtggatgg	gcctggactc	tccagaaact	240
acttggggcca	gagcaanga	aaacctcttg	ttttaaaaaa	attttnttca	nagtgttttg	300
nggaggagtt	ttagggttg	gggagaggga	ggacacatnt	ggaggaaatg	gccttctttt	360
taaaagcana	naacacataa	ccttacaact	gcctggcaag	cccaatatca	cttgtttggg	420
ccctancggg	actccaangn	agccacacgc	cccttctgga	aggggtgtgng	catgtnaant	480
gtgtgccanc	gcgtgggctg	gcgtgtgaan	atctatnaaa	taagtatana	tggngntnta	540

ntatatgtgt	ntaaaataaa	ngantggaca	tatttggnc	tctgnngana	nncttnga	600
ctaagncaag	agtnnnctn	gaaaaacnaa	ananagtnc	ntntanannt	ttacgta	660
atcaatactn	tntccacntn	accctnctnn	tannntncc	natatantcg	antaattc	720
cactcntnna	ttcctngtna	acacnaatna	atnnaactat	naaatatntn	tnctnnntan	780
tngacatann	catncnncc	g				801

&lt;210&gt; 605

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 605

gnttcta	tggttcna	acttgcttn	gctcctttg	aggatcccat	cgattcga	60
tcggcacg	agcctcgct	gggcccgc	gtggctcca	tttcccttc	agcgggaca	120
aggggact	ttaccaggc	atttcttga	tggcctgtg	gatctctgc	cctccaagac	180
cctccaagt	tgagcctg	ccacagctg	gacactga	tcagccctg	gaaccatgg	240
ggcttctat	tgacaccag	ctgcagcct	cccaatcca	gcccacttt	ctgtgtctc	300
ggcgggct	cctccttgg	gggagctgt	ctgcacact	taggatgct	aaaggatat	360
ctggccttc	cccatncct	gccagcagc	cccagtcag	caacagccg	aaatgtctc	420
agactctgc	cagcctcca	ggtagccac	ctcgagacat	gacctcag	tctctgtgt	480
tcctagaag	ctgacagag	ccccanggc	agtgggtgg	tggcgggct	gagaccctt	540
cctgtgtcc	ggaccctgg	gccgntctt	cctcctgtg	atcccttcg	acttacaag	600
gttctnaant	gggcagacg	ctgggcaccc	cttgggccc	gcccancat	ggccatngn	660
cangctttt	naaccgcg	nggntttcc	ngcctgtgt	atcttgc	tccangga	720
nnttggaac	tttctncg	ggcggggccc	ccnagcnc			759

&lt;210&gt; 606

&lt;211&gt; 809

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 606

tctncgtna	tcnnnnntt	aaaagcctt	gcttttgct	nctttgctt	atcccatcg	60
ttcgtgact	tgtacctgt	ccaagctgat	ggggttttg	tgtgtgtg	ccaggcagg	120
gtctgactg	agaacaaact	aagggttgc	caacaaaca	ggacctctt	caagaaggg	180
tcccaggcct	ggcgcagtga	ctcatgcct	tgatccagc	acttgggag	ccnaggcgg	240
tggatcatt	gaggccagg	gttcgagac	agcttggcc	acatgatg	accccgctc	300
tattaaaaa	acaaaaatta	nccaggcgt	gtggcgcct	tagtccca	tactcagg	360
gttgaggcag	gagaattgt	gaacccggg	ggcggangt	gcaatgag	aanatagc	420
cactgcact	catccttgg	tgacagaag	gagactcc	cttaaaaga	gggctcct	480
gtctacgtc	tgggtgggct	anagagang	ccncgcag	gggctgtgt	gagtganng	540
ctnntcttt	naannccag	caatagtgt	tcttgactc	gtccttttc	gngtccac	600
gacattttac	atntttncn	agtttnc	atttaaagt	gnctaattt	accattata	660
attttnaatt	ggcatttct	ttaccnatc	tttttgtnt	aaaatgg	tnnttgaa	720
cngnatcng	tctaagtng	tnatatttn	ccnaatgcc	atnntacct	ctttgnaa	780
atntattcgt	ttcnaagnt	tnaacctc				809

&lt;210&gt; 607

&lt;211&gt; 788

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 607

tnttttctaat	acnagtttnc	aagncttgct	ttnnnatccc	tttgcaggat	cccatcgatt	60
cgcaaggccc	gaggtgccat	cccctctggg	aagcagaagc	ctggtggcac	ccagagtggg	120
tactgttcgg	taaagagctc	accctctcac	agcaccacca	gcggcgagac	agaccccacc	180
accatcttcc	cctgcaagga	gtgtggcaaa	gtcttcttca	agatcaaaaag	ccgaaatgca	240
cacatgaaaa	ctcacaggca	gcaggaggaa	caacagaggc	aaaaggctca	gaaggcggct	300
tttgcagctg	agatggcagc	cacgattgag	aggactacgg	ggcccgtggg	ggcgccgggg	360
ctgctgcccc	tggaccagct	gagtctgac	aaacccatca	aggatgtgga	catcctcgac	420
gacgacgtcg	tccaacantt	gggaggtgtc	atggaagang	ctgaanttgt	ggacaccgat	480
cttctcttgg	atgatcaaga	ttcantcttg	cttcatgggtg	acgcagaact	ataaagccct	540
gtgtncactt	atagacagtg	aaaaccacag	ggtcttcac	tttattaatc	nngaaacctt	600
ggaatgcctg	ctttgttttg	taaccccttt	ttaaaacctt	cctgttttta	aaaagtggtc	660
atttttantt	nacgntttan	aaanaaaaaa	tcctatttct	ttttcctttt	natttttaaaa	720
aaaaattngn	ttttgtttgg	ggggnntttg	ggggaattaa	aataatttgg	cccccaactt	780
taaaaaat						788

&lt;210&gt; 608

&lt;211&gt; 796

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 608

tctttttaatg	cttttttncaa	gccttggttn	aaatcctttg	caggatccca	tcgattcgaa	60
ttcggcacga	gactacccccg	gctacgggtc	ccccatgcct	ggcagcttgg	ccatggggccc	120
ggtcacgaac	aaaacggggc	tggacgcctc	gcccctggcc	gcagatacct	cctactacca	180
gggggtgtac	tcccggccca	ttatgaactc	ctcttaagaa	gacgacggct	tcaggcccgg	240
ctaactcttg	caccccggat	cgaggacaag	tgagagagca	agtgggggtc	gagacttttg	300
ggagacgggtg	ttgcaagaga	cgcaaggggag	aagaaatcat	aacaccccca	ccnnaacacc	360
nncaagacag	cagtcttctt	caccgcgtgc	agccgttncg	ttccaaacag	agggccacac	420
agaatacccc	acgtttttat	ataaggagga	aaaccggnaa	aanaatttaa	aagttaaaaa	480
aatanccttt	cngttttaca	ctactgntgt	agactcctgn	tttcttcaan	cacctgnaga	540
ttcttgattt	ttttgttggt	gatgntctct	ccattgcttg	tngtttgcnt	gggaantttt	600
atttaaaaaa	aaaaaaaatt	cttgtgagtn	gactttggnt	tttaaaccan	tgntagattt	660
taacngnacc	cttaatgggt	tgtacntata	tgntttnaaa	acatgnnaan	aaatatttaa	720
tgtaaagggn	ctgttnntaa	atntaaccac	ntanagaant	tnnaaanntn	ttnanccctt	780
tagaacnatt	nntgng					796

&lt;210&gt; 609

&lt;211&gt; 790

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 609

gnnnttttaa	nacctntttc	aatncttgg	tttnaatcnt	tttgcaggat	cccatcgatt	60
cgcacccagg	gagaacctcg	gggctgggac	acctcctggc	cctcaccctg	ggcatgtttt	120
acagtccctc	gtgccccaca	ccggtggccc	cctgaggaca	cctccaccct	gaccttgatt	180
ttcccaaacy	ctgcctcttg	gtgacagact	cagcccaaaa	ccccttcctt	ctgtctcttg	240
agacccttga	gcttggggaa	atatggaggg	gtgtgtgtct	gcaatcaagg	cctctgcagc	300
tcacggctgg	cccgggtggc	tgggacttcc	gtctgaattt	taaatactta	gggntcattt	360
tttttctctg	gcaacaaagc	ttgatgtttt	caactgttta	gtttcctgtt	tgtctgggtg	420
aggggatcac	gtctgtgact	ctggacttgc	tctgggggaa	cagttgtcac	tgccccngg	480

gagaggggca	gcttgggctt	ggaagaaagc	acaccccnga	gaccagagcc	ccttcnagag	540
ggatncttgg	ctgcttcatt	gnctttcccc	cagcaagccc	tgctcttcca	caagcncctt	600
ntggggctct	gggtatggtc	ccccgntcac	cttctttcca	nantccctga	nntgggtgtag	660
ggttgtgggt	tggcacangg	aattttgggg	cattggggaa	ggggntttca	aaacttttnc	720
caaanacccc	cgtgttcctn	ngnaaaattn	aanttggtgg	gcttnggggtg	ntnaccccca	780
antcttngnc						790

&lt;210&gt; 610

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 610

gatgtttnnn	annctgggtc	taatncttgg	aaanctnctn	ctttgttann	ngcnntttct	60
gcaggatccc	atcgattcga	attcggcacg	agcccagctg	gacctgggtg	ccctttccta	120
gtgcctctgc	tgggggagga	gaacctctgt	ccacgtggag	gctaggaggt	ctcagggtgct	180
gccctggcag	caccagagt	tgggcccggc	ccgagtgtct	gcccctcggc	cctcagggtg	240
gggcacttag	caccagaag	ggacaaaag	cagggcatgg	cggtgcagag	gagtttggga	300
ggtgtaaa	gccccatgca	cgtggaggag	gagctggctt	tcagccccag	acccacgct	360
agcactttcc	acgctgcttg	cccgtgtgtg	atgtgcagtt	cccagtgcct	gtgtgagccg	420
acatctgctc	agtcctatcc	ctcgtcagcg	tgtggagacc	cagctcctgc	aagcccttct	480
gcttccacgc	ccccagacag	cttgggtggag	ggtcctgcat	ctgggccaag	ctgggggtgca	540
cccagccaaa	gacaaagctg	ccttcacgtg	cccaaaggat	tcaagatggg	gcactggccc	600
cgggaggagt	cttgacaaa	aatgggagcc	cgctcttgtg	gggaaanccc	cgacttcccc	660
caccnanaaa	ccgntcccac	ggtgccggan	cttccccctt	ttcctttgtg	ggggcaacaa	720
nattggcctt	gggcnctttc	aattntnctg	gaagctttcc	tgggtgtngg	cttttgacct	780
taaaat						786

&lt;210&gt; 611

&lt;211&gt; 938

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 611

tgttttaaa	ccctntttng	aatncttggc	ttncgncccc	ttggcaagat	cncctctctgc	60
aggatcccat	cgattcgttt	gtatttttag	tagagacagg	gtttcttcat	gttgggtcagg	120
ctggctcnaa	actcctaacc	tcgtgatccg	cctgcctcga	cctcccaaag	tgctgggatt	180
acaggcatga	gccaccatgc	ccagccaaag	atcatttttt	tatatagact	tcagnccttt	240
gtaaatattg	taactgggga	gtatagagta	gaaaaaaagt	atagntaaaa	catttgttct	300
acaaattaac	ctttaaaaat	ataattactg	ctaaaaatag	agtgcgtgta	cacttaagga	360
aaattagtgc	cattttggaa	atgagatctt	gtgccataaa	tncagctgaa	ctgaatataa	420
atgttcacaa	attaatgctg	tnaaaggaat	gagttaagca	gaaaaacttt	taaccagcac	480
ttctcaaaaa	anaaaannna	nnaattaaat	nntataancn	ncatnnaan	ntatnttann	540
tttncntctn	nattncanta	attttgnnt	ncaaataant	nnacctnnan	ctntgttntn	600
nttnnnncna	tnnantatcn	ntttatcnan	tatatnatta	nctnatntn	nngnanngna	660
tcntnctcta	tncnnnatnn	tncatatnnc	gtccnntnnn	nnaantatgc	ctcatnatat	720
ntacnnnaaa	ngtntangta	tgnttantgc	atnnncatna	ctnntgatgt	cnnagttnna	780
nataattttg	cncctattat	tntgctnatn	tatntgtttg	acacannata	ctnnnancna	840
ttcatcttct	cgcaatnnng	gnacttttna	nttacnnnna	tgntannnnnt	nataatatnta	900
tcattagana	cctttttnaat	tntnnntnnc	nanacgcg			938

<210> 612  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 612  
 tgtttgnaan nncggntntt gaaatncntg gtacnnaaac nctttngnaa ancncctctc 60  
 nctgtntgat cccatcgatt cgaattcggc acgagataga aactaggcac tgatttgttt 120  
 atatttntcc tgctcgagac acatgatgtt tcatgtatct gtggcttttt atagttttaa 180  
 ataatttctg gaaaagtcac agtcattatc tctttaaccg etccctctct tccattctct 240  
 ttgttctctc ttcctcgaaac tcctgttagt catttgatcc tccatattct tgaatatttt 300  
 tgtatttctt ttattattta tttcttgtct ctgctacatt ttacattgag taaaagtggg 360  
 atgtgacagt gggaaatcat tagtgactta gaaattccag ttggtcattg ggccaatttt 420  
 gatgtacct tctctctttt atttctcact tcaaaataaa atttgcaaaa acaaaaaatt 480  
 aaatatagta tgagtccagt tactggccta aggagctaaa agcattcttg gtttgtatga 540  
 agacagctga gttataacaa atgagagtac tgttgtgtga ctgcattaat tattcccttt 600  
 ttaaatgtac aagagcaang cattctacct gactgngtta ttgagctctg cancatacat 660  
 ggtgacanag ctaaaacaan acaagccnaa ccnanaagga aaaccccagc tttagggata 720  
 ctctgntcat ngaatatagc ctgaaaaatg gntaatcaag aaagtnaact t 771

<210> 613  
 <211> 774  
 <212> DNA  
 <213> Homo sapiens

<400> 613  
 tttgaatcct tgctttcaaa tncctggcac tngccctctc tgnaggaatc ccatcgattc 60  
 gaattcggca cgaggtaacg tgacacgtat tttacttctt ttantaggcg gacacacttt 120  
 cttaaagtaa taatacgtca tggccctgct ataaggtagt agttctagaa gactgntat 180  
 ctaataattc agactaaagc tatttatatt gctgtgacac cacgtggaaa acttttataa 240  
 ttccatctta tttctgatgt atatgtttta tttctctgc cttcataaga actaaaaacc 300  
 aaagtatttt acgtgaaaac aagatttttg tttgagttca tttacttgag atatgtttta 360  
 aaaatccacc ttctgtcaca ctatagaagt atattttgaa ttatcaaaag gtagaattat 420  
 aactttcana aaagaaaaaa atggtcaatt tantttaact ctatgtcaaa aatttattta 480  
 tagtctcata tattcattcc acaccccccg ttcttctttc cttctttctc cctctgcctt 540  
 nttcttaan atnatTTTTA aattctgacc aaaaaataag tngtggcaag tactttctta 600  
 gcataacctg gactggttga agnagtaatt ctgntccttt aaaaaaantc cccaactggg 660  
 nccnngnca ggnacaaaaa nttntaanga acatntggga attangcnaa atggatnttc 720  
 cttggaggtc caaccccaa aaatcattag gncnaccaa attnaaaata atcg 774

<210> 614  
 <211> 754  
 <212> DNA  
 <213> Homo sapiens

<400> 614  
 ttggantctt ctngaaacn cttngcnatt gcncntctctg naggatccca tcgattcgaa 60  
 ttcggcacga ggttcttcaa agccaaccaa gacaggcttn tnagtttttag agcttcagaa 120  
 caaattgccaa aaagccagag ttgtttatgc tagtgcaact ggtgcttctg aaccacgcaa 180  
 catggcctat atgaaccgtc ttggcatatg ggtgagggg actccattta gagaattcag 240  
 tgattttatt caagcagtag aacggagagg agttggtgcc atggaaatag ttgctatgga 300

tatgaagctt	agaggaatgt	acattgctcg	acaactgagc	tttactggag	tgaccttcaa	360
aattgaggaa	gttcttcttt	ctcagagcta	cgttaaaatg	tataacaaag	ctgtcaagct	420
gtgggtcatt	gccagagagc	ggtttcagca	agctgcagat	ctgattgatg	ctgagcaacg	480
aatgaagaag	tccatgtggg	gtcagttctg	gtctgctnac	cagaggttct	tcaaatctta	540
tgcatagcaa	tccaaagtta	aaagggtttg	tgccactagc	tcgagaggaa	atcaangaat	600
ggaaaaatgt	gttgtaattg	gtctgcantc	tacaaggaga	agctangaac	atntagaaag	660
ctttggaaag	aaggccggng	ggagaaattg	aatgattttt	ggtttcaact	nccaaaagggt	720
gtgttgcnct	cccttctttg	aaaaaacatt	ttct			754

&lt;210&gt; 615

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 615

tgttttnaatg	ctgttttgaa	atcttgtttc	aaatcctttg	gctacttgct	ctntctgnan	60
gatcccatcg	attcgaattc	ggcacgaggg	attctttcac	tgagcacaaa	gagttggttg	120
ggcttttagca	tctgactgat	tttgttacgg	ggttgattct	gaccatagga	agtatgcaat	180
gtgaatcact	atttacagag	aaacctacaa	cagatgcttg	atgttgtaga	aactgggaca	240
tatagatacc	aagcaaaatt	ataagaaacc	tataagggtg	tcaatacgtc	tgtgtttcca	300
aaattcactg	tncatgatca	gtttgggtgt	cttgtaccac	agtttttaac	tgaagggaacc	360
agttgtaaca	gtctcaattt	ttaactaaaa	cttgaagaac	taanacaaca	atgcaaacct	420
ttcagcattg	tttggccaaa	cttgttaaaa	ctgtaatgca	agaaccaa	gcactgtgat	480
gtggcaccaa	ctaattagca	agcatgaatt	tttcacccaa	naagtga	aggaaaatct	540
accatggcct	naagtttaag	agcagaactt	cctgactncc	attctatgac	tgatcaaaaa	600
nactaatagt	ttaaaacctn	agcangcctt	gttcacgata	tgcnagaaaa	aaaagtgcct	660
gcagtttann	atccttatgg	aantttttca	cantgtnaca	nggtnttgta	atacnttgga	720
ngccctacat	tttcntanga	atntattttn	cttggcctaa	nttggnttca	ange	774

&lt;210&gt; 616

&lt;211&gt; 769

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 616

atnnentttt	tgnaatcctc	tctgaaatcc	tttgctactt	gctctttntg	caggatccca	60
tcgattcggc	cagtcctcac	cttccctagt	cctcgtgtgt	attttaggag	atgcgtgggt	120
gtggaacagc	ctcctgcctc	cgggtccagg	gtactggggg	ctgtgtgttg	tgtttctgcg	180
tgttctcggc	agaaagtggc	atgctgtccc	gcctgggtga	tttgctcttt	tacactattg	240
ctgaaggaca	ggaacgaatc	cctatccaca	agttcaccac	tgactaaag	gccactggac	300
tgagacatc	agatcctcgg	ctccgagact	gcatgagcga	gatgcaccgc	gtggtccaag	360
agtccagtag	tggtggcctc	ttggaccgag	atctcttcgg	aaagtgtgtg	agcagcaaca	420
ttgtgctcct	gacccaagca	ttccgaaaga	agtttgatcat	tcctgatttt	gaggagtcca	480
cgggccatgt	ggatcgcac	tttgaggatg	tcaaanagct	tactggaggc	aaagtggcan	540
cctacatccc	cttntcggcc	aagtcaaacc	cagacctgtn	gggtgtctnc	ctgtgcactg	600
gtggatngtc	aanngcactc	ttgtggggcca	cacaanagat	tccttttttg	cctgcaanac	660
cntgtntgaa	acccccttaa	cttatngccn	attnentna	agcaaccctt	aggcnanttg	720
actnnenttc	acaanttttt	ggggcnaaag	anncnaattg	gcctgcctc		769

&lt;210&gt; 617

&lt;211&gt; 766

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 617

```

aganntcttc ctttctaata nctngctacn ttctctntct gcaggnatcc catcgattcg      60
cttcctcaaa gcatgggtgc tgagnaccca nagttgagag gngttttttt actgatttag      120
ccagggtggca atcatgagtg aatggatgaa gaaaggcccc ttagaatggc aagattacat      180
ttacaaagag gtccgagtga cagccagtga gaagaatgag tataaaggat gggttttaac      240
tacagaccca gtctctgcca atattgtcct tgtgaacttc cttgaagatg gcagcatgtc      300
tgtgaccgga attatgggac atgctgtgca nactgttgaa actatgaatg aaggggacca      360
tagagtgagg gagaagctga tgcatttggt cacgtctgga gactgcaaag catacagccc      420
agaggatctg gaagagagaa agaacagcct aaagaaatgg cttgagaaga accacatccc      480
catcactgaa caggagagac ctccaaagac tctctgtgtn gctgggggtnc tgactataga      540
cccaccatat gggtcacaaa naantgcagc atctctaatg aganttatcc ttgcccttng      600
ttcaangata ttattgaaag gacatcttac agcttttccc aatgagaang cccangaagt      660
gttaaacata ctgnnttgaa aaaagcactn tatntnttcc cntnttaana tggtnctctaa      720
aatgtanaaa naaannaaaa naaaanctcg atccctctnn aacnct      766

```

&lt;210&gt; 618

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 618

```

tttnnagnnt cttcctttct aatggcttgg ctactngttc tttntgcagg atcccatcga      60
ttcgctcagt gcagcgatca tggctcagtg cagcctcaaa ctcttgggct caagcagtgc      120
tccaacctca gctcctgag tagctaggac tataggcaca cagcaccatg ccccggtat      180
ttttttatct tgtagagatg gggctctcact atgttgccca ggctagtctt gaactcctgg      240
cctcaagcaa tcctccacc tcggcctccc aaagtgtctg gattaaaggc gtgagccacc      300
gtacctggcc cttggtggaa tctttagggt tttctattca tacatataaa atcatatcat      360
tggcaaacag agataatctt acttcctcct ttccaatttg gatgccttag atttcttttc      420
cttgccctaac tgctctgtct agaactccca gcactatgct gaatagagtg gcaagagcag      480
gcatttgctt tgttcctaac cttagagaaa aatccttcag cctttttacca ttgaggatga      540
tgtttgtgtg tagtttttca taaatgatct atatcaggct tgaataaatt tctatttcta      600
aaaaaanaaa atataacnnn ntanttnatn aantnnttaa naaaanaaaa actggnacct      660
ntaaaactta tagtngagtc gtttnaccgt anacccana ntttgataaa gatacattgg      720
atnanttttg gacaanccnc aactaggaat ngcnntgnaa at      762

```

&lt;210&gt; 619

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 619

```

tttgagntc tttctttcta atncttggct actngntctt tntgcaggat cccatcgatt      60
cgaattcggc acgagcggac ccatcgagc gtaacctgga tctccgagg cctggcgagg      120
gccggccacc tggaggggca ttgcttgggt cgcgtggtag cagaggagct tgagaatggt      180
cgcactctac cacatacagt tctttacatg gctgattcag aaactttcat tagtctggaa      240
gagtgtcgtg gccataagag agcaaggaaa agaactagta tggaaacagc acttgccctt      300
gagaagctat tccccaaaca atgccagtc cttgggattg tgacccagg aattgtagtg      360
actccaatgg gatcaggtag caatcgacct catgaaatag aaattggaga atctgggttt      420

```



gctttattat	tccctcaaat	tgaaggaatn	aaaatacaac	cctttcattt	tattaaggat	480
ccaaagaatt	taacattaga	aagacatcaa	cttactgaa	gtaggctctt	tagataaccc	540
ctgaacttcg	tgtggtccct	tgtctttggn	tataaatgct	gtaaggtggn	agccantaat	600
tntctgcaan	aagtangnca	gcacttttca	gtgatttgaa	tatcatcttg	gcttngangc	660
cangtggaaca	accttgtcat	aactgacttc	tgaaaagaac	cctntngata	tttgatgcct	720
cnggtgtngg	tggaactgtc	atttantngg	anna			754

&lt;210&gt; 620

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 620

gcgttctttg	aaagccctnt	tttgaaaggc	ttgcttctaa	ttacgggaaa	cctttgcaac	60
tgcagatccc	atcgattcga	attcggcacg	aggacccagg	tagaccagct	caagagttca	120
tgttctttgt	natectctcg	tgagctctct	gtaagtcnnt	ttcttgccca	tcaccacatc	180
cctagtactg	ggatcagtc	tgcccaactg	gctttctggg	ttgccccaat	gtggtctatt	240
cttgatgcag	ctaccaaagt	aatgttttaa	aaccattata	ccaagttact	atccttgtca	300
aaacccccag	taactgcaa	tctcacttag	aataaaatcc	ggactcctgt	gaagcacagc	360
ataaactggc	cactgcctat	gcagcaacct	catctttacc	gnttctgccc	ttgctcactc	420
ccttccagcg	ccgttattct	tctgatgcc	cctagtacac	aacaactcct	tcctgtccca	480
agagtaggaa	aattactggg	ctctctgcca	gngagaancc	tcttctggna	ttacctttgc	540
ttcattgcng	aatcttctnc	aatatcatct	tctaaaaaga	gcctttttaa	aatcaccttt	600
nctatnatgc	cctactcatt	tccagtcctt	gaaanggcc	ttcccacttn	antannactt	660
attgctaacn	tgaatacac	taaatgnnan	ccttcatgaa	nggtanggca	anttaaagtc	720
nttngcactg	gnnaggcnaa	gagaacaagc	ancntggntt	canaagn		767

&lt;210&gt; 621

&lt;211&gt; 828

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 621

tttctaatag	cttgccttct	aatnctnggn	aacgctnggt	ctctgnagga	tccctcgatt	60
cgaattcggc	ncgaggggtg	acagagtga	actcgatctt	ccaancaaac	aaacaaaaag	120
tncttaaaca	tatgtgaaca	aaaatttngt	gatggaagga	ttctagttaa	tgagtattgc	180
atcaagattt	acatctttct	tactaaggaa	aagagttaat	aaaaatngnt	ctttatttta	240
caggcagnta	ctgaggctct	tcccanntcn	cagtanaacg	ccactcagcc	ttgaaaatgg	300
agtgttggtg	tttctaaaca	tatatttatg	tcatttattn	aggtacagtt	cacttaaata	360
accataagtn	gantctctct	tgtnagtgat	ttgggtagga	agaggccatg	tctanagttc	420
natttctctg	ttgggtccna	ntgaaattgg	accttttnag	ttgttcanaa	aaatnaanat	480
aaattnctca	tattaaatca	agannctcnt	caanttatag	atgtggggta	gggttccnng	540
taaaacccat	tatnaatcta	gaaaattatc	nctatngana	angcntttta	tatctnttac	600
cntgaaattc	attacttttag	tncaaggcct	accttttaan	gtttnnncnn	gaaccatttt	660
tannnnntcn	ncttttgnnn	caananntca	ttttaancca	ccaaaantcn	caattntnt	720
tncatttnaa	tannngatgn	naattatnnn	atcnatgtgt	catatttnac	canganaata	780
ctgngctncn	tgnaataatn	ggtacactaa	anncnngann	tttnntcn		828

&lt;210&gt; 622

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 622

```

gtctttgaaa cctttttcta atncttgctt tctaattctt ggcnaactcn ctctcncctgc      60
agnncccatc gattcgtttg ctttcagtgg ttggetttca ctgaaagaaa gtgtaaanaa      120
agtcagaatt tatagctttc actatgtcca agactaggac tgggttataa agattttctt      180
ttgtgaagga aaataaaaga aaatttgcca ctactgcatt tactttacta ttgtaaactt      240
aagattcatt ccttagtctt tggaattttg atgtctcaaa accagatgag tgggaagtgc      300
gaatttgcaa aataaagcta agaatgctta actctgcact ttaagttcta ctctgaccaa      360
attgaagatg agcagagcag ccctgaacag catttngttt atacagtctt gtttaagaat      420
agaatttttt taactcttca tttnttgtct ctgtggaagc tgtgtaactc tttttaaaat      480
gcaattttaa acattntggg attctaacaa ttctctcaan aaacagcatt tccaatggna      540
atnggtattg ntacgctgta ccttatgtat tncctgtacc tgaacacttg atgctgcctn      600
acangaaaat agaactttat gttaaaaaat aaaagtctgg tncctctttg naaaaaaac      660
nncnctnctn ctcnaaatcc ncnacannnc tnnnaatntn ctaanntnag tctnnmttn      720
ngcanncttn tnnnccnct nanctccctn tntctnttcc atatctanan tnacancct      780
ccct                                         784

```

&lt;210&gt; 623

&lt;211&gt; 1164

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 623

```

gggacttntt angcctttt cgaaatccnt tncctccnaa tcccttngca actntcnnct      60
ntctgcanga tcccatcgat tccaattcgg caccnagnga gcnnattcnc gtttttnagng      120
ttctntttct ntnatnnaca ngngaaant ccaggnnato ntgnnnccnt atctgantna      180
ngctngnttn aacntngnna caccnngnct mnaancaaa tttanaaaaa ggganncnctn      240
nanancatnn nanntnncca atctaccaa atcanaaac ncantgaaca acacananna      300
tnnnatacnn tctacncaa ancnnncat nncacgcacg ataanacanc nnnnaaaan      360
ancnaancan atatcanann caacntana cnannaatca nacnctnanc tccncacag      420
cannngnacn aanaacnanc antgataaan cncacctnnn tannacacac ctnannancc      480
nntntantcc cgaataacca atngccacnn ctannccnat aacanantcn ctnancctc      540
ntgcatacaa ttantaatc cncnancata aagnanatca cagcctcntt cnaccntga      600
tcnaancntn anaccnangn nanncnntat naaacnctat ancantnnna ctnnaacntt      660
nnatcngcnc ntanaaatta aanatcnaa actcaatatn ncggaatant nncntctcta      720
nataannnta naacggngna aanacnctc anacataann gncntacnaa tcgatctatc      780
anntnancat aaagtcaccc gcataatnac cnacgnncaa cataannnaa atnctactct      840
cagaccatat aaatntcgc tccntanac agngcnanan taaaaaacg tcgcnnnngt      900
ntggaccaca cgnctagat aaacacnnat aaacantttt tanatgtaac acatttcnna      960
tctatnaaat ancatcattn atgnanacga tnacaacaaa nntacncna tgntactaaa      1020
nacaantaaa nntnanatta aaaaagttgc aannatncng ngaaanntcc cnanaaacan      1080
tanatnenta tttannntn acnncggngt nncntaaaa anaactctnn nntnnctggn      1140
ttgtanatnt annncnanc cgcg                                         1164

```

&lt;210&gt; 624

&lt;211&gt; 798

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 624

ttgttaagcc	tnttttcnaa	ntccttcctt	tnaaatcttt	tgnaaacctt	ggtaanttgca	60
ggnatcccat	cgattcgagt	aaagcatcct	gcctcagaat	gactttccta	tcatgcttta	120
tgtgtcattc	caaggtttct	tcatgagtca	ttccaagttt	tctagtccat	accacagtgc	180
cttgcaaaaa	acaccacatg	aataaagcaa	taaaatttga	ttgttaagat	acagtagtgg	240
accctactta	ttcagtcaat	taagagtaag	tttttttatg	tggttattaa	aacagtatga	300
acaattagtc	taactctgca	tagacagggg	ctagattttg	ttaacccaaa	tgtataactg	360
cagttagctt	aaattacaat	ttgaagtctt	gtggnttnta	tatagctngg	cactttatta	420
ctcttttgaa	ctgaaagcac	actcccttat	aggttcattg	aactgtcctg	taataagggtg	480
cttataaatg	ggaacaacta	cacagcctag	ttttgncaca	accttttagca	tctaaaaaag	540
ttttaaaagc	ttcttaaatg	nctaataata	anggagatgc	tnatanccac	aacatctatt	600
ttaccaatat	tngtttcctt	acacttacct	tgggantttg	cattgagtga	ngttttngta	660
aaccccaaan	atnccatta	atanaaaaaa	nttggtacgt	tttnatgact	ttaatccann	720
ttntctgtng	gnnttcncct	aaaangcttn	ccnnnggnnt	ggaantnnna	ntnatttntg	780
gggnaaggtt	ttnngttnt					798

&lt;210&gt; 625

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 625

ttcttaagcc	ncttttctaa	tgcttgcttt	naaatctttt	gnaancgctc	ggctntntgc	60
aggatcccat	ccgattcgaa	ttcggcacga	ggaaatgcct	ctatgtangt	gaagtgttct	120
ctctgcatgc	aacagtaaaa	attaatataa	tattttcccc	acaaaagaaa	cacttaacag	180
aggcaagtgc	aattttataa	tttatatcta	aaggggaatc	atgattataa	gtccttcagc	240
ccttggaactc	taaattgagg	ggattaaaaa	gaattttaaa	taattttgaa	cgaattttatt	300
ttcccctcag	tttttgaggg	cattaaaaag	gcattaaatc	aagacaaatc	atgtgcttga	360
gaaaaataaa	attaatgaaa	acacagcact	tatgttggtt	tagctgcagc	ctccttgag	420
gtagaatttta	tttattttaa	attactgggt	gcattcaaga	cccatagggt	tgtacaaaag	480
gttctataaa	atctgcatta	tagagacaaa	gangcaggca	aatncatgtc	acaagggtna	540
agcttacagt	ttacaaactg	gggaacgccc	agggtgtang	atttnaaaaa	cgncactctt	600
gagaaaacan	atgtaatcan	ggntgctgaa	aactttgcat	ggnggctttt	aagacattta	660
gnccttgctc	aaacaaaaat	ttnttggnat	ttgccagatt	ccttantntt	gccatgggcc	720
atgacaccat	tttgggcctt	tatgncnctt	taaaattttt	aattaaaaat	accntttcca	780
gtaannctaa	ttn					793

&lt;210&gt; 626

&lt;211&gt; 825

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 626

ntttgaatnc	ctttgnaaat	ccttntttct	aatntntgga	tccttggcna	ctcgtntntt	60
ctgnangatc	ccatcgattc	gaaacggcnc	taggaatcat	cgaagggtga	gaccgtgacn	120
anttacatag	tgatnaatac	ccatctatgt	actgnngcct	nctaaatgtn	tntctnctnn	180
atggannttn	cctttaanct	ctagatccat	tgacancctg	ancatntcta	aaaggcatta	240
ngaaaactgaa	cacatctgat	acagaactct	gcattnnctt	ccnaantntg	cccannccna	300
gcctgntcct	ntttcacgct	tancacttat	natatgatcc	cactattcac	tnantctctg	360
aagcttaaaa	cctangattc	atgcttgact	actgnataat	nttacaatct	actcctaagt	420
cattagcaat	tcttgctagc	tctaccttca	aaatatattc	tgaatagact	atntcttgcc	480
gnttcccttg	cctnncatt	tcccatctgc	accccttctc	tntncccaa	aatcaatata	540

ctagntgttt	ctaaaaaaaa	tatnganann	tagnnnaaaa	ncntaaataa	atntaaaana	600
angnntancn	tnacanaana	ttntaataat	aggnnanntn	ntgncaanaa	cnntaantnt	660
tnaatacgnn	aaaactctct	cnaannngann	aanntatnnn	agttaaaagn	naaatannnn	720
aanantncca	aatntanaag	ataangncat	aannntatna	gncnnaacgc	taantgnnga	780
tgannntntaa	tnngnatana	nnantngtta	nnacaaaatn	tacnn		825

&lt;210&gt; 627

&lt;211&gt; 772

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 627

tttttaaatgc	ttngtcgnac	ttctcccagn	aatcgnttng	aaactengcn	actcgttctc	60
tctgcangat	cccacgcatt	cggaaatttg	cactgatggc	tcanaaggct	tacgttttgg	120
agagtatgac	ctacctcaca	gnagggatgc	tggaaccaacc	tggttttccc	gactgctcca	180
tcgaggcagc	catggtgaag	gtgttcantc	ccgaggccgn	ctgncagtgt	gtgagtggag	240
cnctgcagat	cctcgggggc	tngggctaca	caagggacta	tccgtacgag	cgcatactgc	300
gtgacacccg	catcctactc	atcttcnagg	gaaccaatga	gattctccgg	atgtacatcg	360
ncctgacggg	tctgcagcat	gccggccgca	tcctgactac	caggatccat	gagcttaaac	420
aggccaaagt	gagcacagtc	atggataccg	ttggccggag	gcttcggggc	tnccctggggc	480
naactgtgga	cctgggggctg	acaggcaacc	atngagttgt	gcacccagct	cttgcnagca	540
gtgccaacaa	atttgaggag	aacacctact	gctttanctc	ngaccgtgag	acacttgctg	600
ntnccntttg	gcaaagacca	tcatgganga	ncanntnggt	nctnaancng	nntggccaac	660
atnctcatca	acctgtattg	gcatgnaccg	cncttgctgn	acnnncngnc	caaancnctc	720
nantccgccca	ttggggcttc	cggnaaccac	tnnacaccaa	ggttctnttg	gc	772

&lt;210&gt; 628

&lt;211&gt; 808

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 628

tcnctcgnaa	cnnttnannc	ttggctactc	gntctctctg	caggatccca	tcgattcgaa	60
ttcggcacga	gatgacatcc	tcattatcca	cantgcaaag	ccaaccatcc	ctatgatggg	120
ttcattgtgg	atcatgactt	antgggtcaa	gagtttgga	gtggctcagc	tgggcggnct	180
tctgctncat	gtggctgccca	natggtnccc	tgctggtnng	cagnctngtc	tagagggtcc	240
atgatggctt	tactcacatg	cctggcatct	tgacaggggc	agctgggnang	caaagnnnat	300
ctgggactgt	ncacagagct	ncttctntgtg	gcctttccag	catggtggtc	taagggtagc	360
tggaacttnt	gcatnacagc	tcagggtccc	cagagctact	gtcccaagag	atnnaaagtg	420
gnaactgnca	atcttttang	ctaangncca	gaaaccatta	cccctgcacc	ncacagtctt	480
tttntanctg	ntgaaataaa	cattnnnttt	atcaattnta	ancattcgca	aattggaatt	540
aaataccttt	tactaatttt	gncgtgacca	tctgccccctn	gttcaagatc	taaaaaactt	600
ttatngntca	tcntgnngat	ntaaaaaact	nttgtgttng	catttanaac	cnntaagcan	660
nttnggcant	tanannnaan	annttnnnaa	acccttntat	anaaccttat	taagttgang	720
catnngnant	ttnccttna	aatecnaggt	ccttagggct	angnnatacc	nttcntatng	780
naacttttng	gaacctaaan	cctctcct				808

&lt;210&gt; 629

&lt;211&gt; 827

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 629

```

ggccnctttt gaaccttttt caaatctttt ggcactcgcc nctctctgnt ngntcccatc      60
gattcgctgt gatccaaggc atgaaaagag tgcaaggtaa ncangnggca gcnttnatng      120
aagcatnaaa taangcnaaa gcnnatgctn anctnangga gcangnngct aaagacaacc      180
acannctanc tgnntnctaa tcatgctntg cttnctnang tgancttata gnaacgcant      240
nagactncan gcnttgcttg gcncaacaag gnnacctana ntcatnanga agcnnttgaa      300
ctaangagtg gctacnncct ttntnctca tgcntgacct gtaatnattc ttctganttg      360
aggcaanagc gggtnnaant natngntnan ntgnaaanac tntnnnatcc gnnnntnctg      420
attannttnc attnntntna atgatanann ctcactcngc tegncctgna ctttganang      480
ctnnnmtcnn anntnntga ctttaggagn nnacctncag cganatgtna agnanngaaa      540
ttnanntncc tnnegntccn cettgcngac tnanngtctt gngnaacntn angtanntan      600
tctacngggg gnnacnttg gnaattgggg ncttataaan tnttctnna agaattgntg      660
naccaattnt nnaanntcta agnttgggga aatctnngtt tcctgnatnn gnacaaaaan      720
tcgatttann ngncnngntt nnttgggcnt catntgccat tgatgcnatt cnacttatgt      780
cctctggng ctnnttnnaa nnnngnngnn aacatttttt gtgtgcc      827

```

&lt;210&gt; 630

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 630

```

ttcnaatgct tggncnngag tccncccttg aacnttttca aatnncttgg caactcgenc      60
tctctgcatg atcccatcga ttcgaattcg gcacgaggcg ngttgttcta cactgcnntc      120
ngaagnttt ntaanaagcc accacttagc ngaggcnct acangtcttg gggnccttagc      180
gaagagaaat cncgctggca cttgnccgt tcaactaagn actnntgnt gantccnagg      240
gtannngtnc acctgngnn ccancagaca naccaannt gncntaaaan gggcaggtct      300
aagcttacnc tngactncac nggcaagctg nangcctgtn ctgccttccn ctgcnntnac      360
aaatngacag tnnagccaag agtcanagna aaaactncaa ggatacatnt atcccantct      420
nttctacacc tntanattcc ntganctatt gctcanaccn atcgtgcggg caaaggcaag      480
acttgggcaa cattnttnaa tacaatgatg ctgacaanta atttccngct ngttgccagg      540
natntttacn cgagctnttg tgattccaaa ctaaagaatg gngccnnnan gccntcntt      600
antnctggnc cccanaang ancctaactn gcgaaagggn agnatggcat tnacccaaac      660
caactntng gattacnca actccanaan atccgacggc atnnaanang caaaacaaca      720
acttcncnan natnnaanna atngnccnn aaananaacc cgngcntctn aaacnattgt      780
ggacccatnc ccc      793

```

&lt;210&gt; 631

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 631

```

gnagtnnct tngancctct ntnaaatcgc tttngcnant cgcctcttct tgntngatcc      60
catcgattcg aattcggcac gagatgttac agacatgaaa tatgaacaga atnctaaaag      120
aacataaaag aataagagct ccttaaagat tataaataaa tgggtgatgt aaagtaatat      180
caccattgga cgaagctagg gaatcaacac ttgacagaaa gatacatatt tttttatatac      240
aaactacata tatttgagca atcaagtagt agacatagag aattttcttt ttatggaagt      300
actctaataa gtaaagggt gatagaatta tatcagcatt ttctagctcc tgggtgaatta      360
tgcatggggc atccatggct gccttagatc acaaaaatac caccagatat atgctgtgg      420
atgaaagatc acaccaccac ctgtgaaata gtcttcccca caaaaaatcc aaccctaatc      480

```

ctatccagcc	tgtagatggt	actcgagatc	ttctataaga	aataaagaga	gcangetggt	540
cacggtggat	tgtgcctgta	atcccagcac	tntgggaggg	caangcaggt	ggatcgccctg	600
angtaaagaa	gttcnagacc	agcctgccaa	catggtgaaa	ccccctctn	tacttaaaag	660
taccnaggat	gagcccggcc	gttgtggcaa	gcacctgtgg	tccccagcta	cttgggaagc	720
tgagcangaa	aaatcgcttg	aanctgggga	ng			752

&lt;210&gt; 632

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 632

gnnnnnnnttn	nnnnnttcta	atgcttggct	actcgttcct	tntgcaggat	cccatcgatt	60
cgcaactaga	gaagattgga	cagcaggtcg	acagagaacc	tggagatgta	gctactccac	120
cacggaagag	aaagaagata	gtggttgaag	ccccagcaaa	ggaaatggag	aaggtagagg	180
agatgccaca	taaaccacag	aaagatgaag	atctgacaca	ggattatgaa	gaatggaaaa	240
gaaaaaatttt	ggaaaatgct	gccagtgtct	aaaaggctac	agcagagtga	tttcagcttc	300
caaactggta	tacattccaa	actgatagta	cattgccatc	tccaggaaga	cttgacggct	360
ttgggattttt	gtttaaactt	ttataataag	gatcctaaga	ctgttgcctt	taaatagcaa	420
agcagcctac	ctggaggcta	agtctgggca	gtgggctggc	ccctggtgtg	agcattagac	480
cagccacagt	gcctgattgg	tatagcctta	tgtgctttcc	tacaaaatgg	aattggaggc	540
cgggcgcant	ggctcacgcc	tgtaatccca	gcactttggg	aggccaaggt	gggtggatca	600
cctgagggtca	aggagctcga	gaccagcctg	gccaacatgg	tgaaacccca	ttcttttctt	660
aaaaataacca	aaaaatttag	cccangtgtt	gaatggntgc	atgcctgtaa	ttcccagctt	720
ctnanntagg	ctnanacaag	gagcttnctt	t			751

&lt;210&gt; 633

&lt;211&gt; 806

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 633

ttnnannnncn	ttttnaaaag	gcctnnnmtt	gannctttcn	aatgcttggc	tactngntct	60
ttctgcanga	tcccatcgat	togaattcgg	ctntagggaa	ggggagggtt	ggtgagtcct	120
agaccttaaa	aatacaaggt	taagaggggac	cccaaagcaa	aaaattccaa	cccttttctt	180
cccagtcatt	gaaacaccaa	aactattata	cgggagggtg	taatagtgtt	gctgcccagt	240
tgtggttaggc	cagtagtggc	ctcccaagat	gcccattgtc	taatcccagg	aacctgtcaa	300
aattaccttg	tatggccaaa	ggggctttgc	agatgtaatg	aagttaagga	tctttcgcca	360
ggaagattat	cccagcttgt	cangagggtc	tgatgtcctc	acccgggtct	gtataacaga	420
agagcaggtg	acgggagag	aggttggagg	tgtancgatg	gacangaaac	tggagttata	480
ggaggggcagc	tnaagccaca	gaatccaggc	cancttanga	gcccaggaaa	atgcatttct	540
ttccacaaaa	gcccttggaa	ggccccaanc	cctgcttccc	acccttggac	tnggcttcaa	600
tgaggcttaa	tttttataaa	ttcntggctt	gatttttagaa	ctcntaaggg	gaaataaatt	660
ttgtgttngn	tttaantcan	aaaataaatn	aattaaaaaa	aacttgaanc	ctttanaaac	720
tnantggaa	ttcntattan	cttaaanccn	aancttggat	taaaggatnc	atttgtttna	780
anttttggga	cnaaccccca	anttnt				806

&lt;210&gt; 634

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 634

ngggacttcg	cctnacgaac	cgctnggaaa	tcccntntnt	gnaggatccc	atcgattcga	60
attcggcacg	agtataaact	ttattttatt	ctcttctggg	tttgtgttac	atgacaagaa	120
attgaattaa	nncaatanaa	ttttagtctg	gggtgcttag	gtttttactg	ctccattct	180
tgcttttact	aatttatcca	agattagatg	tgattactat	ttaataataa	tttagtcctc	240
acacttacaa	accacttaca	ataccagcat	gcttctatca	ctgtaattct	attcaattct	300
caggcccatg	aggcatgcca	gccagacgac	cagacagcat	ttatagagtg	ggcactcaat	360
accagccaca	aaagatcctg	tgtcagaagg	ggaaacaggc	ttggaggctt	ggagtatgtc	420
gtgatagcct	ccctccagtc	cacacaactg	gtactgctgg	ggctgaaact	agaactcang	480
cctatgcctc	tcaagctcaa	gggtcggatg	tccatgtntc	tcgcctctag	aactatannn	540
gagtcgnaat	tacgtagatc	caagacatgg	gtaagataca	tnggatgagt	tnggaccaac	600
ccaccaacct	aagaatgcan	tggaaaaaaa	tgcttaattt	ggtgaaaaat	ttgtgatggc	660
tattnnngctt	aaatttngnn	aaccatttna	taaagnctng	cnantaaaaa	aaaggtttaa	720
ccaaccaaac	caattggcaa	ttccatttca	anggtttcaa	gggtccaang	ggggg	775

&lt;210&gt; 635

&lt;211&gt; 784

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 635

ttgagngtcc	tncttttnacc	ctttcnaatn	gcttggcnac	tcgctctntn	tgnaggcatc	60
ccatcgatcc	gaattcggca	cgagatatag	ctctggagggt	caggacatag	gagatattga	120
ttcaggactt	gccagagtat	ggtcttgggg	tgtgccctga	tattacaaac	agggatctta	180
gtggcttaggt	gatgaggcca	tggcaaatgt	agatggacca	agatcaattt	gcctttctag	240
atgaggtttt	ctaggtgaaa	tgtttttgaa	actattttgt	agcctagtat	aatttataaa	300
agtagagaga	aactataaat	ataaatttgg	aanggggttag	ctaaaaggag	aaaacagcan	360
aatcttcata	tatatanaaa	tggatattaa	tttgctagaa	ttaanagact	gcaggtaaag	420
atagnttttt	ttaataacctc	tttttgctgt	anaaaggaca	ggattaaatg	atnaagggat	480
gctggaatga	ggaatggtaa	ctttaggcaa	gatagtcttc	tgngacggct	gatatgaaca	540
atngagagta	anacatttnn	aatacaanaa	attgtcctgc	tgctcaccca	tcaagccttt	600
tcangtttct	tccttgcca	aaantngtaa	naactnttgg	tacttttnna	ncttgatnn	660
ttcngtttna	ttggttanaa	ccccttogat	naanaanncc	atantttnaa	tttgggnttg	720
accccnagg	ttaaaanttn	centttntct	aatttccctt	tttcaaagnt	ttaacntaat	780
taan						784

&lt;210&gt; 636

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 636

ttnnannctt	tcnaatnctt	ggcnactcgt	tctttctgca	ggatcccatc	gattcgctct	60
gcgcaggagc	cgcagggccg	taggcagcca	tggcgcccag	ccggaatggc	atgggtcttga	120
agccccactt	ccacaaggac	tggcagcggc	gcgtggccac	gtggttcaac	cagccggccc	180
ggaagatccg	cagacgtaag	gcccggaag	ccaaggcgcg	ccgcatcgct	ccgcgccccg	240
cgctcgggtcc	catccggccc	atcggtgcgt	gccccacggt	tcgggtaccac	acgaagggtgc	300
gcgcggggcg	cggttcagc	ctggaggagc	tcagggtggc	cggcattcac	aagaagggtgg	360
cccggaccat	cggcatttct	gtggatccga	ggaggcngga	acaagtccac	ggagtccctg	420
caggccaacg	tgcagnggct	tgaaggagta	ccgctccaaa	ctcatcctct	tcccaggaag	480
ccctcngccc	ccaagaaggg	aagacaagtt	cttgctgaan	gaacttgaaa	cttggcccac	540

ccaactgaac	cgggacccgg	tcatgcccgt	tccnggaaan	gtctattata	aaggagaaag	600
cttcgagtc	tcanttgang	gaanaagaag	aatttcacaaa	gccttcgctt	atnttcngta	660
ttngcccgtg	ccaaacnccc	cngctttttt	ggcttaccgg	ccaaaaagaa	gccaanggan	720
gcccnnanaa	cagggatntt	gaaaaagaaa	naatnaaacc	ctcnn		765

&lt;210&gt; 637

&lt;211&gt; 853

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 637

ttttggancc	ntttcttgan	nctttcta	atgctgggntac	tcgntctctc	tgcaggntcc	60
catcgattcg	aattcggcnc	gaggatcagc	ccacctcggc	ctcncaaagt	gctgggatta	120
caggcgtgag	ccaccttgcc	cagcccacat	catacagttt	gaaatgaaac	tttgccacaa	180
ccagcctttg	ctgtagcaca	cacatatatc	actgaacctg	tttgaaataa	agtttttttt	240
ctttntcctc	tggtattctg	ggttctgaag	tctgggtattc	tggtattctg	ggttcaaaag	300
tatgacttga	gagtgttgct	ctgggtattct	gagagttgct	ctgtattctg	ggttctgaag	360
attatttgaa	aaataactcc	tactacattg	aaatgcagac	ttaaaaattt	aaacattgga	420
ttangcagtc	aaaaaaacca	agcaagcata	aaaggtcaat	aagttgtaat	cttgatagta	480
aaggtggaaa	acttattata	aatggnaang	aaagttttat	ttcctttttt	gtttgaatgg	540
gcaagtatgc	catattatac	ccaaaagtgc	ttttaaaaaa	atatttccca	ttcaaccat	600
ttttaattna	aaattaaaac	cattttgnaa	gggaaanttt	acccaanggc	aanccttttt	660
tttctcccaa	aaaggttnac	cntgttnatc	cttctttttt	ggnaaattta	nccaccaatt	720
tttttaaggg	ngggncaatg	gggnttaaaa	ntanccctgn	aagnnathtt	ttnancttc	780
caggtttaaa	antccccttg	gatnggggtc	taacctgggn	gggtngnata	naaaaaata	840
natcctnttt	anc					853

&lt;210&gt; 638

&lt;211&gt; 740

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 638

anttgntctt	tntgcaggat	cccatcgatt	cgcagcaaag	actttatttt	tgtacagaag	60
atggtgaagt	ccaagacggt	ggctcagtg	gtggagtact	actacacgtg	gaaaaagatc	120
atgcggetgg	ggcggaacaa	ccggacacgc	ctggcagaaa	tcacgcagca	ttgtgtgaca	180
agtgaagaag	aagaagagtt	agaggaggag	gaggaggagg	acccggaaga	agataggaaa	240
tccacaaaag	aagaagggag	tgaggtgccg	aagtcctcgg	agccaccacc	cgtccccgtc	300
ctggctccca	cggagggggc	gccctgcag	gccctggggc	agccctcagg	ctccttcac	360
tgtgaaatgc	ccaactgtgg	ggctgtgttc	agctcccgac	aggcactgaa	tggccatgcc	420
cgcacccacg	ggggcaccaa	ccaggtgacc	aaggcccgag	gtgccatccc	ctctgggaag	480
cagaagcctg	gtggcaccca	gagtgggtac	tgctcggtta	agagctcacc	ctctcacagc	540
accaccagcg	gcgagacaga	ccccaccacc	atcttccctg	caaggagtgt	ggcaaagtct	600
tcttcaagat	caaaagccga	aatgcacaca	tgaactta	cangcagcan	gaggaacaac	660
agangcaaaa	aggcttaaaa	aggcggtttt	tcagctgaaa	tggcaccnnc	aattganagg	720
actacngggc	cccgtggggg					740

&lt;210&gt; 639

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 639

tttttncnt	taataaatcc	tttgttgact	ccttggtctac	ttgtttctttt	tgcaggatcc	60
catcgatncn	aattcggcac	gangtgatgn	cagattgnna	ntnactaaa	ctgggcannn	120
catcaggatc	acctgtgggc	cttcannaat	cananatnca	ccccaggcc	atgccctnga	180
cccagtgcac	caggacaaga	aatccacccc	aggcctctcc	cnagacccac	tnnaccagna	240
caagaaatcc	acccccangc	cangcccnt	acnactgcc	ctangatntn	nnggtgtnaa	300
ccnggtggtg	ctttgtaaag	acgtgcangt	ggtaacccca	cgcgcncncn	ctcnnnacnt	360
tggacacatg	atcatccacg	tgtctgtgat	ttgnttcttc	ggnttnnttt	gtgaatngaa	420
aataantgtg	ncgtttgact	agggtttaag	agcagcaggc	agnccctcag	ctcagcaagc	480
ngccctctca	gctcagcang	cagcccaagt	ctcctgtang	acttctatgg	accatnctgg	540
cgggaatgaa	gaaactggtc	aagctggatt	cgggactgaa	agtgtacct	ggtgacaccg	600
tatgactnan	ctgactnana	aagatcactn	atctttccac	acttgngggg	naggagccnn	660
tannangttc	aatatgcnn	ggtngantcc	catngctaca	atttcatgga	cacantttga	720
ttacttnnga	taannnaggc	ccttgagggc	ccctntccc	cttttaacng	gaat	774

&lt;210&gt; 640

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 640

ctnnncctcc	ttgatccntt	cctnctttga	anncatnngc	tacttgttct	ttttgcagga	60
tcccatcgat	tcgaattcgg	cacgaggctg	acctacatca	gaagctgctg	gatgcagnaa	120
agtgaataca	gacaaaaca	acacngggcg	aatcttnaca	ccattntggg	tgccnnatnt	180
nncennngat	atttgcttgc	tnagctctac	tcctccaaga	nannangnnt	caaacnctnc	240
agcangntag	agcanntnaa	gaccgcntnt	nctnacctnc	tnaagannct	ctgngaggan	300
cgcaatcctt	tngtgaana	tagaatcaac	agaccacact	gcncctctga	ccatgngctc	360
tcaaangngc	tagaagggtg	tgaccttttn	agactcttgc	agaagaggcg	angtgggtng	420
anacccttna	ggaanacttt	cccgaactag	accnncnctt	ncngaacnng	ntcaactgtt	480
ggggnngaaa	ncntgtgann	tgtngnccct	cngagagacg	gcataattcta	tgatggcnga	540
cttnatnctt	ctgcggaacc	anactngacn	tactgaaaga	aanctganac	caagcgtctt	600
ccttaaggac	ccttatatcc	agacnatect	ttggataata	ccnctngggc	aaaacctnnt	660
aactntgcat	acaatcngga	tggcaacatt	tgaactggng	gccttnanna	ccnttaccgg	720
cttttcncat	tatgnaagag	ntn				743

&lt;210&gt; 641

&lt;211&gt; 740

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 641

ctttcctttg	antcttcttc	tannaaacgt	tngaacgaan	tcngcacgag	accactaaca	60
gcattctactt	gactactgat	actttgatca	tggagtgttg	gcattgccact	tgatagaaat	120
ttgaagagca	atttatattt	tcaaaaagag	ttttgaataa	tgtaagata	gattgcaaca	180
tgactatcaa	ttcttccctt	cccatcaaag	gagagagtcc	gtttatccag	cctttgaatc	240
ttgattattc	aagtgacttg	cttcacccaa	tgtaacatta	ataagcacia	tacaagcaga	300
ggcttgccaa	gaacttggtt	tgtttcta	gcttagaaga	agaatggtgt	atgccatatt	360
tctgcattta	gaactcacgt	ggagacatgt	gtggcccaat	tgctcctctt	tcattctcagg	420
caataaccag	acacgggact	gaggccatcc	atgaccagcc	agccctagtc	aacacacaac	480
acacaagctg	atcacagatg	catgagtaag	cctaactgag	accagccaag	accagcctag	540
aatagaactg	ctcagcagca	ataaaaacta	aataaattgt	taccttaagc	tacttttaga	600

gctatattgga agtgtatttt tgtgcagcta acatttacta tcagataaaa tgggtgattgn	660
ttatctctgn tttaatgatg ntttaaggaa atgggttctat taaaaggaaa tatctggggc	720
tttgtcaccg ttaaaaaaat	740

<210> 642  
 <211> 737  
 <212> DNA  
 <213> Homo sapiens

<400> 642	
tancctttga nnttttctcn ncntgnentn nnnngnaacga cctcggcacg aggacacccc	60
agatgcagcc accaccagca gaagcgatca nctgacccca caagggtttc gtggctgtgg	120
ccgtgggctc aggtggcagc tatggagccg aggatgaggt ggaggaggag agtgacaagg	180
ccgcgtcct gcaggagcag cagcagcagc agcagccggg attctggacc ttcagctact	240
atcagagctt ctttgacgtg gacacctcac aggtcctgga ccggatcaaa ggctcactgc	300
tgccccgggc tggccacaac tttgtgcggc accatctgcg gaatcggccg gatctgtatg	360
gccccctctg gatctgtgcc acgttggcct ttgtcctggc cgtcactggc aacctgacgc	420
tgggtgctggc ccagaggagg gacccctcca tccactacag cccccagttc cacaagggtga	480
ccgtggcagg catcagcatc tactgctatg cgtggctggg gccccctggc ctgtggggct	540
tctgcgggtg cgcaaggggtg ttcaggagcg catggggccc tacaccttcc tggagactgt	600
gtgcatctac ngntacttcc tctttgcttc atccccatgg tggctctgtg gctcatccct	660
gtgccttggc ttgaatggct ttttggggcc tggncctggg ctgttaaacc gccgggctgg	720
natttaacct ntnggcn	737

<210> 643  
 <211> 748  
 <212> DNA  
 <213> Homo sapiens

<400> 643	
cttttaaccn tttgancnt cctcnaaac cttngatnccg anttcggcac gaggaaggca	60
gaagtgtaaa tgaacataca ntttaaggag aaagcctgct gtgtttnnct tgttcagcag	120
ggtattatga attagcacia gtattgcttg ctatgcatgc taatgttgaa gatcgaggga	180
ataaaggaga cataactccc ctgatggcag cttccagtgg aggttactta gatattgtga	240
aattattact tcttcatgat gctgatgtca actcccagtc tgcaacagga aacctgctgc	300
taacttatgc atgtgctgga ggatttgtat gacattgtta aagtgtcct taatgaagg	360
gcaaatatag aagatcataa tgaaaatgga catactccct taatggaagc agccagngca	420
ggtcatgtgg aagttgcaag agttctttta gatcatggng caagcatcan cactcattct	480
aatgaattca aagaaangtg ctctaact ngcttgctac aaangccatt tggatatggg	540
gcgctttcta cntgaagctg gtgcagatca agagcncaaa acagatgana tgcacactgc	600
cttaatggan gcctgcatgg atnggacatg tanagggtggc acgtttgctt tttggatant	660
nggtgctcan gtgaacatgc ctgcataatc atnttgaatc tccattgacg ctagctgcct	720
gtgganggac atgttgaaat tgcngcct	748

<210> 644  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 644	
tcnnncnctt ttcgatcttt tgagncttgc ctttgaaccc cttggntacg anttcggcac	60

gagggaaacca	tgananccna	gagctagaat	tgctattgga	tnnecgtctat	tctctntttg	120
cttattgggn	cgngntnecgt	ggttnctggc	ctcangggtn	nccccgaang	anggggtatc	180
tnngagcnan	ttntgcnntt	tacnggctag	cttgntgggg	gcttaanntg	ccactnttan	240
acatgctnta	ctantcantg	aganntnncn	ntcgaccatn	tannacnatn	ctgtgnnttc	300
cngtacnctn	tgcccgatg	gagctattag	cttcaanatg	nntcgnantg	ttacatgcan	360
ncactgannt	nactatccan	natntaagtn	ctcttngctt	actgtgaaca	nnngctactn	420
ncttgatata	tatagnaagg	ntcnttgata	cncgatnatc	ntnctgtca	gatcnataaa	480
tancanctat	accnactgtn	naaatnccat	ctggngnct	tncnatccan	acataattgc	540
attannnecgt	cnaattgnga	tanagtnttg	aaagantctn	ggttttagacn	ttggatggtg	600
caatgnttgt	gncttanaan	ttatgtgctg	gctactgant	aanctggggg	catgacntta	660
ctggnnttgac	ctaagngng	aantcnatgg	tccgattgct	ggncctanc	cttaagnttt	720
gccatgaata	ggncttttgc	cctaaaataa	naccctttt			759

&lt;210&gt; 645

&lt;211&gt; 766

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 645

tnnnnnnntt	tcaatntttt	ancgtccctt	aggatccntc	gattcgatcc	agatgggata	60
cctctaaaca	cgaaaagaaa	gaagattcca	ttantgaatt	tttaagtttg	gtttnatcaa	120
aagccgagcc	acctangcaa	cagtccaccc	ccttagtaaa	caaagaggaa	nagcatgcac	180
cagaatcatc	cgcaaataag	acagtcaaca	aagatgtgga	cgcacaggct	gaangagaag	240
gganccgcca	tccatggact	tattcatggc	catctttgcc	agttcctcat	atgaaaagtc	300
ctnatcctgc	gangatganc	acggtgacag	tnaanatgat	caggcacgct	ctggngagga	360
caacttccaa	agctggnaag	acactgactt	ggnggaaaca	tcactctgtg	ctcacgctnt	420
tgtgccagng	ccctaggagc	cgtcaccttc	cttcccata	caaangatgc	agatagatna	480
naganaagag	ntcgccngn	ngctgcctcc	cgtcttatgt	nccaatgctc	gtcagacact	540
tgaagttnct	canaaagaga	aacattccaa	gaacaaagac	nagcacaang	gcaatanaga	600
acacaggccn	gaaagaattg	anangaaatt	ggaaacactn	gaagcacnaa	acacctaang	660
naatccaaaa	naattggcaa	accaggggaa	aagtaggtnc	ctncnggaag	tttcgacagc	720
cngcggacaa	gccanaattg	acnatgaaac	cgcatacgtg	tcttnc		766

&lt;210&gt; 646

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 646

tnnnnnnntt	tttatccntt	natncttnct	ctttggatcc	atcgattcgc	tccaaggaaa	60
atccacctcg	cagcttgtaa	atctacagcc	tgattacatc	aaccccagag	ccgtgcagct	120
gggtccctt	ctcgtccgcg	gcctcaccac	tctggtttta	gtcaacagcg	catgtggctt	180
cccctggaag	acgagtgatt	tcatgccctg	gaatgtatct	gacgggaagc	tttttcatca	240
gaagtacttg	caatctgaaa	agggttatgc	tgtggagggt	cttttagaac	aaaatagatc	300
tgggtccacc	aaattccaca	acctgaaggc	agtcgtctgc	aaggcctgca	tgaaggagaa	360
cagacgcata	actggccgag	cccactgggg	ctcacaccac	gcaggggagg	ggggaagaca	420
gggtccagc	taccacagga	cgggtctctg	gtatagccgt	tccagtcagg	gacagccgtg	480
gagagaccag	ggaccaggaa	gcagacagta	tgagcatgac	cagtggagaa	ggtactagtc	540
aaccttcaga	aagagtatgg	agagaaaaag	aggcacacct	ggacgcagag	ccctgccagc	600
gccctctctg	ctgttgacg	tgcaaggaga	ccatgcctgt	gggagccagg	cctcgcttgc	660
atgaanaagg	aacgatgcct	ttttcaatgg	tgtcttccct	ccattgtgca	naanaacctt	720

ttggtggcctt ctcttccgac ttgtgcctga tt

752

<210> 647

<211> 743

<212> DNA

<213> Homo sapiens

<400> 647

ttaatccttt	caattcggtc	ntctttggat	ccatcgattc	gaattcggca	cgagccctcc	60
ccggcttccc	ccggagtggg	tcaccacact	gttttttatc	atcatgggaa	tcatttcatt	120
gactgtcaca	tgtgggtttg	tgggtggctt	ccactggcga	agagaagcta	caaaatatgc	180
tcgatggata	gcattcactg	gaaccactat	gagaagatta	taggaaaaac	accaagacta	240
gaggactctg	ggttcctttt	atgcaaagtc	aactcttctg	ggtcacagtt	acccagcaac	300
aaaaataaag	agaggaccag	gacgatgcca	gcaccccggt	tatcctgagt	gaactctccg	360
gaggcctctt	caagcttgtg	ggttctctgc	tgtcttgaag	ccatccatcc	atttgatagg	420
ttttgcaaag	acttggtcct	gccaagatgg	ttttaatcat	ttctgctaaa	aggaatggac	480
tcgaggattt	gatctcattt	tagatgcagt	tgtcctcact	tggccatttt	acagcacttt	540
agtaaataatg	gccagtgtat	ttggtcacta	ttaaataaat	ccccattcat	tatctgtcan	600
ggcaactcag	tgaactaaat	actatgttct	gacctctggc	actctttctc	atggttggtta	660
aatatattaat	attgnctaag	gcaattcaag	tatttttctt	aaataaaaaa	tatgaaaact	720
caaaaaaaaaa	aaaaaaaaaa	ana				743

<210> 648

<211> 759

<212> DNA

<213> Homo sapiens

<400> 648

ttttaatccc	tttcatttcn	ttccttngta	ggatcccatc	gattcgtttt	tttttttttt	60
ggtgattgga	ttaacaattt	tattctgnnt	ccactacaaa	ngggctggtg	ttttgttcca	120
aatgttttagc	tgggagggct	gtagggaccc	ctgttacccc	cattaaacac	agtaaagcat	180
ggatccagtc	agccccctgc	tggcaggtgt	gggcctggca	actacacaga	tccaacccca	240
ccctcctggg	tgcggccaga	ggccaaggca	gtcgcccgag	ctcctgaatc	ccaagaatgg	300
ttctggcaag	tactgctgtt	tgtttgtagg	ggcaaagagt	taaaataaaa	cgaggttctg	360
ccatggctaa	gccttgtgga	aaccagaccc	caaagcccct	gccatgccan	gggtctcaac	420
nccagacgct	tggtatggag	gcaccancng	gtantggccc	ctgtaagcan	ggccagagtc	480
gggacaaaaga	gcaagantga	aacanccaag	agacanagga	ccatgctgga	ccattgggca	540
cncangaacc	tgcttgggaa	aaaccggggg	gcaangctgg	catgggaatg	aacacctgct	600
tgntgacacc	tatntgagct	tcanttnccct	taacttgaag	aattgaacan	gcccggtncc	660
gtggctcata	ccctgtaatc	ccancacttt	tgggancttt	tangccgntt	ggatcattga	720
ngttaggaag	attaaagaac	cancctgggc	cnacattgg			759

<210> 649

<211> 746

<212> DNA

<213> Homo sapiens

<400> 649

tnancctttg	aatccttgaa	ngnngatccc	tcgattcgcc	ggaacctcat	ccagtgccac	60
ccatcttgac	accttctccc	tcttcagctt	ttccaacagt	cactactgtg	tggcaggaca	120
atgatagata	ccatccaaag	ccagtgttgc	atatggtttc	atcagaacaa	cattcagcag	180

acctcaacag	aaactatagt	aatcaacag	aacttccagg	gaaaaatgaa	tcaacaattg	240
aacagataga	taaaaaattg	gaacgaaatt	taagttttga	gattaagaag	gtccctctcc	300
aagagggacc	aaaaagtfff	gatgggaaca	cacttttgaa	taggggacat	gcaattaaaa	360
ttaaatctgc	ttcaccttgt	atagctgata	aaatctctaa	gccacaggaa	ttaagttcag	420
atctaaatgt	cgggtgatact	tcccagaatt	cttgtgtgga	ctgcagtgtg	acacaatcaa	480
acaaagtffc	agttactcca	ccagaagaat	cccagaattc	agacacacct	tcaaggccag	540
accgcttgcc	tcttgatgag	aaaggacatg	taacgtggca	tttcatggac	ctgaaaatcc	600
ataccatac	ctgattttatc	tgaangcaat	tcctcagatt	tcaactatca	aaactagggg	660
aaactngag	tttaacacca	agtnctacaa	cacaagggtg	gaaacacctg	aacttgngng	720
atcatgatac	cacttnacca	ctccnt				746

&lt;210&gt; 650

&lt;211&gt; 789

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 650

tgaccctttt	gaaantcctt	gcatntttca	nacnttttgg	tacnnncant	ttngntgga	60
tcctctgttc	gctgnacaaa	agatgttttt	caattaaaag	acttgagaaa	nnttgctccc	120
aaagagaaan	gcattactgn	tgtgtcagtn	aaaggaaanc	ttcaaagctt	tattngatga	180
tgggttttgt	tggactgtga	gaggatcgga	acttctaatt	attattgggc	ttttccaagt	240
naagctcttc	atgcaaggga	aacataagtt	ggaggttctg	gaatctcagt	tgtctgaagg	300
gaagtcaaaa	gcattgcaagc	ctacagaaaa	gcattgagaa	agctaaaatt	ggcccgatgt	360
gaaacggaag	agcgaaccag	gctagcaaaa	gagctttctt	cacttcgaga	ccaaagggaa	420
cagctaaagg	cagaaagtag	anaaatacaa	agactgtgat	ccgcaagttg	tggaaagaaat	480
ccccaagcaa	attaagtagc	caaaagaagc	tgctaacagg	atggactgat	taccatattc	540
gcaataaaat	cttgggccaa	aagaaaattt	gggttttgaa	agaaaataaa	aattgatnng	600
aactttttgg	aattccagaa	gactttgact	acatagactt	aaaatattcc	atggttggtg	660
aaaggatgta	ccaagctttg	tgaatatattg	taaattttta	aacctattat	ctactaaagt	720
ngtactggaa	ttgtccnttt	gcctgttnac	ttngngtnta	ntcatttnta	tttaatgntn	780
aaattaang						789

&lt;210&gt; 651

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 651

tnnnnnctaa	ncctttgaaa	tcgtccntgc	atgatccctc	gattcgaatt	cggcacgagc	60
agatattttac	tgaaggaatc	taggttggtt	tttcagtgga	caatgggaat	aanncatttc	120
taaagcaccg	actggagagg	aaggcaacag	agacaaggag	agaagccgag	agacatgtct	180
gcgtgctgcc	acgcatctga	gcgattgtct	tgtgaagagt	tgtacactga	acattttcag	240
gggaggctgt	ttaccagggc	aatgtcctca	aacaagcctg	tgccgggggtg	tccttggaatc	300
tgtgccagga	ctgtgttttt	agcccttcac	ctctcagctt	tagcaggaca	tgaaccagtt	360
ataacaagat	ggccctgcag	ctggttacag	gaatgtgaca	tggcaggatc	tatggaacca	420
aatggaagg	tttnaggtga	tgtaggtcct	tcacagttag	ctttggggaa	tacagaatac	480
tcaataaag	tgtctttgta	ttatttcaga	gggaatggcg	attgaaatgt	tacaacagag	540
atttcttggt	ggtagctatt	tggttaaang	tatatggata	ttntctgta	catgtgaaat	600
tatntaaaat	aaaagttata	taaattacat	tgacaaaaaa	aanangtana	aaaaaaactc	660
gaaccttta	aaactatngt	ggagtcgcta	ttacgttaga	tccagacctt	gataaganac	720
cattgatgaa	ttttggacaa	acccactng	aatgcnn			757

<210> 652  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 652  
 tcnnnccttt aatgctttga actcgttgca ctgcangatc catcgattcg aattcggcac 60  
 gaggtcgncc aggcagttnn atggcctnct ggttggtgct cttcacaccc gcctacagcc 120  
 ccacctcacc atcaagcgct gagccaatgc ggntgtggct ggccctgagt tcctgagtca 180  
 gtccttgcc agggccagag ctggtnacag cggggcanca nggtgggtag cctctaccag 240  
 ncagggcagt ccctgagggg ccagcanggg ggctgactgc ctagtggctn aacctactga 300  
 acccaccac tcccagegat gctaccaga accccaacgg cntgaatcct gcacantgcc 360  
 gggcantgcc agactcnaaa gggctcgtcg tggggacagc cccgtcatgg ccacanactc 420  
 tgtcctcacc tttgattgtc aggatgacag nccccaccac catgatgagc gtctgcaggg 480  
 cgtccgtgta gattacagca gccaggcccc ctgccaatgg aagcaagggt gctggaaggg 540  
 gccctgggtc agggaggaag gacaccggga ggaacttctg ggcttctgct ggggccactt 600  
 cctgggctgn tntcnggnc tgtatgggga agtggccttn tgacccttt acacgttccc 660  
 tgggtggacc ttccctgntt gcangcacc atacctgctg atgggtgnca nggctnttga 720  
 tgcccnaaac tttaggattg ttggatangt nnaatctnc 759

<210> 653  
 <211> 820  
 <212> DNA  
 <213> Homo sapiens

<400> 653  
 tgcaatcccn cngnnaatcg ctttgaaanc nccntcctg tatgatccca tcgattcgca 60  
 acagtccagg ctctgcagac agcatccac ctgtcccagn tngctgacct gaggagcatc 120  
 gtggnggaga ttgaggacct tgtngctcgc ctggatgaac tcgngggcnt gtatctccag 180  
 ncanaanaan gacngcatac aacagaccat tangangntg tcatctacan tntnanngat 240  
 catntgngna cngaccatc cattaatgag gatcanggn tccanctgat gaacgctgat 300  
 cttctgcaan aagaacgttc tagntctanc nnanngcent canctnecn ctcttgagct 360  
 cagtngtca ngctcntaan atcttnncac ntgccaant gtngngnctg ccttnagnct 420  
 tccggatagg cactntnatn ngacntgcc tatanttgcc ngcngnnant naaccaantg 480  
 naccatngtc actctgttga catcanggn atntgnntaa actaatnnct tngcngcact 540  
 ctagtnngcg ttgncactgc ccnctnnnc tanctacca nttcncattn cccntttaat 600  
 gggnaaagan atnatcccta cnatcatatt ncccntnnaa tggattcgag ncgnaantct 660  
 tnnntantna tctnaancct aaatgntcac atnnaaactt tanangncat cnnnnatgna 720  
 accnancnat ggctaaang cctcattaan gccngnttt tcaaacttga aaantgcatn 780  
 ccncattga naaagganta cacgggcccc cntgngnggg 820

<210> 654  
 <211> 768  
 <212> DNA  
 <213> Homo sapiens

<400> 654  
 tttnncccn ttttgtncct nttgattcnc ttgctacntn ttcaaactng tnggatccca 60  
 tcgattcgcc acatttaagt gagatatggg aaggaggagc agattgtttt tgaagggagg 120  
 aagagcagtt acttagggtc aaattaagtt gtaaaatccc ccccgggatt ttgtatgtaa 180  
 gtcaaagtga attgtatttg gaagaagaac tggggagccc acctctggta ttttttttat 240

gtccctcata	tggaacaaata	aacctctggt	attaaatgaa	ttttcttttg	ggggattcta	300
tatatctggg	atttcaacca	ccaacctatc	tggtttttcc	cgctgaaatg	ttgggtgatg	360
gaatcaggag	agcagatttg	gagactcttt	atattttata	attgagagag	acaaagagaa	420
aaccgtttga	tttgaaaaag	ttttctaggt	tccctcaggt	agatggaaat	tttcatcaaa	480
aacagtttat	tcaaggtaca	tagcctacta	gtttcccat	tgagagtacc	gcagaatgat	540
acgacgtgta	ctgcttctct	acgcagaatg	aagtataaaa	ttagcaccna	atagtacttt	600
aatttgcagg	tgctaaactt	tttacctgct	tnatctcatt	taattcttag	aagaaactaa	660
ttttaccaag	taaantgtct	ggaccaacca	tntgcaggtc	caaaannctg	gaaaaaccgt	720
naggtttgga	ctcctacata	gcctnttttn	taagtnnct	nntaaatn		768

&lt;210&gt; 655

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 655

tntnccnttt	gattccttga	ctannaaatc	cgtggatccc	tcgattcgaa	ttcggcacga	60
gggtaaacct	atttatataa	tagaaggatg	attataaaca	tttaataaat	tatatcaaat	120
agatattata	tattaaatgg	gcagataata	gaaatctgtc	caagcaaaac	tctggataat	180
ttttatgttg	ccttattttt	tgttttctgt	gaactccaag	aaaaatgaga	taccagtttg	240
gaacagatgt	aattattgtg	atttaacagt	ttagggatac	tccccaagtt	caataatttt	300
gccaaagatac	aaattttaaat	ggaacctttt	atgaagcttc	atagtgtgtg	aagaacttac	360
cttgttttata	tgtttgaaga	catacatatt	tcacatttca	gaagagtcta	tacatagctc	420
accaaataatc	aaaaccacct	tgtagaaaa	cattaaggtc	tgtcttattt	atttgttcat	480
ttgnttatga	gacacantct	cactctgtaa	tctcactctg	ttgtagaggt	tgagtgcagt	540
ggcacgatca	cggctcactg	caacctncat	ctccctgact	caaggaatcc	ttccacctca	600
gccttccaag	tagcanggac	caccaggtgc	acccactat	gccagctta	attttttgna	660
ttttattgga	cagattgggg	ttttgcccat	gttattcagg	ctggatcctt	nnggcctcaa	720
actcctgggg	cttcaagcca	atctggcctg	cc			752

&lt;210&gt; 656

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 656

ttttctttt	natcttgtct	nanaancnt	ggatccctcg	attcgagag	gctggttcag	60
aaaaggagga	agaggcccg	ctggcagccc	tggaagagca	gangatggag	gggaagaagc	120
ccagggtgat	ggcaggcacc	ttgaagctgg	aggataagca	gcggctggcc	cangaggagg	180
agagtgaggg	caagcgccctg	gccattatga	tgatgaagaa	gcgggagaag	tacctgtacc	240
agaagatcat	gtttggcaan	aggcgaaaaa	tccgagaggg	caacaagctg	gcngagaagc	300
ggaaagccca	cgatgaggcg	gtgaggtctg	agaagaaggc	caagaaggca	aggccggagt	360
gagtgcctgc	ggccctcac	agggtctgang	ccagccctta	tcagctggat	gtggcagagg	420
catgccanag	gacctaatgt	tgatggacca	gantcacttc	tnctcctcct	ttctncacca	480
gccctgaccc	ctcatgtctct	ctggctgggc	cantgggcaa	ccctcgcttc	cttggatgga	540
ctgcctgctg	gtgcctgggc	agagaanagc	ctnttttccc	agnctgatcc	tntgctccca	600
ggaaccaatt	gacctatnaag	gtgcaaangc	cnanccaatc	cccttaacnta	ctggccccc	660
ttnatctctg	gctttttcan	aagccccent	gccaaacann	ttgggacccc	ctgattnttt	720
aagggtgcct	tttnatnggg	gttaaagggt	aant			754

&lt;210&gt; 657

&lt;211&gt; 734

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 657

tntgttcnc	natgaacgnt	ngaancnna	tncnttga	tcccatcgat	tcgctgcggc	60
cgcaggagct	gtggcggtt	tcctaactct	gcgnttatgg	gtagtgcttc	nttccatgga	120
cgttacgccc	cgggagtctc	tcagtatctt	ggtagtggct	gggtccggtg	ggcataccac	180
tgagatcctg	aggctgcttg	ggagcttgct	caatgcctac	tcacctagac	attatgtcat	240
tgctgacact	gatgaaatga	ntgccantna	aatnaantcn	tnngaactan	ancgagctga	300
ttganaccct	agtaacatgt	ataccaaata	ctacattcac	cgaattccaa	gaagccggga	360
ggttcagcag	tcctggncct	ncaccgnttt	caccaccttg	cactccatgt	ggctctcctt	420
tncctaatt	cacaggnga	agccngattt	ggtgatngt	tacngaccac	gaacatgtgt	480
tcctatctgn	gtatctgncc	ttatccantg	ggatactagg	aataaagaaa	gtgatcattg	540
ntactttcaa	agcatctgcc	gggttgaaac	gatntncatg	tccnaaaga	ttgttgatn	600
tgagctnct	cantgctann	gtcggttttg	aanaaagttt	nccaaatnnn	tgtaccttgg	660
gccaatntt	ngacaantng	aactgacttg	tnagaatctt	gcagntaacn	gtcttgtntc	720
ntccaattng	ggng					734

&lt;210&gt; 658

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 658

ttctcctgaa	acgcttngca	cttccctcnc	tgcaggatcc	catcgattcg	aattcggcac	60
gagacactgt	cccactccat	caccaggt	ggagtccagt	ggtgtgatca	tagctcgctg	120
catcctccag	ttcctgggtt	caagccatcc	ctcctgcctc	agcctcccca	gtagctggaa	180
ctacaggtgt	gtgccatcac	acctggcttt	acatttttct	gtggggtctt	actatgttgc	240
ccaggccggt	ctcaaactcc	tgagctcaag	tgatcctctg	nctcagcctc	cagagtatct	300
gggattacat	atgtcggcta	ccgtgtctgg	ccgttcacat	ctttggccac	tattngcttg	360
tgaaaaggta	tnatgagggt	gtacttatca	tngttactgt	gtctcatgtt	nngtatattt	420
ttgcttcatc	aactaagatg	cactgtaaca	tctgtgaaat	ctggatatat	tatcaaangg	480
tttatcatag	ttttgttaac	aatacactgt	cgttttactn	ggtgcctaen	ataatgggat	540
agttgngagg	tgatcttaga	tttgatgaag	cacagtatgc	aangtaggcc	taatggnggg	600
aaagaatggg	naattttcan	angcnnggaa	gtatttgnnt	ttttgtaaat	ggacttgaaa	660
agcttgttct	gnnggattgg	acccaacccc	tttccctttn	aaaccccgaa	ttctnatnga	720
ctnttccaac	ttngaaaact	ttgctcnaac	ttaaatacct	tnaaaaaatt	aacctngacc	780
ccg						783

&lt;210&gt; 659

&lt;211&gt; 741

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 659

tcttcttttg	tatacctgct	nttgcctttt	ntgcaggatc	cctcgattcg	ctttgagcta	60
ggataaaaaat	tgggtaaagg	acatttgctt	acctgcaa	gaatcactgt	ggaaatgtga	120
tcttcccata	tcataagaa	acttgttttc	tggatgaata	ctgggagaat	aaaatgagaa	180
ctctggagtg	agctaaattg	atcccaatta	agtttttctg	cttagcagac	agaaggata	240
attttttgac	accctttccc	acctggtgcc	tatgctaggc	ttgtcctgag	aacatccctc	300



agtaacttga	tattcacatg	acctacagga	tgtcccatct	gcagggctga	gtcagttggg	360
gaacaccaga	ggctacacag	tagctcttcc	tgctactcgg	ttaatgagct	tggcaggttc	420
tttgtctcac	tgaattctta	tcatggaaac	agcagcagca	gccgctagga	aatcttcaag	480
tgtagtgtct	gtgctaacc	agtggtaaat	cccttagatc	ccctgctggg	ctctggcagt	540
ctccttgatt	ttgggtacca	tgtatatatt	ccgctttgac	tttaacgctt	tctaggatag	600
ggtaagcac	cttaattcan	gcactgtcca	ttagcttcc	ttgcaaaagc	tacttatggn	660
cggtcacaat	ncaacactna	nacagagcca	aggcaatatc	ctcttgccca	tggctatgat	720
gtcagacagt	ggatggctcn	t				741

&lt;210&gt; 660

&lt;211&gt; 734

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 660

tctgnnctnt	gtntccttgc	tctgtgttctt	ttgcaggatc	cctcgattcg	aattcggcac	60
gaggactgga	gaagtcagaa	gtagaaaagc	agattgctag	gagagacagg	atgacagatt	120
ttgggtcagaa	aatgggatat	tggagttaa	agtatcaa	acagaatagt	tccagatggt	180
cagagatcca	gcatgggatt	aggtactgaa	atggattaga	actaaaagtc	actagaattt	240
agaaattgag	aaccatgaga	gtggatgcaa	tgacttgttg	cttgattgaa	aaataaatta	300
ataataataa	aggaccatga	gactagcctg	ttataggggt	tatctccatg	aacattgaat	360
tttcccagga	tcatagcagg	aattgggtag	agaaaaagat	tatgagaagg	tgccagagtc	420
ttcagtgaat	gtcaggaaat	taccaggaag	tcagcatatg	acagagaaaa	ggacagtatg	480
ttatctgcat	caaaggaaaa	tgtgcttttg	ttgaaaagta	cagaaaaagc	caatactaca	540
atactgtgct	aagcccctac	ctgtactcct	ctcccacagc	tgcattccag	ccctgtggta	600
taaaaggtgt	gagaatgagc	ttttccacca	gaatcagcag	gtttagttaa	agcatgagca	660
gaacaagcat	nctatgaaga	gactgaggat	gtaggtgagt	ggtctaaatc	tcatnnaagg	720
acattgcagt	ngat					734

&lt;210&gt; 661

&lt;211&gt; 762

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 661

ttnnnnnnct	ccnaatcctc	cngatnanat	cnctttgnan	ctncctgcag	gatcccatcg	60
attcgaattc	ggcacgaggt	ccatacatgg	agctccctgg	agcccgtgtg	ntntcgtgtg	120
actgaacgtt	ttgtgatgaa	aggaggagag	gctgtctgcc	tttatgagga	gccagtgtct	180
gaattgctga	ggagatgtgg	gaattgcaca	cgggaaagct	gtgtgggttc	cttttacctt	240
tcagctgacc	atgaactcct	gagcccgacc	aactaccact	tctgtcctc	accgaaggan	300
gcentngggc	tctgcaaggc	gcanatcact	gccatcatct	ntcagcaagg	ngacntatat	360
gtnnntgacc	tgnagacctc	agctgacnct	nccttngtan	ggttngatnt	nggaagcatc	420
ccaaggngat	ttagngacnn	tggantcctn	atnactgata	anacncnaac	tatantnttt	480
tacccttggg	agcccaccag	caagaatgag	ttggagcaat	cttttcatgt	gacctnctta	540
acanatatac	tctgaatgaa	tctacgttgt	atztatcagg	nggacaatgg	gaataaagcn	600
ttntntaaagc	accnantgga	catgaaagca	acagacacna	ggagnnaagc	cttgagacat	660
gtctgnnntc	tgaccgcatn	ttgatccant	gntctgtgan	ganttnttca	ctgaacattt	720
tcaagaggag	ggtgnatacc	cctggcaatn	gccnaanaa	ag		762

&lt;210&gt; 662

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 662

```

nanatccnnc nantncttnt tgttctgtgc cgnangatcc catcgattcg aattcggcac      60
gaggtttcat ttaagaagaa tgancatagat anatgtgtgc ttctgggttac cccaccctga    120
cagagtgcac ttttacacgg ctacgagggg ttgagactgc agcctggcct gccagccatt    180
ggaggtgttt aaggaagggc agataatgtg actctttgcg ggggtgccatc tgcttaccac    240
ttagcgagca naggggggttt ctgcgggtga cccccagcat atttctaggt tacttatggg    300
cagatttgta agtgacaaaa ctccagctga tgctgggaat ggggagaggg cccttgaggg    360
actttgtggg tttgtgcttc tggtttcctg gccaaaccca gggtcacttg tctggaggcc    420
cagctgggca ctaatgtctg ccaccgacta tgttaaagtg tataaatgat tcctctatct    480
gggagagatc ttccaatcca gaggagcccn tcttggactg cctgggttaa atctgcatan    540
cagangtggt tgatgaagtt catctgaaga aattcagccc cacctnccca ccctgccttt    600
cctgtccctt tttgatagtg gcttctgggt actcgggcnn gtcttgaggc caccancctt    660
ntctgggggt ctnaagccat cccgttgggg ctgtcggcca agcctaagtt aatcgtgtgc    720
ctntattggg aggatngctn ntccct                                     745

```

&lt;210&gt; 663

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 663

```

taatcctntt gataanaatc cttgtncctt ctnntgancc ntcgattcga attcggcacg      60
agggcaagtt tccaaagatc agtgtggagt gctacagaaa taattatagg agaggaaatc    120
ataatcacag aaggtataat gcttgtttga ggctccggaa taagaactaa aaaaaaacia    180
aaaacactgg tttcatgctt acgggggtaca cactttggtg catcccgtga acacaaatct    240
taataccaaa caatccttga tgcttcacct ggggctgcc aagcagtttg aaaacagagg    300
aaaacattta gtgcagtctg tattatcctt ttccaacttt tctgtttgtg caagtttttg    360
aagattcatt ggccaaacia tgaacaacia aggttttctg agagaagaca aggtggactt    420
ttcattttgt tagtaaatac cagtggcact gttgaacgaa acaaatactt ttatctcagt    480
ctttcaaatac agtattaatg tctgtgtttc cttccactga cagctcttct tctagtttca    540
ctgaaaaaag ggtgttagta tttttatctt ggacactctc ttccaaatcc ttcagcagct    600
cctcttcttt atattctgcc acatcgacct cttaaaccgga attgtccttc agtttgccgt    660
ggtgcttgag atantacccg ctggttctga aagaacttga tgatggtgta ctttgggaag    720
gtcnaactgg gcanacagag tctggatt                                     748

```

&lt;210&gt; 664

&lt;211&gt; 785

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 664

```

gtnnnnccnc nnaccctnnt gaatntaatc cttgttcttg ctgcatgac ccatcgattc      60
ggtcaagctg gccctggatg tggagatcgc cacctnccgc aagctgctgt agggcnagga    120
gtgcaggctg aatggcgaag gcatatggac aagtcaacat cnntgnagng cagtccaccg    180
ncttcagtgg ctatggcgnr gccagcgnr taggcagcng cttaggcctg ggngnnggaa    240
gcagntactc ctatggcant ngnccttgnr ttggatgcnr cnntagtncc agcagcggna    300
nagccactgg ggggtggcctn agctctgtng gaggcggcag ttccaccatc aagtacacca    360
ccacctcctt ctccagcatg aagagctaca ngcactgaan tgctgcgcgc agctctnagt    420

```

cccacagctt	tcaggccccct	ctctggcagc	atagccctct	cctnangttg	cttgtcctnc	480
cctgnccctc	antctccctc	gccctaccgn	gnagagctgg	gatgccctca	ctttntnctc	540
atnaatacct	gtttcactga	actcctgttg	cttaccatca	tgtcncagtt	atcagcactn	600
aaancatgct	aatgnccttt	tataagnccc	ngtattttatt	acaagnatct	tgaantctgc	660
cattaaattc	ttgaggaang	aaaatgacct	attatccccc	ataaagaacc	tgaaacttca	720
agnctaangt	cccagcntnc	aacanggaag	gagntccntt	tttttnattn	gctaaaccan	780
tcctc						785

&lt;210&gt; 665

&lt;211&gt; 763

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 665

ggnngntgnn	nntnntaatt	nctnttnaat	nncantcctt	ggntctngnt	ntagganccc	60
atcgattcgc	tgaaccctaa	aggaaaagcca	gcaaaccagc	tgcttgctct	caggactttt	120
tgcaattggt	ttgttgcca	ggcaggacaa	aaactcatga	tgtcccagag	ggaatcactg	180
atgtcccatg	caatagaact	gaaatcaggg	agcaataaga	acattcacat	tgctctggct	240
acattggccc	tgaactattc	tgtttgtttt	cataaagacc	ataacattga	agggaaagcc	300
caatgtttgt	cactaattag	cacaatcttg	gaagtagtac	aagacctaga	agccactttt	360
agacttcttg	tggtcttg	aacacttatc	agtgatgatt	caaatgctgt	acaattagcc	420
aagtctttan	gtgttgattc	tcaaataaaa	aagtattcct	cagtatcaga	accagctaaa	480
gtaagtgaat	gctgtagatt	tatcctaaat	ttgctgtagc	agtggggaag	agggacggat	540
ntttttaatt	gattagtgtt	tttttcctca	catttgacat	gactgataac	agataattaa	600
aaaaagagaa	tacngtggat	taaagtaaaa	attttacatc	ttgtaaagtg	gtggggaggg	660
gaaacagaaa	taaaattttt	gcactgctna	aannnaaann	actttccagc	naanctaaaa	720
aactnnancc	tttaaactat	antgagttcg	nanaccnggn	ccn		763

&lt;210&gt; 666

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 666

nnttnnatat	nngctcttgt	tctttttgca	ggatccctcg	attcgtctag	acctctgaca	60
tcatgggtgt	ttcttaatgc	ctcacattgc	tggcacgggg	atgtgccttg	cctgccagca	120
cctaggactt	cgagttgggt	tgcagcttat	gacatgcatg	ataggttttg	gaaggtaact	180
tttaactgca	aacctataaa	gtactatttt	ttattttata	aatgaacagg	gttttaacgt	240
gtcacaactt	aatttttttc	aattgtatga	aggccttaaa	aaagctacat	taagcgtagc	300
taaaattatt	tattggacta	aaaactaaca	gaacttcatt	tccagaattt	ttttttttgg	360
caaagtgtta	cattcaatta	aggggaaaaa	gtagaaccag	cacaaatgag	tggcagttgc	420
tggagcataa	ctgcttcaat	aaatcttcat	cttggggtaa	ttacaggcaa	gtcattttca	480
catcctcttg	aggttcagag	catcagaatg	aactctatga	atacatgtgt	aagtgccaga	540
cagctgaatc	tttatcaggt	attgnaaaga	tacacatatg	atatgnttat	taaaattgaa	600
ataatgtaaa	acacatgaat	aaatttgcaa	aaccaagatc	acagtccacc	atatgcactc	660
tggtacctta	aatttttttt	ataaataatt	naaaagggaa	tattggaagc	ttcttaaaaa	720
aaaaaaaaan	aaaaaactcg	agcctntana	acttttgng			759

&lt;210&gt; 667

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 667

ggnnntnaaa	ctnctaata	ctc	tgtnttgcag	gatcccatct	atnctntatan	angctctagg	60
cggngcggnt	cccactctcg	gaaccttgtc	ctgtttgtcc	cccagctcgg	caagcgccat		120
atgagcctgg	cggcgccaga	tgcgaatcct	gttctgggct	ttttggccta	ttcccgcctc		180
tcagtcttgc	cgggatggca	ccgcccgcac	aggacttcca	gggttgggct	gantgggagt		240
tcgactgctg	ggcctcgtaa	ttctcgcttt	ggggctgtct	cttccaggct	gggacacact		300
ggggcccgcct	gtcggctctc	cgtcctccga	catcttgtct	ggaacttccg	cctggcagtc		360
tccagtagga	gtggagctct	gtgcggcgta	ntttgggtga	aaaacnggcc	ttgcgtcggc		420
ctcaccacca	gtgtttgtgt	ttcagaatga	agactattct	cagcaatcag	actgtcgcaca		480
ttccagaaaa	tgctcgacatt	actctgaagg	gacgcacagt	tatcgtgaag	ggcccagagg		540
aaccctgcgg	agggacttna	atcacatcaa	tgtagaactc	anccttcttg	gaaaagaaaa		600
aaaagaggct	tccggtttga	cnaaatgggt	gggtaacaga	aagggaactgg	ctaccctgtc		660
cggactatct	gtaagtctng	tncagaacat	gatcaaaggg	tggttacctg	ggctttccgt		720
tacaaagatg	aangtctgng	natgcttaat	ttccatnaaa				760

&lt;210&gt; 668

&lt;211&gt; 763

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 668

gntctatgtg	gctctngttn	ttttgoggat	cccatttgac	gccttggcac	gagaagaaaa	60
cccattgaaa	gtagcagtg	tgtgagttgc	agagacagga	aagatagaag	acgttccatg	120
tggtattctg	atggctgaag	tttacatttg	gaaaaaaatg	gaaatcacac	accatcctcc	180
agtgtgggca	gctctgtaga	aattagttta	gaaaattctg	aactgtttta	agatttgtct	240
gatgccattg	agcaaacctt	tcagaggaga	aatagtgaag	ccaaagtgcg	acgtagcacg	300
aggctacaga	aggattttag	aaacgaaggt	cttgtatgga	tttcacttcc	acttccttcc	360
acttcccaaa	aagccaaaag	aagaacaata	tgtacatttg	acagcagtg	atttgaaagt	420
atgtctccca	taaaagaaac	tgtgtcctcc	agacaaaaac	cgcagatggc	acctcccgtc	480
tcagatccag	aaaacagcca	gggcccgtct	gctgggttct	ccgatgaacc	tggttagagg	540
aggaagagct	tttgtatatc	tacacttgca	aataactaa	ccactttcca	gttnaaaggc	600
tnccggagaa	gatcctctct	ttaatgggga	aaggagagga	gctctcttga	ctggccttgg	660
gaaagggatt	ggaacataat	ggggagaaaa	gaaagccgta	attgacattt	tctggcanan	720
tcttgtnanc	aagaggggna	aagtnaccct	tntntgcttg	aaa		763

&lt;210&gt; 669

&lt;211&gt; 754

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 669

tgntttcta	gctngctctc	gttctttctg	caggatccca	tctattcgaa	ttgatgagcc	60
ttattaacta	tcttttctc	atgagacaaa	ggttctgatt	atgcctactg	gttgaaattt	120
tttaattctag	tcaagaagga	aaatttgatg	aggaaggaag	gaatggatat	cttcagaagg	180
gcttcgccta	agctggaaca	tggatagatt	ccatttcta	ataaagatct	ttaagttcaa	240
atatagatga	gttgactggg	agatttgggt	gtagttgctt	tctcgggata	taagaagcaa	300
aatcaactgc	tacaagtaaa	gaggggatgg	ggaaggtggt	gcacatttaa	agagagaaa	360
tgtgaaaaag	cctaattgtg	ggaatgcaca	ggtttcacca	gatcagatga	tgtctgggta	420
ttctgtaaat	tatagtttct	tatcccagaa	attactgcct	tcaccatccc	taatatcttc	480

taattggtat	catataatga	cccactcttt	cttatgttat	ccaaacagtt	atgtggcatt	540
tagtaatggg	aatgtacatg	ggaatttccc	actgacttac	ctttctgtcc	ttgggaagct	600
taaactctga	atcttctcat	ctgttnaaat	gtgnattaaa	gtatctacct	aactgagtng	660
tgantgtant	gaaagaaagg	ncatatntta	aacnttgaat	ttancaagcc	cacnctcgna	720
ttttatgncc	tttcttttgc	ctngggattg	aanc			754

&lt;210&gt; 670

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 670

tgnttcta	anttgctact	tgttcttttt	gcaggatccc	ttttgacgnc	tttggcacga	60
gaaagaaagg	gctcgtgaca	gagaaagaag	aaagagaagt	cgttcacgaa	gtagacactc	120
aagccgaaca	tcagacagaa	gatgcagcag	gtctcgggac	cacaaaaggt	cacgaagtag	180
agaaagaagg	cgagcagaa	gtagagatcg	acgaagaagc	agaagccatg	atcgatcaga	240
aagaaaacac	agatctcgaa	gtcgggatcg	aagaagatca	aaaagccggg	atcgaaagtc	300
atataagcac	aggagcaaaa	gtcgggacag	agaacaagat	agaaaatcca	aggagaaaga	360
aaagagggga	tctgatgata	aaaaaagtag	tgtgaagtcc	ggtagtctgag	aaaagcagag	420
tgaagacaca	aacactgaat	cgaaggaaag	tgatactaag	aatgagggtca	atgggaccag	480
tgaagacatt	aaatctgaag	gtgacactca	gtccaattaa	aactgatctg	ataagacctc	540
agatcagaca	gaggactact	gttcgaagat	ttttggaaga	atactgagaa	cggcataaag	600
tgaagatcga	catttaaaaa	atgaggtgaa	agaaagctnt	tgtggcatag	aaaaagtntt	660
aagctcaant	agttttttta	ttattattat	tattaaaagt	tattcaggac	tgatgtgact	720
ncngatttna	gaacatgtgg	taatagtnta	nt			752

&lt;210&gt; 671

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 671

tgnttcta	gttgctactc	gttcttttgc	ggatcccatn	ttattcgaat	tcggcacgag	60
gatattcaca	cagtatgtat	tatattaacc	atatcacact	taagttatta	aattcagact	120
atttgtaact	tattgttata	gggcctgccg	tatggcttag	gatatttgag	taatcatata	180
tttaaagtaa	aaacttttggg	ctgggcacag	tggtcacac	ctgtaatccc	agcacttggg	240
gaagctgagg	tgggcagatc	agttgaggtc	aggagttcta	gaccagcctg	gtcaacatgg	300
cgaaacccca	tctctactaa	aaatacaaaa	attagctggg	cgtggtggca	cacacctgta	360
atcccagtta	cttgggaggc	tgaggcacaa	gaatcgcttg	aaccgaggag	gaggaggttg	420
cagttagcca	agatcgccct	gctgactcc	agcctgggca	acagaggag	actctgtctc	480
caaaaacaaa	aacaaaaact	gttagtgaag	gttcctggg	acttttgata	ttttaaaaat	540
tggtcttatg	actagtagat	aaattcattg	ccataatgag	gctagctccc	agataaacag	600
tgtattttct	tctttttttt	ttttggtgag	tggtccaaac	tttaagctac	tttttccagt	660
antttgccac	tttctccgan	gtaantttgg	ctggctcttn	agtaatgcta	attgngtgctc	720
aaaatttgctc	tacaacagtt	nggcaacaga	tn			752

&lt;210&gt; 672

&lt;211&gt; 792

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 672

tgnttcta	actngctact	ngttctttct	gcaggatccc	tctattcgaa	ttcggcacga	60
ggctgcttct	ggctggggg	tccttggcct	tcacctgct	gaggtgagg	aggaggagga	120
agagccctgg	aggagcagga	ggaggagcca	gtggcgacgg	gggattctac	gatccgaaag	180
ctcaggtgtt	gggaaatggg	gaccccgctt	tctggacacc	agtagtccct	ggtcccatgg	240
aaccagatgg	caaggatgag	gaggaggagg	aggaggaaga	gaaggcagag	aaaggcctca	300
tgttgctccc	accccagca	ctcgaggatg	acatggagtc	ccagctggac	ggctccctca	360
tctcacggcg	ggcagtttat	gtgtgacctg	gacacagaca	gagacagagc	caggccccgn	420
ccttctgccc	ccgacctgac	cacgccggcc	taggggttcca	gactggttgg	acttgttcgt	480
ctggaonaca	ctggagtggg	acactgnctc	ccacttttct	gggactttgg	agggangtgg	540
aaccggcaca	ctggacttct	tccgtctcta	nggctgcatg	gggagccctg	gggagcttna	600
atnnttgggg	gatcccnnaa	aangaccccc	tgtcccccat	anacttgggt	ttttngcttt	660
cancccttcc	cccttggccc	cnnttgacca	cttcatggag	tttaattaaa	atngcccttg	720
gtangaaaan	anaatantnt	tcctcntttt	antgntnttt	tnntataatt	tnatnatcct	780
antnatcntn	nt					792

&lt;210&gt; 673

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 673

nttcta	atnc	tngctacttg	ttctttntgc	aggatccctc	gattcgaatt	cggcacgagg	60
cagcttcgag	ccaatggtga	gctccttctg	gatcagctcc	ttcagctcct	tcttgctcag		120
gatgctgaaa	ttgcaaggct	gatggaagac	ttggaccgga	acaaggacca	ggaggtgaac		180
ttccaggagt	atgtcacctt	cctggggggc	ttggctttga	tctacaatga	agccctcaag		240
ggctgaaaat	aaatagggaa	gatggagaca	ccctctgggg	gtcctctctg	agtcaaatcc		300
agtggtgggt	aattgtacaa	taaatttttt	ttggtcaaat	ttaaaaaaaa	aaaaaaaaaa		360
ctcgagcctc	tagaactata	gtgagtcgta	ttacgtagat	ccagacatga	taagatacat		420
tgatgagttt	ggacaaacca	caactagaat	gcagtgaaaa	aaatgcttta	tttgtgaaat		480
ttgtgatgct	attgctttat	ttgtaaccat	tataagctgc	aataaacaag	ttacaacaa		540
caattgcatt	cattttatgt	ttcaggttca	gggggagggtg	tgggaagttt	tttaattcgc		600
ggccccggnn	gccaatgcat	tgggccccgg	tacccaactt	ttgttccctt	tantgagggt		660
taattgcnc	ccttggccgt	aatcatggta	atagctgttt	cctggtgnga	aattgtttcc		720
cgtnacaatt	ncacacactt	ttcancggg	ggacn				755

&lt;210&gt; 674

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 674

tgcttcta	at	gcttgctact	cgttctttnt	gcaggatccc	tcgattcgca	gatttttgac	60
aaggaaaggct	aattctaaac	ctgaaagcat	ccttgaaatc	atgcttgaat	attgctttga		120
tagctgctat	catgaccctt	ttttaaggca	attctaattc	ttcataacta	catctcaatt		180
agtggctgga	aagtacatgg	taaaacaaag	taaatTTTTT	tatgttcttt	tttttggtca		240
caggagtaga	cagtgaattc	aggtttaact	tcaccttagt	tatggtgctc	accaaacgaa		300
gggtatcagc	tatttttttt	taaatcaaaa	aagaatatcc	cttttatagt	ttgtgccttc		360
tgtgagcaaa	acttttttagt	acgcgtatat	atccctctag	taatcacaac	attttaggat		420
ttagggatac	ctgcttctc	tttttcttgc	aagttttaaa	ttccaacct	taagtgaatt		480
tgtggaccaa	atttcaaagg	aactttttgt	gtagtcagtt	cttgacaaat	gtgtttggtg		540

aacaaactca	aaatggattc	ttaggagcat	tttaatgttt	attaaataac	tgaccatttg	600
ctgtanaaag	atnanaaaac	ttaagctttg	ttttactaca	acttgtaaa	agttgtatga	660
cagggcatat	tctttgcttn	caanattttg	ggttgggggc	actanggggt	caaaaccctg	720
gcanaattgt	cnactttagn	ctgaccataa	tnc			753

&lt;210&gt; 675

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 675

tgntttctaa	acnttgctct	cgtnntttnt	gcaggatccc	atctattcga	attcggcacg	60
aggttccctc	accttattcc	tccaagttcc	cccttgggaa	cctctgagat	taacttgata	120
agctccttgg	gcaagctctt	tatcctaaga	ttcctcagtg	agccttatag	agttgctgcg	180
agaattacat	ttgttcatga	tgtcaagtgt	ctggatgta	gctaattgctt	attgaacaca	240
tagtaattta	ttgaataatt	gtcatgatca	ctggatgaga	tatagccact	gtggaggtag	300
gcacaccagg	gttttagagg	cttgggatct	tgcaacagga	ttttcctctt	gcctctccaa	360
actgcctttt	gcccagatgg	cttcagcatc	tttttgcata	cctgtttcct	tgtttggtga	420
acacctgtct	caacctgtct	gcaaggcgtg	gtgagattct	gcataccttg	taagcactca	480
tgctactcca	aaacagctgt	ttgatgctaa	tagcacacat	gaggtcttgc	aaatttgtct	540
gaggaaactac	aggacattgg	agagatattt	atcaaacacc	cactacatgc	ctgatactta	600
actanggaac	tatnaaagtg	ggtggtgaag	acaagtngga	agtaaantgc	aaacctattt	660
ccatatatgt	ttgnncgcta	gattgntncc	ancaattngc	ntcttggaat	tgttgaattn	720
ggccctgtgt	gtgtgcctgt	ggtaantgga	nntgngtttc			760

&lt;210&gt; 676

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 676

ntttgaaact	tnctactngt	tcttttttgcg	gatccctcna	ttcgaattcg	gcacgaggca	60
gaaccttttc	ccctctactc	ttgtctaaaa	gttctgtgtg	gcacacagag	atgcgacctc	120
ctcaatctga	cttagtaaaa	ccatgctgta	gaatttttgt	cttaaaaaga	ccacataccc	180
agcaccatg	aaataaaaaga	ttcatctgta	attgggattc	aaagtgatta	aattcctttg	240
ttcatactca	taaatagcac	ttaaagtgtta	taacattttc	atttaacctat	ttttagttcc	300
ttcattttta	cttaataaaa	atcttgggatt	gatattcttt	tttttttttt	ttgggacgga	360
gtctcgctct	gtcaccagag	ctggagtaca	gtggctctat	cttggctcac	tgcgagctcc	420
gcctnccggg	ttcacgccat	tctcctgcct	cggcctgccg	agtagctggg	actgcaggcg	480
cccgcacca	caccgggcta	atttttttgt	attttttagta	gagacggggg	ttcaccttgt	540
tagccaggat	ggtctcgatc	tcctgacctc	gtgatccacc	tgccctnggc	tcctaaagtgc	600
tggaattnca	ggcgtgagcc	accgcgcccc	ggncctaaatt	ggatattctt	taaccattaa	660
aaggtttact	gggtgnccna	tttgccatat	tattggaaac	ttggaaaggg	taatttgaaa	720
caaagntttg	aagttaactg	aaatttgggg	a			751

&lt;210&gt; 677

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 677

tgctttgaat	cctttgtaan	cgccctntnt	gcatgatccc	tcnattcgaa	ttcggcacga	60
ggataaactc	ttcagtgacg	aataattagaa	ttagttagtt	atacatttga	ggaaaactat	120
aaaagtacca	ataatgagta	ggaaatcact	tctgcagtat	ttttggagca	ttttccttaa	180
gcatgacata	aaagccaaag	gtcacaaggg	aaaaaactga	tagatttgtc	tgtgatattg	240
agagatgtat	gcacatatac	atacaacagt	catagtaaga	caccgttaga	caaaagggtga	300
tgtatgaaaa	agaggcaaaa	caacaagaag	aaaagattga	aaaaatgaga	gctgaagacg	360
gtgaaaatta	tgacattaaa	aagcaggcag	agatccata	agaatccagg	atgatgatcc	420
cagattgcc	gcgcagggtg	gaagccgcat	atgttgatct	tcaacggata	ctagaaaatg	480
aaaaagactt	ggaagaagct	gaggaatata	aagaagcacg	tttagtactg	gattcagtga	540
agtttagaag	cctgaaactt	ttctcgtatg	gggtgggttt	tgcattaaat	nctgggggtcc	600
attttacaat	ccattatttt	tgaccactgc	tatgtgttca	agtagtatga	gaatgtgatt	660
gntnttatct	ggntcatata	tatttctttg	gctaatttaa	tatgtcaa	aatgagttc	720
atttaaaaaa	aaaaaaaaaa	acccggactg	ttttnt			756

&lt;210&gt; 678

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 678

gnnnnnnnnn	nnnttnnaat	agnnagctac	ttgttctttt	tgcaggatcc	catcgattcg	60
aattcggcac	gaggggtgtt	ggagcagatt	gtagttgatc	cacagcaaag	agcatcacca	120
aagccattcc	aggaggaact	agatccacca	cttcctctgc	tgggcatgct	ccaaaaatgg	180
ttgtggcttc	cagagaggac	tccaaaagaa	agcacaaaaa	ctagacagt	ggagggcata	240
cccaaaagcc	ctgagtttct	gaaaaaatat	tgaaagtttc	tatgggtgaa	taggaagtta	300
atgtgcttag	gaagaaaaaa	gtggtaatga	ttcaaggaaa	cataatcaca	cacggtttta	360
gttttaatgg	acatgggagg	agccataaaa	gtagtctatc	tatcatcagt	tacatatcta	420
atgaactgtc	tatctgggat	accctatcct	gttttaatct	gagtgaactct	ctctcagctg	480
agagagctgg	acagactcca	ttttagcctc	ttcacttgca	gtccccttat	ccccctccct	540
taaggggaata	actagtgcaa	gctgacttca	agcacattca	ggaatgcact	tactgataag	600
atattgaggc	aagctgtacc	agcagcttct	gggggacctg	ctcantggat	ggcccccaacc	660
cctgcattta	tctctttggg	atagtttaag	cccctgnacc	tggaactgng	tatttttctg	720
tactatctct	gtancattaa	tttttttact	ttttgg			756

&lt;210&gt; 679

&lt;211&gt; 747

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 679

tctaantnctt	ggctctcggt	ctttctgctt	gatccctcga	ttcgaattcg	gcacgagaaa	60
tgactccctg	caaaacccaa	cccatgctgc	tggtgtggg	atttttggtg	taagcctatc	120
tatgcactct	atcagccaga	atttggcatt	tagctcttag	ttaaatctag	taaaggacag	180
tctattgttt	aaagagaagg	tgcatttgtt	cctcaatcaa	gcaagagcac	ctgtgttgta	240
ctgctttata	tctcatgtat	atttatagta	atgaaaagac	tttttaaatt	gtacacgttt	300
cagtgccttt	cttgtgttat	gaaaggcagg	tagatattat	agccataggt	aaaaatccat	360
agttaaattg	caactgacc	ttaaatctct	ctgtgtatgc	ccttgatct	tgcatgttaa	420
aagttggatt	attgggcag	tgtggcagcc	tgccctgcta	catgctagac	aagtgtgctt	480
tagtacatag	ccacaagttc	ttcattcttt	aaaatgtttt	gacagatcat	ctcataataa	540
aaataattca	ngaaaactat	ggggaaatag	ttacatttca	caaaagatat	tttaaaactct	600
ttgtaaaact	tagataatag	agcctancaa	gttactttgn	atctaattgg	atacatttta	660



tgnttaattt taccaccata catttttatta atcaaaattg gtttagcatgt gactcttttt 720  
 ggcttcanaa gttntcaaaa aaattat 747

<210> 680  
 <211> 750  
 <212> DNA  
 <213> Homo sapiens

<400> 680  
 ttctaattct tggctctcgt tctttctgca ngatcccatc gattcgaatt cggcaccgagg 60  
 accggctggg cctacaaaaa gatcgagctg gaggatctca ggtttcctct ggtctgtggg 120  
 gagggcaaaa aggtctcgggt gatggccacc attgggggtga cccgaggctt gggagaccac 180  
 agccttaagg tctgcagttc caccctgccc atcaagccct ttctctcctg ctcccttgag 240  
 gtacgagtgat atgacctgac acaatatgag cactgcccag atgatgtgct agtccctggga 300  
 acagatggcc tgtgggatgt cactactgac tgtgaggtag ctgccactgt ggacaggggtg 360  
 ctgtcggcct atgagcctaa tgaccacagc aggtatacaa gctctggccc aagctctggt 420  
 cctggggggc cggggtaccc cccgagaccg tggctggcgt ntccccaaca acaagctggg 480  
 ttccggggat gacatctctg tcttcgtcat cccctggga nggccaggca gttactcctg 540  
 aggggcttga acaccatccc tncactagc ctctccatac ttactcctct nacagcccaa 600  
 attcttgaaa gttgtctccc ttgaccttc tttaatggca acttaactga anaaagggat 660  
 gtncncttat atccaaaatt cagctatttg gcaataaac canatggatt aaaaaaata 720  
 attntntctt aananaanaa actccggcct 750

<210> 681  
 <211> 748  
 <212> DNA  
 <213> Homo sapiens

<400> 681  
 ctaatncttg gctctcgttc tttctgctng atccctcgat tcgaattcgg caccagccca 60  
 gctgctcagg aggtcaggc aggagaattg ctggaacca agaggcggag gttgtgggtga 120  
 gccgagattg cacctttgta ctccagcctg ggcaacgagc aaaaaactct gtctcaaaaa 180  
 aaaaaaaaaa aaagaaaaag aaaaatggct tccaggacag agcatgctca tttgctggcg 240  
 gacagttcca gaaacagacc ctgttagtcc ttctacttac ctgctggatt tttcaagcac 300  
 taaatttata actttttgaa acaaaataat gtgtaatttt ccatttgggg gcaaactcta 360  
 ttcttgtgag cattattaaa atcttgtttg taaatatatt gtctttctct taatatttgc 420  
 tctgggtcan gaagaagctg ttcacggtgt gataatactc ttanattgt gctttcatta 480  
 ttatagatgc atcatgtctt ctgctttcac gtgtctggga tggggtcaga aatgcatnct 540  
 ccagntgaca naaaaatccn agnatgagat caanaaggat actggtgttt tctgactttt 600  
 acaaaaatta ctttgntgtt ttcattaaaa aaaaagcttt aacctantgn ttncntantc 660  
 cttttagaaa ntattaaatt tnaaatgaa ttcnatanaa atanaannac naaaaaactt 720  
 nntnccctta naactttagt gangcgtg 748

<210> 682  
 <211> 755  
 <212> DNA  
 <213> Homo sapiens

<400> 682  
 ctaatgctng gctttcgttc tttctgcagg atccctcgat tcgaattcgg caccagcagg 60  
 agcaatcaat tctgtcgaa gtgaatacca tgcagctttt aacagtatga tgatggaacg 120

catgaccaca	gatataaatg	cactgaagcg	gcagtactct	cgaattaaaa	agaagcaaca	180
gcagcaggtt	catcaggtgt	acatcagggc	agacaaaagg	ccagtgacca	gcattctccc	240
gtctcaggtg	aacagttctc	cagttataaa	ccaccttctt	ttaggaaaga	agatgaaaat	300
gactaacaga	gctgccaaga	atgctgtcat	ccacatccct	ggtcacacag	gagggaaaat	360
atctcctgtc	ccctaccgaa	gaccttaaga	cgaagctcaa	ctncccgtgg	cgaactnaca	420
tccgagtcca	caaaaagaac	atgccaaagg	ccaagagtca	tnccggctgt	ggggacaccg	480
tanggtgat	agatgagcag	aacgaggcca	gcaagaccaa	tgggctgggg	gcagcagagg	540
cattcccctt	tggntgtcan	gagacagctg	ggagagaang	caagnaagcc	ctgaangcna	600
gtccaggagg	accnncnaag	ggcagtttcc	ggagcccgtt	gttccggaga	tgctgatgtg	660
ggntgtgtct	gcanttcang	gccaaanttg	gggacccctg	ggaactgtac	cctangggnt	720
ncttgnagnt	taaaacttga	ccttaanggn	ngcct			755

&lt;210&gt; 683

&lt;211&gt; 755

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 683

ggnttttnnt	ctttctaagt	cttggtcttc	gcctntctgc	ttgatcccat	cnattcgaat	60
tcggcacgag	aattagtatc	aacttacaat	ccaagtccaa	gtatcatctt	ataatcactt	120
ttttctacta	tattaagatc	taatgaattt	gatttctttt	ttgaagtgtt	ttcttgtaac	180
atctgagatt	agaagttaa	gatcacttga	cccaaacct	ttgtttatgt	aagaattttt	240
aaacataaaa	gtgtttgttt	ctgttatgtt	accataattt	gatgtatata	gtgtccagat	300
ccatttagaa	atttaatat	tattaataac	tgaactgtt	tgtcttctt	tggtatatag	360
tctcgatat	tattattatg	caggccaaga	taaaattttg	acagctcttt	aagcccacat	420
gcagcagtg	gtcagataac	cctgtggcag	tgacacgggc	aaattggcat	ttgaataaag	480
ccctgggacc	acctcaacat	gcgtagcctc	ttgtcttaaa	tgtactcccc	atggcagcat	540
ggaggaggca	agacctgtgg	gtcaattttg	aactggncct	actttgattt	taaaacaaga	600
gactcagggg	aaagtactaa	acaaaaaact	ctgattntac	tttgcgtttt	ctgggaagtn	660
ttggtttact	gagatgcttt	tgtaaaggaa	aataatgctt	gngacanttt	agtaattttt	720
acanaattcn	ttaatatatt	ttctctntgg	gcttn			755

&lt;210&gt; 684

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 684

ggnttttnann	cttttnaatn	cctttgctnc	tcgntctttt	tgctggatcc	catcgattcg	60
caagatctgg	aggaatgcag	agaggaactt	gatacagatg	aatatgaaga	aaccaaaaag	120
gaaactctgg	agcaactaag	tgaatttaat	gattcactaa	agaaaattat	gtctggaaat	180
atgacttttg	tagatgaact	aagtggaaat	cagctggcta	ttcaggcagc	tatcagccag	240
gccttttaaaa	ccccagaggt	catcagattg	tttgcaaga	aacaaccagg	tcagcttcgg	300
acaagggttag	cagagatgga	tagagatctg	atggtaggaa	agctggaaag	agacctgtac	360
actcaacaga	aagtggagat	actaacagct	cttaggaaac	ttggagagaa	gctgactgca	420
gatgatgagg	ccttcttctg	agcaaatgca	ggtgctatac	tcagccagtt	tgagaaagtc	480
tctacagacc	ttggctctgg	agacaaaatt	cttgctctgg	caagtttttna	ggttgaaaaa	540
acaaaaaaa	tgacatgggt	gcagaagctt	gtaacattga	tcacattctt	aatgtaaatg	600
gtgtctttct	tctgggggtt	cagtatttgc	aaagaaantg	aagaagaatt	ctggaaatgc	660
cattcaatta	accctnagga	aaaaagccga	ccttanaaat	ttaccttant	gcnttgnnnn	720
ttaaaaaana	aaaaaantna	aaaaactttn	accctttana	ccttttgtgg	ggnc	774

<210> 685  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 685  
 ggnttttnnan ncttttcta ncttggcttn agttcttttg caggatccca tgcattcgaa 60  
 ttccggcacga gagtaccag agttgcgagg agttttttaa ctgatttagc cnnntggcaa 120  
 tcatgagtga atggatgaag aaaggcccct tagaatggca agattacatt tacaaaggag 180  
 tccgagtgac agccagtgag aagaatgagt ataaaggatg ggttttaact acagaccag 240  
 tctctgccaa tattgtcctt gtgaacttcc ttgaagatgg cagcatgtct gtgaccggaa 300  
 ttatgggaca tgctgtgcag actgttgaaa ctatgaatga aggggacccat agagtggagg 360  
 agaagctgat gcatttgttc acgtctggag actgcaaagc atacagccca gaggatctgg 420  
 aagagagaaa gaacagccta aagaaatggc ttgagaagaa ccacatcccc atnactgaac 480  
 agggagacgc tccaaggact ctctgtgtgg ctggggctct gactatagac ccaccatag 540  
 gtccagaaaa ttgcagcagc tctaatagaga atattctgtc ncgtgttcaa ggatcttatt 600  
 ggaaggacat cttacagctt ccaatgagaa gccaaagaag tgtgaacata ctgattgaaa 660  
 aaagacttta ttttaataccc tcattaaaaan ggttttaaat gttaaaaaaa aaaaaaaa 720  
 acttcgagct tttaaactat ngtgagtcga ttcntataa 759

<210> 686  
 <211> 749  
 <212> DNA  
 <213> Homo sapiens

<400> 686  
 ggntttnnnn nctttgaaat ccctnngctn ctagnctttt ttgcaggatc ccatcgattc 60  
 gaattcggca cgagggaat tagcctcgct taagttgcct tttttacaca ccaaaacttt 120  
 ttacatgaag ggctgggttc acatgaatac tatactgaaa tctgtgctct caagatctag 180  
 cagtgcaccag ggctgcccgg cgggggctct cctggcaagt caggaagggt tctgttgcta 240  
 atataacata gaaacacatt agtgcactgg gcctctctga ggtcagcata tttgtactct 300  
 tggaatattt gtttttttct tcagtaacaa cagaaacccc agttgggagt ttaacaaata 360  
 actgactacc actcactcat gcatttttat ttccaattaa agcaaagcac tgtgctgtgc 420  
 tcagataata atagtttgta agtaaaagtt tttagttttc agtggttcagg ttatagaata 480  
 taactgacca taaaaattac ctgcaggat tttcttttta tgaacttggt tttaaattac 540  
 caagtaatta ctggtgtcat tttgttttat gacagacaca cgtatctaac aaacaaacaa 600  
 acagtgcact tctccatggg tcaaggactt ccttacaatt tctnctgagt taacttttgt 660  
 gaaaataatc ctaaggtttt ctggcttatt gaggaatttn ctacaaacaa caaaccaaca 720  
 acngaagaga agatcatcaa ccactgttt 749

<210> 687  
 <211> 760  
 <212> DNA  
 <213> Homo sapiens

<400> 687  
 ggntttctaa tgctttctaa taccttggt ctngctcttt ctgcaggatc ccatcgattc 60  
 gaattcggca cgaggaaatg tgtatttcag tgacaatttc gtggtcttt tagaggtata 120  
 ttccaaaatt tccttgatt tttaggttat gcaactaata aaaactacct tacattaatt 180  
 aattacagtt ttctacacat ggtaatacag gatatgtac tgatttagga agtttttaag 240  
 ttcattggtat tctcttgatt ccaacaaagt ttgattttct cttgtattac attttttatt 300

tttcaaattg gatgataatt tcttggaac attttttatg ttttagtaaa cagtattttt	360
ttgttgtttc aaactgaagt ttactgagag atccatcaaa ttgaacaatc tggttgtaatt	420
taaaattttt gccacttttt tcagatttta catcattctt gctgaacttc aacttgaaat	480
tgtnnttttt tttctttttg gatgtgaagg tgaacattcc tgatttttng tctgatgtga	540
aaaagccttg gtattttaca ttttgaaaat tcaanaagc ttaataataa agtttgcatt	600
ctactcanga aaaagcatct tcttgatat gtcttaaaat gtatttctgt cctctataca	660
naaaagtctt taaattgatt ttacagctt ggaatgcttg gatgntttta aatantaaca	720
ttttatattt tttaaaagac aaancttata ttnatcctng	760

&lt;210&gt; 688

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 688

tgnttttctaa tgcttctaata agcttggctc tngttctttc tgcaggatcc catcgattcg	60
aattcggcac gagacaaaac ctacagatgg agataaaaat tactactgtt attcaacatg	120
tgttccagaa ccttattttg gggagttaaag tcaattgggc agaggatcct gcccttaagg	180
aaattgttct gcagcttgag aagaatgttg acatgatgta ataagaattc atttctgaca	240
tattttacat ttctggcaat ctcaactctt atttggataa cttctgtgca tttgtctgtc	300
caccgtaatt ttagaaaagc atatccataa cgtttacagt tgtagtacag ttgtggtag	360
ttatttgtag tgggattgaa agtaattttt ttctttttat atttctatat ttagtttgtt	420
ttttgttgtt tggtgttttt tgagatggag tctcgctttg ttgccagac tggaggcag	480
tggcgcgatc tgggctcaat gcaacctctg cctcccggtt tcaagcagtt ctgcctcagc	540
ctnccaagta gctgtgacta aaggtgcacg ccgccatgcc canctaattt tttggatttt	600
aagtagaaac cgggtttcac ccgtgttgcc caagctgtc tnaaaactcc tgagctcaag	660
cagtcacccc gncctngcta ccggantgct aggatccaga cgtaagcccc cgaanccctg	720
ctagtttgcg tntttttctn tcattttata ag	752

&lt;210&gt; 689

&lt;211&gt; 806

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 689

gtgnttttcta atgcttctaa tngcttggct actcgttctt tntgcaggat cccatcgatt	60
cgaattcggc acgaggannt cntgtctatn gaacagnggc tggtnnacac tnnngantta	120
nnnntgnacn ntannnattg nancanntan tactggnnt ccntaatncn nttaatgtna	180
cntnttgcaa gnngnntga tnaaatacac gacaggagg aaanctantg cgtcataggc	240
acaggcagac ctaccgnnta aggagatnat ntncennang gntggctgtt gagnncatgc	300
aactctggna tgtatttccc tttataggac cacttgttnc atngtggata aagcccctaa	360
agnaggatgn naaagatgat cngatccaat acgttacnct gacannaaan nntgtnatac	420
ntcngctgan caatctntcc ancnnntnta atatcgtgna tcacctaggg tgtatgaten	480
taggaactct gcncctncan tcnggactgt ccatcacnga ctnntgggct nctactgtac	540
antangcna gaanancnnt canntctacan ntaaccagat tgggtgctggn anatggtant	600
gcnnnttnan cncacacgac ncaataaagn ncnnctntnc cccanancct nttnaggga	660
gaaaggaatt ttncatagtg ggctcaatga anggggtacc cttggntttt ntaaaaaacg	720
ttncatggnn cctaccttaa acctgngtna actnanancn nttngncata angggcttaa	780
cgnctatang gggnacnnat ttttnc	806

&lt;210&gt; 690

<211> 772  
 <212> DNA  
 <213> Homo sapiens

<400> 690  
 ntntttgaat ctttgaaata cttttgctat ngttctttnt gcaggatccc atcgattcga 60  
 attcggcacg agaggttgc cactgaagg agcacaggag gggtttccag gccatgtggc 120  
 tcagcttccct caagcacaag ctgcccctca gcctctacaa gaaggtgctg ctgattgtgc 180  
 atgacgccat cctgccgcag ctggcgcagc ccacgctcat gatcgacttc ctaccccgcg 240  
 cctgcgacct cggggggggc ctcagcctct tggccttgaa cgggctgttc atcttgattc 300  
 acaaacacaa cctggagtac cctgacttct accggaagct ctacggcctc ttggaccctc 360  
 ctgtctttca cgtcaagtac cgcgcccgct tcttcacact ggctgacctc ttctgtcctc 420  
 cctcccactn cccgcctacc tgggtggccgc cttcgccaag cggttgggcc gcttgccctc 480  
 gacggctccc cctgaggccc tgctcatggc cctgccttcc atctgtaacc tgctgcgccg 540  
 gcacctgcc tggcgggtcc ttgtgcaccg tccacacggg cctgagtttg gacgccgacc 600  
 cctacgacct tggagaggag gacctagccc aagaccggg cctttggaaa acttcctgtg 660  
 gggaagcttt aagnncttc nanangccac ttaccaacc ttgaggggnt ccaaangccc 720  
 gccanccggt nattaaccaa ggccttgnc aatgcctgaa ggtcaaacia tn 772

<210> 691  
 <211> 755  
 <212> DNA  
 <213> Homo sapiens

<400> 691  
 ntgctttcna atctttntaa atgcctttgg cttctcgntc tttctgcagg atcccatcga 60  
 ttcgaattcg gcacgagaaa aagtaaagct tttcatgagc acaaatnctc tgcattgttt 120  
 gatgttactg atattcgtaa aatgaatatt tttgttttg tttgtttta ttttttgag 180  
 acaagtcttg ctttggtgcc caggctggag tgcaatggca tgatcttggc tcaactgcaac 240  
 ccctgccttg cgagttcaag tgattcttct gcctcagcct cctgagtagc tgggattaca 300  
 ggcgctcacc accacaccca gctaatttct gtatttttag tagacacagg gttttaccat 360  
 gttggccagg ctggtctcaa actcctgacc tcaaaactcct cacacctgta atctcagcac 420  
 tttgggaggc tgaggtggaa ggatcacttg aagccagagt ttgagaccag cctgtgcaac 480  
 acagcaagac cccgtctcta caaaaactta aaaaattagc tggctgtggt gttgctcacc 540  
 catagtcca gctactcggg aagctgagca ntaagatcac ttgagccan gaggccnatg 600  
 cttncantga actgtgattg tttccantac agnccacctg ggtgacanag taaanaaaan 660  
 gaaacattac ataatttggc tagagcataa taaattgatt tctgggttnt gaaattnnag 720  
 ttgccataaa aggnntttna atngcnant tcant 755

<210> 692  
 <211> 748  
 <212> DNA  
 <213> Homo sapiens

<400> 692  
 tgnttttaat cnttctaata cttggctctt gttctttttg caggatccct cgattcgaat 60  
 tcggcacgag gtccgaagaa aaagactgtg gtggcggaga tgctctctcc aatggcatca 120  
 agaaacacag aacaagtttg ccttctccta tgttttccag aaatgacttc agtatctgga 180  
 gcatcctcag aaaatgtatt ggaatggaac tatccaagat cacgatgcca gttatattta 240  
 atgagcctct gagcttctta cagcgcctaa ctgaatacat ggagcatact tacctcatcc 300  
 acaaggccag ttcactctct gatcctgtgg aaaggatgca gtgtgtagct gcgtttgctg 360

tatctgctgt	tgtttctcag	tgggaacgga	ctggaaaacc	tttcaaccca	ctgctgggag	420
agacttatga	attagtgcga	gatgaccttg	gatttagact	catctccgaa	caggtcagcc	480
atcaccacc	aatcagtgc	tttcatgctg	aaggattaaa	caatgacttc	atctttcatg	540
gctctatcta	tcccaaaactg	aaattctggg	ggaagagtgt	agaacagAAC	ccaaaggaac	600
catcaccttg	gagctncttg	aacacaatga	ggcatataca	tggacaaatc	cacctgctgt	660
gtgcataata	tcattngggg	taaactgtgg	atcgaacagt	ntggcaatgt	ggaaattnta	720
accncagact	ggggacaaat	ntgtgttg				748

&lt;210&gt; 693

&lt;211&gt; 881

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 693

tgnnnngtna	accagggaaa	agctnngttt	gaactccttg	ggcatgatcc	catcgattcg	60
aattcggcac	gaggcggtag	cccacgtgtc	cttttgattg	ccctactgct	gtggagacct	120
cgtgctgacc	atctggcagt	gntcttcgta	ttctctggcc	tgtggggcgt	ggcaagatgc	180
ccgtctggca	gacacaaaac	aatgctctct	acggcgttct	gtttganaag	agcaaggaag	240
ctgccttcgc	caattaccgc	ctgtggggagg	ccctgggctt	cgtcattgcc	ttcnggtaca	300
gcacgttttn	gtgcntgcac	gtcaagctct	acattctgct	gggggtccng	agcctgacca	360
tgggtggcgt	tgggcttggt	gantgcgtgg	agtcccaaga	accccgaaatc	anaccnact	420
ctttcaggac	aggtcaanca	agtcagagga	tgaagaanat	tcanacaaan	atgtgatanc	480
cngngaggcc	naangaggan	naantnataa	aagcaccagc	cagaagaatt	ttcttanaan	540
atgcctnagg	gacatatcan	ccggggttct	cattacccat	cttaancncc	anatttngnc	600
ccattcttga	aataagantc	nttgnttnaa	ttntcaactt	ctttttatgg	tnatttcnat	660
ntatctantt	antaaaacca	caaatntggt	nncnatnacc	accantttct	ttaaaccatn	720
tagnaattca	aangntgtgt	nnttacnaat	ntntaanggg	ttattcaaan	ttcnaaat	780
taaanattnt	tatgcantnc	ncacaatnta	tataanangg	tcctnaaaac	gngnnccaat	840
atnncannnc	nataatntag	nanatntntn	nncctgtan	n		881

&lt;210&gt; 694

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 694

atngcttggc	tctngttctt	tctgcaggat	cccatcgatt	cgaaaattta	tagtaatgac	60
aatgacttta	tcagtgttca	tcacttgaaa	gctaagtgg	tcgttcaatc	actttttcaa	120
agttgatagt	agattgcatg	gtttcatggt	tcctcatatt	ggtttattaa	ttctatttaa	180
tcaaggaaaa	taacttcaga	ttccataaa	tttcagttta	tttttagttt	actactaggt	240
gagatagcac	attacatact	tttactatca	aatattattt	tagcagcttc	ccatagtacc	300
aatgatttg	attccctact	ctcatttttt	aaagcatata	aatatttatg	ggcttaaaaa	360
gggggttttt	aaaaactgag	gatatcanta	ataaattgca	gaatattttg	caaagctttc	420
ttttggaaag	caaacttttg	tgcttgctta	tatgcnaagt	attttatcag	ggacttgaac	480
aaagacctca	ctctttttca	cttgtcttat	gtcgagagaa	aagggttattg	gcagnccat	540
tcctaanact	ggggaatgg	gtgtntcttt	naaatgtgaa	gataactttt	agggtaatta	600
tggaaactcc	tcaaangagg	ganaaagtna	tttttttcca	gacatttttc	ctcaattctg	660
ggtctttcac	acactanntt	tccatagtnc	nagaatttct	gnntttttac	catttgggct	720
gtgaaatgtt	cacaatntcn	ng				742

&lt;210&gt; 695

&lt;211&gt; 745

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 695

```

tttcaaatng cttggctact tgttcttttt gcagggatcc catcgattcg aattcggcac      60
gaggctagac gaagtgggtga agcccaaaga cttatttttg agctcgctgt aagactgaga     120
aatcacgtag tccttcctga aaccactaag aggaaaaatg tctgtgacac tgcatacaga     180
tgtagggtgat attaaaattg aagtcttctg tgagaggaca cccaaaacat gtgagatgga     240
gtctcgctgt gtcccccagg ctggagtaca atggcgcgat ctgggctcac tgcaacctcc     300
gcctcctggg ttcaagcaag tcttctgcct cagcctcccg agaactggaa gaggaggcaa     360
cagtatttgg ggcaagaagt ttgaggatga atacagtga tatcttaagc acaatgttag     420
aggtgttgta tctatggcta ataatggccc gaacaccaat ggatctcagt tcttcacac     480
ctatggcaaa cagccacatt tggacatgaa atacaccgta tttggaaagg taatagatgg     540
tctggaaact ctatgatgag tggagaaagt tgccagtaaa tgagaaagac ataccgacct     600
cttaatgatg tacacattaa gggccntaac tattcatgcc aaccatttg ctcatgagct     660
attgatngan ctggacaaat tactttgncc aaattgctng aacacacttt attgggggggt     720
taccocgntt ttaattatgt canaa                                     745

```

&lt;210&gt; 696

&lt;211&gt; 795

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 696

```

tttcaaatng cttggctant ngttcttttt gcaggatccc atcgattcga attcggcacg      60
aggctggcca aagccaaatc tcctaagtcc accgcccagg agggaaccct gaagcctgaa     120
ggagttaagg aggccaaaca tccagctgca gtctgcctcc aagaaggggt ccattggcct     180
agtcgagtcc atgtgggctc tggggaccat gactattgtg tccggagcag gacccccca     240
aaaaagatgc ctgccctagt cattccagag gtgggctccc gatggaatgt caagcgccat     300
caggacatca ccatcaaacc tgtcttgtcc ttggggccag ctgcccctcc gcccccatgc     360
atanctgcct cccgggagcc gcttgatcac aggactagca gtgagcaggc agatccctca     420
gcacctgcc ttgcccac cagcttctgt tcccctgagg cctnaccctg ccggaatgac     480
atnaacacta ggactncccc tgaacctca gccaaagcanc ggtcaatgcg ctgttaccgg     540
aaaaagcctg caggtcaagc cagcccctta agccagggtc tggcangggc ccgcnaagg     600
ccgnaacaag accgntctgt naactcttgg gttccaaacc cggaaacttg cccgaaagca     660
ttnttttccc ttaattcctt caattcaatc cggnttttcc ttaatttccn ggattcttng     720
ggtccaaggg tccccttttt tcccccccaa naacaaagaa aagggtgggc ccgaaanggt     780
cccaaccttn ttnnt                                           795

```

&lt;210&gt; 697

&lt;211&gt; 734

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 697

```

ctaatagctt ggctactcgt tctttntgca ggatcccatc gattcgcagc cctcttcctt      60
cccctgtcaa gtcacttacc atgcaaacca caggctctaa gagtttgtcc ccagggacat     120
ccatccaagt catctccatg gctcctgggt cccctgggtga gcatggagtc aggaggatcat     180
caatcatcat gctgggggtg gtgcgagagg ggccacagac ctgaaaccaa atggatctga     240
ctgggggcagc tgcccctcag tgtcagaggg gctcgacccc tccggtctct aaggaagtc     300

```

```

caaagagaat gctctgtggg tccctagcat ctgaggagga cgggctcctt cagaactcgg 360
gctgggtggt ccgagcgact catgatttgc atgggactct ggcaatctgt agccccaatg 420
ccttgatgtc ttccctatta acactgtcac gtctcaccag gaatacagtg acattaaaag 480
tgtgatatgg tntagctgtg cccccacca catttcaact tgaactgtat ctatctccca 540
gaattcccac atgttgtggg anggaccag ggggaggtaa ctgaatcatg gnggctgggc 600
ttttcccggt ctattctcgt gaatngtgaa ntttnacgag atctgatggg tttatcaggg 660
gttttccaat ttttggttct tatttttctn ttgcaatctg catttaagna antgcnttn 720
gtctctaac antn 734

```

&lt;210&gt; 698

&lt;211&gt; 728

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 698

```

ttcnaatngc tnggcttttn gttctctttg caggatccca tcgattcgaa ttccggcacga 60
ggtttaattt aaacctctca tcttttttta agcactcact gantttgacc gagacagcca 120
gtcgccgttg aggaatcctc tgttgtcaac atcgagaccc ctgggttttcg ggaaacccaa 180
tggtgatgca gttgattatc agaaacagct gaagcagatg attaaggatt tagccaaaga 240
aaaagataaa actgagaaaag aattgcccac aatgagccag agagaattta tccagttctg 300
taaaactctg tacagtatgt tccatgaaga tccagaagaa aatgatttgt atcaagccat 360
cgccacagtc accacactgc tgctgcagat cggggagggtg gggcagcgag gcagcagctc 420
tggaagctgc tcccaggagt gtggggagga gctgcgggct tcagctcctt ctcttgagga 480
ctcggttttt gcagacactg ggaagacgcc ccaggactcc caggcatttc cagaggcggc 540
agaaggggac tggactgtct cccttgaaca tattttagct tcacttctga ctgaacagtc 600
attagtcaac ttttttgaa aagccactgg acatgaaatc caaacttgaa aatgccaaaga 660
tcaatcagtn caatctcaaa cttttgaaat gaccncaatc caatctggac ntaagctgag 720
tacttgn 728

```

&lt;210&gt; 699

&lt;211&gt; 746

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 699

```

tttcaaaten cttggctntt ngttcttttt gcaggatccc atcgattoga attcggcacg 60
agggaaaaac aacaggtttg agtcctataa agccataatt taactccagt agctgatgtc 120
agacaagctt gtctatgtc ctatttgagt ggcagcagcg ccagcccagc agaaggctg 180
ggggttgta aggttgctcc cagaccttgc ttgcagtggg ttgagaacct agggggctgc 240
cttgggccct ctggccagag ggaagcgggc agctctagcc ctggagattg tggtcacatt 300
ggggcttggt taggattgga gggccaggtc acctccccag ccacctccc ttctctctc 360
tggggtcccc actttagggc gactttgccc gagccccgc atccatccac tcttttagtg 420
ccttgaatct cattcacaag cagccccctc ccttccccct cccttctcac tctgttgatg 480
taatcctncc acccccagtg tccatcctaa gacaggcatc aaaaagaggc cctaacttta 540
cttnccaaat ggtgcttttt aaaaaacacc atcactacat tangggcaat tttttcacac 600
cttctgtct tcagaatgta aaaggggtgg ggaattattg tctctgggta aatntgcacn 660
cccttgactt gtggggggtt tggggcatgt tcanntattt angaatgaat tncaattnga 720
caaaaggggg tttantnaat tgtnt 746

```

&lt;210&gt; 700

&lt;211&gt; 759



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 700

```

gntttgaaat ccctttgctt tnaaatcctt tgctanttgn tctttttgca ggatcccatc      60
gattcgaaatt cggcacgaga taaggggtggg gccttaattc agtagaattg gtggcctcct      120
aagcagagga agagagattt ttctttctct ctctgccatg tgaagacagt gaggagtctg      180
cogtctgcaa gccaagaaga gcccttatca ggaacagact tggctagcac cttcatcgtg      240
gacctccagc ctccagaatt gcaagaaaat acatttccgt cgttgaaacc acccagtctg      300
tgggtattttg ttatggcagc ccaggcagac taatacgtga agcctgctct aaatagataa      360
aataagaaat tactacagag ggctcttttag aaattgtatt taaaaacaag acaatccata      420
tttacctaag atttacagaa tgtatgtcta taaaaggagg gatttctgga ctagatgatg      480
atgaaaaatg ttcataataa ggcaccttca gcttcgagtt gccaacacag gaggaagaat      540
gctccctgct gttcagatgc tgatatgtgt cctgtgcttt ctggatggcc agtgggatca      600
taagctggta gaagccagaa ctttcatcca ctgacttcat attcttncac atnctggaac      660
tgtgggtgtt tgacctttta aaaaataaat ttaagcaaat tgaaatgntt tcctttgaga      720
nttttggcca naaaccaca tnganatttt ncgctctncc      759

```

&lt;210&gt; 701

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 701

```

gcttnnaatt ccnttccaaa gnaaaccctt tgnaaattnc cctttctgnt tggatcccat      60
ccgattcgaa ttcggcacga gggtaagtca ggtgattgaa tcccgggaant nttcattgtc      120
ttcaagctca caatactatt ttgggacaaa cagttgtcta gtgtttggac tcatagaacc      180
tgattcttga ggggtggtatt ttactgcttt tgtgatttgg tttcaacata tatagtcttt      240
tctccggagt taccttaggt cagtggccag tgtttcagcc cctggaaagg gcatgggctg      300
ccactgaggt tggtcacagg cctctcagct catggtggga gtgggttcag gatttggtaa      360
gtagggttca gttctgttgt tgccaccgat ggcaacaggg gtttgtaata atccctagtt      420
gtgtcaatta tgtcacttaa ttttcacaac aggtctctga agtgtttctc atctcathtt      480
tacagatgag gctgcctgt gttatacac ctagttagga gtggagctga atttgaatgc      540
aagccttggc accttaattg agcaagtttg aaacctcgct tgttgccctt ctggaaggag      600
tcangaattt ncagttcttg gcctgggctg tgggtctggc agacagacct ctggccctaa      660
ggtttgggtn ccangttctc tgttccaga atgagaagct ttgctgtgca ccaagnanct      720
gggcccctct ggnatctcnt gaatnaaaan n      751

```

&lt;210&gt; 702

&lt;211&gt; 748

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 702

```

gntttgaanc ccctttnttt naaatccttt gctacttgnt ctttttgag gatcccatcg      60
attcgaaatt cggcacgagc tgaatataaa gaggaggagg aagaccaaga catacaggga      120
gaaatcagtc atcctgatgg aaaggtggaa aaggtttata agaattgggtg ccgtgttata      180
ctgtttccca atggaactcg aaaggaagtg agtgacagatg ggaagaccat cactgtcact      240
ttctttaatg gtgacgtgaa gcaggtcagc ccagaccaa gagtgatcta ctactatgca      300
gctgccaga cactcacac gacatacccg gagggactgg aagtcttaca tttctcaagt      360
ggacaaatag aaaaacatta cccagatgga agaaaagaaa tcacgtttcc tgaccagact      420

```

gttaaaaaact tatttctga tggacaagaa gaaagcattt tcccagatgg tacaattgtc	480
agagtacaac gtgatggcaa caaactcata gagtttaata atggccaaag agaactacat	540
actgcccagt tcaagagacg ggaatcccag atggcactgt taaaaccgta tatgcaaacg	600
gtcatcaaga aacgaagtac agatccngtc ggataagagt taanggcaag gagggtaatg	660
tgctaattgga cccgaactgt gacgatcctc atgtgatcat gaagtaccag tactgacttt	720
ttatgttaaa aaatgtccat ttactgng	748

&lt;210&gt; 703

&lt;211&gt; 769

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 703

ggnnntnnna gnntttgaan tccctttnt tctaantcta ggcttctngt tctttttgca	60
ggatcccatc gattcgctca gctgaggcaa ttaactgga aaagaaatag attgaaaaga	120
tactacagaa gaagcagtac agaagtggg ggactgaagg agagggagcc actgcaggtg	180
ctagctgctt aaggggatac cagtcccttt acagatataa tagatacagc ttctgaggtg	240
gaggggtgata ggagtgtgta gagaaattgc agttcagaac tggagcatgc agttaggcaa	300
gaggcatccc atgtgaagat gtcaagcaag tactggaaaa tgctgaacta aaactcaggg	360
atggatatgt agatttagag aacttcattg tagaggcagt cattgaaagc taaaagggct	420
gataataaaa ttgccaagga tggaaatagt aagagggagt cagtgttatt aggattagaa	480
ttctgttttg tttttcttt aaacagattc tcgctctgtc accctggctg gagtgaagtg	540
gtgtgatctc ggctcactgc ggctcgacc tcccaggctc aagttatcct cccaactctc	600
agccttccaa gtagctggga ccacagccat tcaaacacat gcctgcctta tgtttggatt	660
tttttgtana aaccaaggtt ttgccatgtt tnccaggctg gnctnngaac ttctgggctt	720
aagccattcc cccacccttg ggtctcccaa aatgctngcc attatangg	769

&lt;210&gt; 704

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 704

cnaannncnn ggnttcnaat annaggctac ttgttctttt tgcaggatcc catcgattcg	60
aattcggcac gagaccgctc cggggccggc caatttgcat atttggaatg cgccgctata	120
aaccggctg gggttttgca gcgatttctt agatgtaaaa atgagatctc aatagcagcg	180
ggctgggcac atcctctcct ctctccttct ctctctgccc ggagctggtt tccgtctctc	240
ggctcggggc tggaactccg gcccaacctt ggcgcgcagc cgccacgaga tggcgcactt	300
ccgatcaatg tcaaagccgc cggggagccg ggaaccccag catgattctt ggcttttgtt	360
cgcttctgat actaagagca gcacgtaca ttatttctact tgtcccgctc cccttcataa	420
cagaaaaagg ggactcacc ccaagaagtg attggtatgg taatttaaag caacgcgcac	480
tcgctaggcc tcgcgagcgt cgccgcgcgg agaagccagc tgtcccttgg cagtgatttc	540
ggaaatgtgt caaggcaatt ccaaaggtga aaacgcagcc aactggctca cggcaaaaaga	600
gtggtcngaa aaaagcgctt gccccttaca cgaagcacca gacactggag ctggaagaan	660
ggagtttctg ttcaatatgt acccttactc gaaaagcggg gcctagagaa taaccgcgan	720
cgttccacct taacggacag gacaagtga aaaatcttg	759

&lt;210&gt; 705

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 705

tttgaaatcc	cntttnttna	aatcctttgc	tncttgttct	ttttgcagga	tcccatcgat	60
tcgtcctgaa	gctcgggggg	ctgcagggtcc	tgaggaccct	ggtgcaggag	aagggcacgg	120
aggtgctcgc	cgtgcgcgtg	gtcacactgc	tctacgacct	ggtcacggag	aagatgttcg	180
ccgaggagga	ggctgagctg	accaggaga	tgccccaga	gaagctgcag	cagtatcgcc	240
aggtacacct	cctgccaggc	ctgtgggaac	agggctggtg	cgagatcacg	gccacacctcc	300
tggcgctgcc	cgagcatgat	gcccgtgaga	aggtgtgca	gacactgggc	gtcctcctga	360
ccacctgccg	ggaccgctac	cgtcaggacc	cccagctcgg	caggacactg	gccagcctgc	420
aggctgagta	ccagggtgctg	gccagcctgg	agctgcagga	tggtgaggac	gagggctact	480
tccaggagct	actgggctct	gtcaacagct	tgctgaagga	gctgagatga	ggccccacac	540
cangactgga	ctgggatgcc	cgctagtga	gcttgaaagg	tgccaaccgt	gggttgggct	600
ttcttaagca	tggaggacat	ttttggcaat	gcttggtttt	gggccattta	aatgggaaac	660
cttgaaggc	caaaaaaaaa	aaaaaantna	tnnaaaaaan	aaacttnnac	cttttaaaac	720
ttttaantgn	ngnccgnttt	tacnttanat	tccagacttg	attaggaatc	cattttt	777

&lt;210&gt; 706

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 706

gntttgaaat	nccnttnntt	caaatnctng	gctacttggt	ctttttgcag	gatcccatcg	60
attcgaattc	ggcacgagna	atgcaaagg	ctgcagttct	cattcaggct	actttcagga	120
tgcacagaac	atatattaca	tttcagactt	ggaaacatgc	ttcaattcta	attcagcaac	180
attatcgaac	atatagagct	gcaaaattgc	aaagagaaaa	ttatatcaga	caatggcatt	240
ctgctgtggt	tattcaggct	gcatataaag	gaatgaaagc	aagacaactt	ttaagggaaa	300
aacacaaaagc	ttctattgta	atacaaggca	cctacagaat	gtataggcag	tattgtttct	360
acaaaaagct	tcagtgggct	acaaaaatca	tacaagaaaa	atatagagca	aataaaaaaga	420
aacagaaagt	atttcaacac	aatgaactta	agaaagagac	ttgtgttcag	gcagggtttc	480
aggacatgaa	cataaaaaaa	cagattcagg	aacagcacca	ggctgccatt	attattcaga	540
agcattgtaa	agccttttaa	ataaggaagc	attatctcca	cattagagca	acagtagttt	600
ctattcaaag	aagatacaga	aaactaactg	cagtgcgtcc	ccaacaagtt	atttgtatac	660
agtcttatta	cagangcttt	aaagttccaa	aaggatattc	aaaaatatgc	caccgggctt	720
gccacactta	attcagncat	tctatcnaat	gccccagggc			760

&lt;210&gt; 707

&lt;211&gt; 856

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 707

ggtgctttga	agcctttgaa	atnctttggt	tnaaatnctt	ggctttngnt	ctntttgcag	60
gatcccatcg	attcgcctcc	ctggatgtgc	agacatggag	gaggacagaa	ggcccagctc	120
agtggccccc	gctccccacc	ccccacgcc	gaacagcagg	ggcagagcag	tctggaggtg	180
gtgntccac	ttgatgaaga	gcaggcgact	ggnttgagga	gggagatcat	gctggctgna	240
aagaanggac	tggaccata	caatgtactg	gccncaaagg	gancttcagg	caccagnгаа	300
gacccaaant	tantncccta	catntccaac	aagagaatag	naagctgcac	ntgtgaanag	360
gacaatacca	gcntcnantg	gttttggttn	nacaaangcc	angnccancn	atgccccnn	420
tttgnaaccc	attacaantc	gntgccccan	tagctggcac	actgancncc	tnntctaaat	480
tacttaaaat	natgctgtan	aagtatannt	tttncagaan	agactaanca	ntncatngnc	540
tacttctcca	aaaaaaantg	anaaaaaatna	taaaantcaa	antaaatact	aaatnannan	600

ataananan	tannaantta	tatttcnnan	atantanann	nancnnttta	naannantta	660
nggnnancan	nnattantnn	tnnatanttt	acattaaant	tattnanann	anaaaannan	720
nananannat	atattannan	anantnacnt	aaactnnnt	naatnntcca	nanacttnaa	780
naanaataag	nnntanatna	nnnnttangn	ntnatatann	ttnanatann	nnnnacnata	840
nnacatnnnn	tannga					856

&lt;210&gt; 708

&lt;211&gt; 766

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 708

ctaatactgg	ctacttggtc	tttcnaagcn	ctggnnnttn	annnatnnag	ctacttggtc	60
tttttgcagg	acccatcgat	tcgcccacac	ttatcggggg	tgccagaggc	agagtagaca	120
agccttagtg	gcccgcattt	gttgaatata	tactgtgcgc	caagcagtg	gtcacaactt	180
tatgaagtag	gtattattat	catccccatt	ttacaggtga	agaaactgag	tctctgagag	240
accaactttt	ccaaggtcac	acagaggtgg	gatccagccc	acttccgtct	gaccccaagc	300
ccctgctggt	aacccctgcc	ccattgtggg	gaggttccgg	cccactctgg	agttctctgg	360
tctgcgtcag	tcctcaggag	aagaaagaat	gggggtgatg	ctccaaatat	tgaggctccc	420
atctgtctgt	cctgcactag	gcagagccag	gcttctccat	ggggcacagg	agagagggca	480
ccagatctga	ggagcaaata	ggttcttggt	ctgagatctc	atgggatcag	gttgccagcc	540
ctgcaaacc	ccgctcangt	ctagaggaca	tggagctgcc	tttcaagggt	catttgcttc	600
ctttacagac	tcggactctg	tnctctggct	actttggggc	gtcccggact	cgggaatgcy	660
tnctacactt	gtaggggcaa	aaccccggtt	tgactctttc	cgggttccta	cccttaacca	720
agcctttact	ttctngggat	caccctgttg	ggactttttg	tccacc		766

&lt;210&gt; 709

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 709

gaannccntt	nnnttgcaaa	tnntnggcta	cttgttcttt	ttgcaggatc	ccatcgattc	60
gaattcggca	cgaggttttt	tttttttttt	tttgagagaat	gaatgcaaga	tttattgagt	120
ggtggaagta	gctctcagca	gatggctggg	gagccagaag	ggggatagca	tggaaggtta	180
gtcttctct	ggagtctggc	tgctcagcag	ccgggatctc	ctactgtcct	tgcccggaatt	240
tcccttggcg	tcgaatcgt	tcaccatca	atggcctgcc	agcgtctttc	gatgtgttct	300
tctgccagt	tggtctctt	gacgtccagc	cgcttggtg	tgtgcccgct	gggtctcag	360
ggtttttata	ggcacagaat	gggtggcatg	gcaggccaga	gtggtcttgg	aaaatgcaac	420
atttgggcaa	gaagacagga	gtccttggtc	tcattaggtc	catgggcaca	agcctgaggg	480
tggaagccct	gccagtgacc	ctgcccttct	ctaccagca	cttccctgtc	cccctcccat	540
atcaccgttg	ccatcttgtc	cttgatgagg	aatacaactc	ccaattcagt	gnttgcttgt	600
gggaagatgc	aatcctcttt	atgacaagtt	tctaanaagt	tgataagaaa	aatggggacc	660
tgcttaaggg	ctagtatctc	atttaatact	ctatagaata	ttatngggtt	ttccctttta	720
ngttttaaat	gttgaananc	nan				743

&lt;210&gt; 710

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 710

```

gnnnnnnnnn nagngttga antcctcctt ngaaatcctt tggcnactcg ctctttntgc      60
aggatcccat cgattcgaat tcggcacgag gggcaatgca gttataatac tgtgttaatt      120
tcagacatct tctggtcctc cgagccttgt atttacatac tagctgaaac tgcaagtgga      180
aatgaatgga gctgatgata tttgccttat cctaattttt ctgtgaggag gagaaaaaca      240
cttgtgcttc aaataagcag atgtgaaaac acttctcact aatcaaatg tttaccacta      300
ggttatgaga gtctgcctct cataggcagt gaatctgata tgtatactta gtaatataag      360
tctatttagt ttgacaaaac cttagagcag aatttttgca gcttagttca ggatgatcac      420
tagcaatgcc aaacttcatt ttttattgaa cttggatcca agaaggcctg ctgtgtctat      480
ttcagtatag actctcatac caatatatatt atgctccaag tctactacacc cagaagtgat      540
gcagtggggg aaatgcaaag acaacatcac tgtaagattc acagaatgga tcttttgtaa      600
aatattttat attgacttaa ggaaaacctt tcattgggaa ttaattaaat taagtctcta      660
atatcctgga agacagtaaa aantnaagcn ggtgntctca antttgaacc cggcnattng      720
naatttcatt ataggaattt ctgaaaataa tcc                                     753

```

&lt;210&gt; 711

&lt;211&gt; 718

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 711

```

naatngctag gctacttggt ctttttgtag gatcccatcg attcgaattc ggcacgagcc      60
tacttattgg atgttggtct tttggtgtca tggagatggc tttactgtag gtttgttgtg      120
ttgcattact tttcattggg attgaactga gaaataacaa acaagcttta agtgggaaat      180
taaaaaaaag aagtaacctt ttagatcca aacttaaaat gtgagaaatt attgaaattt      240
cattttctac aaacttgaat ttagcctgct aattgtaaaag ttgttttaat aatgctgaca      300
aatgtcagtt acgtttgcaa aggagtgtat ggttctaggt atttgcctac tgtaaccgt      360
tgagaaaaac attgtcaggt tagcaagtct attgaaatag agacctcctt agtttacagc      420
aaagaataaa tagctgatga ctggagattg ggactaaggt tttattttatt tatattcttt      480
gaaagaaatc ggacagttaa taagtgggtt gtggttagagt tgaaggatgt ctgagagatg      540
gaaagagagt gacaaaggag gagaaggaat agtatttctt ttttagtatt gntttgaaat      600
taaaactctg ntattttaat atggtaaaga gcaagaattt ggggtggggc gcngtgactc      660
acgcctataa tcccagcact ttgggaagcc ntggtgggca aatcacctga aattangg      718

```

&lt;210&gt; 712

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 712

```

agttgaantn cttgctacnn aaaacctttg gcnactngct ctttntgnag gatcccatcg      60
attcgcaaag atggtcgtat tactaaagggt gaataaccag cgcggnnngc acgtggagtc      120
actggaacat ttgtgcaatg ctggtgggaa tgtcaaccog tgcggccctc tggaataagc      180
ctggcagctc ctccaagagt taccngtgta cccancaatt cactcctag ctccaccac      240
aggaattgaa agcaaanacg caaacagatg cctgtncacc aaagtccacg gcagcatnct      300
tcgncatagt ggcagcatcc gtcgtcacag cggcatcatc cttcatcata gcggcagcat      360
ccgtcgtcac aagcggcagc atccttcgcc acagnggcan gcatctgtcg tcacancggn      420
agcatccttc gacaaagcgg cagcatnctt cgtnatagcn gcagcatcct ttgccatanc      480
cggcaagggt gaaacctgt ccatccactg aggcgtgcat agactaaaca tgggcagtcc      540
agcactggaa ttccaagcgg tacaacggng nccacngtca aaaangaatg aggaccctga      600
ngcacctgng cnganaacaa gaacnngcga nccaanact ttnagacat tattgcctta      660

```

agtngaaaaa cccagngcac caacgggaaa ccngaccgnc ntgnanccct gnttaacntt 720  
 nantnngttn cccgaaaatg ggggcacntt nccaaaaagg ggaataaaaag gggagaattn 780  
 cct 783

<210> 713  
 <211> 765  
 <212> DNA  
 <213> Homo sapiens

<400> 713  
 gttgaantcc ttcctttcaa atngcttggc tactcgntct ntntgcagga tcccatcgat 60  
 tcgaattcgg cagcagccca catgtaccag gttgagtttg aagatggatc ccagatagca 120  
 atgaagagag aggacatcta cacttttagat gaagagttac ccaagagagt gaaagctcga 180  
 ttttccacag cctctgacat gcgatttgaa gacacgtttt atggagcaga cattatccaa 240  
 ggggagagaa agagacaaaag agtgctgagc tccaggttta agaatagaata tgtggccgac 300  
 cctgtatacc gcactttttt gaagagctct tccagaaga agtgccagaa gagacagtag 360  
 tctgcataca tcgctgcagg ccacagagca gcttgggttg gaagagagaa gatgaaggga 420  
 catccttggg gctgtgccgt gagttttgct ggcatangtg acaggggttg tctctgacag 480  
 tggtaaatcg ggtttccaga gtttggtcac caaaaataca aaatacaccc aatgaatttg 540  
 acgcagcaat ctgaaatcat ctctagtctt gctttccttg tgagcagttg tctttctatg 600  
 atcccccagg aagtttttct aaagtnaaaa ggaaaattcc tagtggaatt cancccccaa 660  
 gggaaaaaag ccacttgnc cacannagga agccnggntn ccccttngtt ccggcttaan 720  
 ggccccctgt tcaggaaacc acactggggg ancttntttt ttttn 765

<210> 714  
 <211> 740  
 <212> DNA  
 <213> Homo sapiens

<400> 714  
 gtttgaannc cttngntttc naatgctnng ctacttgctt tttntgcagg atcccatcga 60  
 ttccgcaaaa gcttgtggca aatttgaaat ttctgccatt agggacctta caactggcta 120  
 tgatgatagc caacctgata aaaaagctgt tcttcccact agtaaaagca gccaaatgat 180  
 caccttcacc tttgctaatt gaggcgtggc caccatgcgc accagtggga cagagcccaa 240  
 aatcaagtac tatgcagagc tgtgtgcccc acctgggaac agtgatcctg agcagctgaa 300  
 gaaggaactg aatgaactgg tcagtgtctat tgaagaacat tttttccagc cacagaagta 360  
 caatctgcag ccaaaagcag actaaaatag tccagccttg ggtatacttg catttaccta 420  
 caattaagct gggtttaact tgtaagcaa tatttttaag ggccaaatga ttcaaaacat 480  
 cacaggtatt tatgtgtttt acaaagacct acattcctca ttgtttcatg tttgaccttt 540  
 aaggtgaaaa aagaaaatgg ccaaaccxaa caaactaaca ttcctactaa aaagttgagc 600  
 ttggacatat tttgaatttt tgtaagttaa agatttttaa actgactaac ttaaaaaaat 660  
 agattgtaat tgatgtgcct taatttgcac aaatcataaa tgtatgtcct ctctgtaatt 720  
 ggttaaatgt gtgcttgaan 740

<210> 715  
 <211> 708  
 <212> DNA  
 <213> Homo sapiens

<400> 715  
 ttggcaaatn gcttggctac ttgttctttt tgcaggatcc catcgattcg aattcggcac 60

gagggaggct	agactcaagc	tgtctggaga	gtgtgaaaca	aaagtgtgtg	aagagttgta	120
actgtgtgac	tgagcttgat	ggccaagttg	aaaatcttca	tttggatctg	tgtgccttg	180
ctggtaacca	ggaagacctt	agtaaggact	ctctaggctc	taccaaataca	agcaaaattg	240
aaggagctgg	taccagtatc	tcagagcctc	cgtctcctat	cagtcctgat	gcttcagaaa	300
gctgtggaac	gctacctctt	cctttgagac	cctgtggaga	agggctctgaa	atggtaggca	360
aagagaatag	ttccccagag	aataaaaact	ggttgttggc	catggcagcc	aaacggaagg	420
ctgagaatcc	atctccacga	agtccgtcat	cccagacacc	caattccagg	agacagagcg	480
gaaagacatt	gccaaagccc	gtcaccatca	cgcccagctc	catgaggaaa	atctgcacat	540
acttccatag	aaagtcccag	gaggacttct	gtggctctga	cactcaacag	aattatagat	600
tctaacttga	tgagttactg	agctttggtc	ccttaaaaca	agctgacttg	gtccctaaac	660
cagatgaaaa	tccagatgct	ctatacttgg	ccttaagaac	tgctttcn		708

&lt;210&gt; 716

&lt;211&gt; 730

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 716

ttgcaaatng	ctnggctact	tgttcttttt	gcaggatccc	atcgattcgc	tcccatggag	60
gtggtgggaa	tgccaccgag	aagtttgatg	acagttatct	aatggactag	aggttggcaa	120
actttctgta	aatggccagg	tagtaaatag	ttctgctttt	gaaggcataat	ggtctcttgc	180
acctactcga	ggctgaaagc	agctatagac	aatacataaa	tgaatgagcg	tgagtgtgtt	240
ccaataagaa	aaaaacatgg	ctgtttgctt	cggccccagg	gtttagctt	accagtccctg	300
taacagatca	cagtttgctc	ttttggtcac	aaataacttga	acccctccct	agttcagagc	360
atttgatacc	gtaatattta	aagctcactt	gtaaaacatc	gtttgttgcc	tccatccata	420
gtatctcaaa	cagaatgtct	ctcccaaata	tacctaaatt	ccatattctc	tgaagcaciaa	480
ccagctattt	tcttgacata	cttccctaaca	cacccacag	ttcacaattt	gatctgaaaa	540
cttgtaagg	gaggttcttt	ggcatgtgat	gccataaaaa	gagaggtatg	ggctctcctt	600
taaaaaagag	acccttttta	tgagactcac	aataggataa	aagagcccat	gcctattttt	660
aaacattttt	ttcactatat	aagacatgca	tgcttgnaaa	atgggttttta	attagtatna	720
ntgcttaatn						730

&lt;210&gt; 717

&lt;211&gt; 728

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 717

naatngctng	gctcttgctt	tttttgcagg	atccctcgat	tcgctgcagt	gagattctct	60
gcaatgactg	gcctcagcaa	gggggcagct	taggaccctg	acatcccagg	tcactaagcc	120
acataggata	agtaatgggt	ggacagaagc	gggaaaggag	aagggcaggg	cacatgttta	180
aaacttgaac	tttctgaggc	taagactgga	aaaggaatgg	tttcagctga	tatatattgga	240
taccagttag	ctatttttag	gaaaaaaaca	caaattggctt	ttaaacatca	cagtgtgata	300
cagtctaact	cagaattaga	gacaggcaaa	acagaactcc	atcttaaaaa	ataaataaat	360
aaaataaaaat	aaatgacatc	actttggctt	agagctctaa	aatggaggga	ggaagccatt	420
ctaaaaagga	ctccctacat	gacctgcaac	ttgaaaaaaa	attaaaagct	ccaaaaaaaa	480
caatncagga	gcttaccttg	aaccttttga	attggggcaa	attgccgatg	accactgcat	540
cctggaaaat	tttattttcac	cagcactaca	acttctcaac	agcaccaacc	aatttaacta	600
tggtattttg	tactaanccc	agttgcctct	ttnaaaacaa	cctgtcaact	ttgtctaact	660
accctcagct	tttttttaaa	aaccctnct	ctacccctnt	ctcttcagaa	caccaaagtg	720
gncttttn						728

<210> 718  
 <211> 730  
 <212> DNA  
 <213> Homo sapiens

<400> 718  
 gaantccttn nntttnaaat cnttggtac ttgtttcttt tgcaggatcc catcgattcg 60  
 aattcggcac gatctagata ttgccaatc gctgccaca gtgcacatac ctttccacca 120  
 gtcacatgtg agagggcaga ttttccaaat gctcatcacc acttggcact gtgtggacta 180  
 taattttggc cagttaggaa atggcatctc attgttttca tcttaatttg cgtcagcctg 240  
 attactcatt gaaacttgtg aggttgagaa acttttctta agcttatttg ccattcaagt 300  
 ttccctcttt atgaaatggt tgttcatgtc atttgctcat ttttatatta gattgttttt 360  
 cttttttcca gctgacttgt aggaactcta catcttatca atattaatca tttatcgaaa 420  
 actatttggg tgccattatc ttctcctagt caatgttttt tgtttgtgat atcttttata 480  
 atatataagt ttttaagtgt ggcagaagta aagttaatct ttttggctgt gttgtgtgtc 540  
 ttgtttgatg taaagatagt ttctgtaata gttttgcagt ttgattggtc atcttttaggt 600  
 cttcaattac aacctgcaca ttcacccctc tatcctcttt cttactctgg ttttctccat 660  
 agcacttatc atccaataat atggcatgca cttatttaat ctggtttgca tatatatattt 720  
 ngctggtacg 730

<210> 719  
 <211> 733  
 <212> DNA  
 <213> Homo sapiens

<400> 719  
 ttcaaactgc ttggctactt gttctttntg caggatccct cgattcgctt cagtgcacac 60  
 aacaggagag aggagaaaga agaaacgcta gtaattccaa gcactggaat taagttgcct 120  
 tcatcagtgt ttgcttcaga gtttgaggaa gatgttggat tgttaaataa agcagctcca 180  
 gtttcaggac ctgactgga ttttgatcct gacattgttg cagctcttga tgatgatttt 240  
 gactttgatg atccagataa ttctgcttga ggatgacttt attcttcagg ccaataaggc 300  
 aacaggagag gaagaggga tggatataca gaaatctgag aatgaagatg acagcgagtg 360  
 ggaagatgtg gatgatgaga agggagatag caatgatgac tatgactctg caggcctatt 420  
 gtcagatgaa gactgtatgt ctgtgcccg aaaaactcac agagctatag cagatcactt 480  
 gttctggagt gaggaaacaa agagtcgctt cacggagtat tcgatgactt nctcagtcac 540  
 gaggagaaat gaacagcttg accctacatg atgagangtt tgagaaagtt ttatgagcca 600  
 tattgatgat gatgaaattg ggagctctgg ataatgccag aatttggaaa ggttctatc 660  
 aagtgggaca gcaattcgct ttcnaggaag ttttgaatga ctactattaa agagaangcc 720  
 caanaattnt ntt 733

<210> 720  
 <211> 740  
 <212> DNA  
 <213> Homo sapiens

<400> 720  
 agttnnnttn ntncntttca aatccttggc tacttgntct ttttgcagga tcccatcgat 60  
 tcgaattcgg caggagaaga gaaggaccta gagattgaga ggcttaagac gaagcaaaaa 120  
 gaactggagg ccaagatgtt ggcccagaag gctgaggaaa aggagaacca ttgtcccaca 180  
 atgctccggc ccctttcaca tcgcacagtc acaggggcaa agccctgaa aaaggctgtg 240  
 gtgatgcccc tacagcta atcaggagcag gcagcatccc caaatgccga gatccacatc 300



```

ctgaagaata aaggccggaa gagaaagctg gagtccctgg atgccctaga gcctgaggag 360
aaggctgagg actgctggga gctacagatc agcccgagc tactggctca tgggcgcca 420
aaaatactgg atctgctgaa cgaaggctca gcccgagatc tccgcagtct tcaacgcatt 480
ggcccgaaga aggccagct aatcgtgggc tggcgggagc ttcacggncc cttcaccagg 540
tgaggacct ggaacgcntg gagggcataa cngggaaaca gatggagtcc tttctgaagg 600
caaacattct gggctctcggc ggccgccanc gctntggcgc cttctgaccg tcgctnctac 660
ttncgntttt tcaaattttt ggnataaccc ccgtgtttgn gtaaaatcca gtttttgttc 720
cgntaaaaaa aaaaaaaat 740

```

&lt;210&gt; 721

&lt;211&gt; 736

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 721

```

nnttnnttt tnnaaatccc ttggctactt gttctttttg cagggatccc atcgattcgc 60
atgagtgata ttttggctct ggtttcctct taagatttta gtttgtctga attaaggaaa 120
aatgttttta atatacatc ttattttctc ccccccctcc agaaataagc tggaaatctt 180
aacttttttg ggggtctttt ttggtgtttt aatgggcccc gaactgtggt ttaaattttt 240
atgtatgtat tttctttttt gtggagtata aatttaaaaa ctggatttgg gacctaaaat 300
actcctcagg ttgatgtatt catgaagttt taaaacatct ttagttttca aagtaaacgt 360
gatatgtgga ccttaaagtt attgagttta agctacaaat tgtaacgtca ttactggaca 420
tgtcagcatc aaccctctca aaatagcttg gtcactttat gaaggggctt ttaaagttg 480
ttgttttagc gtgacattta atatggtcca attgcttttc tttttaacgt gacaaaaaga 540
gaataaggaa caaacactat tgctgccgaa tgccataaca ctgagttgtc aaattgtgat 600
tgaggaaatg aaaaggttta tactttttta aaaaaaaaaa cnnaanccaa aaaacccaaa 660
cttcaaattg aataaattat tcatgaagcc cttaaaaaaa aaaaaaaaaa aactcgaacc 720
tntaaactn tngngg 736

```

&lt;210&gt; 722

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 722

```

attnccttgg cttttcaaat ccttggttac tngttctttn tgcaggatcc catcgattcg 60
aattcggcac gagattatag agattaatct cctttgctcg aagtctatct aaatattagt 120
cacatctaaa acatactttt acagcaacat ctgactgggt gtttgacca acaactgggc 180
atcatagctg acacataaaa ttaaccatca caaccatgtt ctaggcactg ttctcactg 240
cctgagaaga caccgttatg tttattaggg tttttgagtt ttatccacag cttttggtta 300
tctgcaacca tgtctccac cattaacata gttcacactg agatgaggat tccctattta 360
acacttggtc ccaacttctt cacagtccat ctggttttgt agagggaaca taactggaca 420
ttctggtcag gttaggtgag gtcaggcctt caggacgcta ttttactga gttgctttat 480
aaggcacatt atgcaaaatt ccatcagctc ttctgttcac tacattcact gttgaaatc 540
taagagtgag actgctgtct cacaccaaag ccagtgggta ctatcttcag taggcacgca 600
gcatcatgtt tgtatttgat ccantagat gacatgtaag agaaaacttt attgnggact 660
ctgtaaagtg tgacattcgt ttgtgactca atttgtcat gtatttggtc ctggggagtc 720
attacatagc taactttcag ctgctttcaa t 751

```

&lt;210&gt; 723

&lt;211&gt; 749

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 723

tttaatncc	ttcnntaatc	cttngtttcn	ngcnctttnt	gcaggatccc	atcgattcga	60
tgctagccaa	agcctgctgc	cagctccata	gcctggacct	acagcactcc	atgggtggagt	120
ccacagctgt	ggtgagcttc	ttggaggagg	caggggtccc	aatgcgcaag	ttgtggctga	180
cctacagctc	ccagacgaca	gccatcctgg	gcgcactgct	gggcagctgc	tgccccccagc	240
tccaggtcct	ggaggtgagc	accggcatca	accgtaatag	cattccccctt	cagctgcctg	300
tcgaggctct	gcanaaaggc	tgccctcagc	tccagcctgg	accttgcccc	caggtgctgc	360
ggctgttgaa	cctgatgtgg	ctgcccgaagc	ctccgggacg	aggggtggct	cccggaccag	420
gcttcctagc	ctagaggagc	tctgcctgnc	gagctcaacc	tgcaactttg	tgagcaacga	480
ggtcctnggc	cgntactcc	acggctctcc	caacctgcgc	ttactggatc	ttcgtggctg	540
tgncgcac	acgcccggctg	gccttcagga	tctgccatgt	cgggagctgg	agcagcttca	600
tctgggcctg	tatggcacgt	cagaccggct	gactttttacc	aangagggca	agnccctttt	660
gaccagaant	ggtgcataca	ctgcgaagaa	ctggactttg	aatggccaag	ggttcaattg	720
agaaagacct	ggaacangcc	cttgctnct				749

&lt;210&gt; 724

&lt;211&gt; 761

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 724

ttnnnnccct	ttttaatncc	ttctactaat	ccttggtctct	cgntctttct	gcaggatccc	60
atcgattcga	attcggcacg	agcctcagcc	ttctaaaaag	ctgggggtctac	acccagctga	120
agaaattgta	actaaagata	gattgtttta	agcaaagcaa	gaaacttctg	aagaaatgga	180
acaaagtgga	gaagcctcag	gaaagcccaa	cagagagtgt	gcaccccaga	ttccttgtag	240
tactcctatt	gctactgaaa	ggacagttgc	acatttgaac	actctgaagg	accgtcaccc	300
aggtgatttg	tgggcccgc	tgacatctc	atccctggaa	tatgctgcan	gagacattac	360
ccgaaaaggg	agaaaaaaag	acaaagctcg	agtgagtga	ctgctccaag	gcctctcatt	420
ctctgggtgac	tcagatgtgg	aaaaagataa	tgagcctgag	atccagcctg	ctcaaaaagaa	480
gttaaaggta	tcattgtttcc	cagaaaagag	ttggaccaa	agagacatta	aacccaattt	540
tccaagctgg	tcagcactgg	attctggact	tttgaatctc	aagagcgaaa	agtttgaacc	600
cagtagagct	ttttgaatta	ttttttgatg	atgaaacatt	caacttaatt	gtcaatgaaa	660
ccnataatta	tgcttctcag	aaaaatgtca	gctttggaag	tccagttcag	gaaaaaaaaan	720
nnnnannaaa	aaactcgagc	ctntanaact	atngtgagtc	c		761

&lt;210&gt; 725

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 725

tttcncccn	tttttanccc	cttnctctaa	tccttggnct	tngttctttt	tcaggatcc	60
catcgattcg	aattcggcac	gaggcggact	ctcaggacga	aaagagtcaa	acctttttgg	120
gaanttcaga	ggaagtaact	ggaaagcaag	aagatcatgg	tataaaggag	aaaggggtcc	180
cagtcagcgg	gcaggaggcg	aaagagccag	agagtgggga	tgggggcagg	ctgggggcag	240
tgggaagagc	gaggagcagg	gaagaggaga	atgagcatca	tgggccttca	atgcccgcctc	300
tgatagcccc	tgaggactct	cctcactgtg	acctgtttcc	aggtgcctca	tatctcgtga	360
ctcagattcc	cgggactcag	acagagtcca	gggctgagga	actgtccccc	gcagctctgt	420

ctcccttgct agagcccatc agatgctctc accagcccat ttctctactg ggctcctttt	480
tgactgagga gtcacctgac aaggaaaaac ttctatcagt actttgatat gtcacagttt	540
catgtttatc cagttcaatg tattttttaa ttttcccttg agacttcttt gactgataga	600
ttattgtgaa gtgtgttttt aaatttncaa atgtttangg attttcatat ctttcttatg	660
ctgatttcca attggattcc ttacaatgat ttttgggttt catctgctct tggatgatta	720
ctatctcttt taaatttggt gtggccaagt tttagggccn	760

&lt;210&gt; 726

&lt;211&gt; 741

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 726

ttntgcctt tgnntnatcc ttgntcttgc ctttttgcag gatcccatcg attcgaattc	60
ggcacgagac aagttctatt gagtgtctatt cagaatagga acaaggttct aatagaaaaa	120
gatggcaatt tgaagtagct ataaaattag actaatctac attgcttttc tcctgcagag	180
tctaatacct tttatgcttt gataattagc agtttgtcta cttggctact aggaatgaaa	240
ctacatggta ataggcttaa caggtgtaat agccactta ctctgaatc tttaaacatt	300
tgtgcatttg aaaaatgctt ttgcgcatct tcctgctggg attacaggca tgagccactg	360
tgccctgacct cccatagtga aaagtgtcta aaggtttttt ttgggtataa aaggaaaatt	420
tttgcttaag tttgaaggat aggtaaaatt aaaggacatg ctttctgttt gtgtgatggg	480
ttttaaaatt tttttttaag atggagttct tgttgcccag gctagaatgc aatggcaaaa	540
tctcactgca atctcctcct catgggttca agcaattctc ctacttcagc ctcccaagta	600
gctgggatta caggcatgtg ctaatttggt gtttttaata gagatgaggg ttttccatgt	660
tggtcangct ggtctcaaac tcctgcctta ngtgatcgcc tcggcctnct aaagtgctgg	720
aattcaggca tgaancncca t	741

&lt;210&gt; 727

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 727

ccttcttccn aangctntgt tgaancnctt tcnnnatcgc gcttgcgctt tgagctagga	60
taaaaattgg gtaaaggagc atttgcttac ctgnntnatg aatcactntt tgaaatgtga	120
tcttgccata tcatcaagaa acttgttttc tggatgaata ctgggagaat aaaaagagaa	180
ctctggagtg agctaaattg atcccaatna agtttttctg cttagcagac agaaggata	240
attntttgac accctttccc acctggtgcc tatgctaggc ttgtcctgan aacatncctc	300
agtaacttga tattcacatg acctacagga tgtcccatct gcagggtga gtcagttggg	360
gaacaccaga ggctacacag tagctattcc tgctactcgg ttaatgagct tggcaggttc	420
tttgtctcac tgaattctta tcatggaaac agcagcagca gccgctagga aatcttcaag	480
tgtagnggcc tgtgctaacc cagtggtaaa tcccttagat cccctgctgg tctctggcaa	540
aactccttga tnttgggtac catgtatant ttgcctttga cntttaacgc tttctacgat	600
anggtaanca cncntttaat ttangenctg gancattaac tttctttgca aaggctactt	660
atngccngnc acaantgcag cctcggacan ancnnangnn atatcctgtt ggccatggct	720
ntgatgtttg acanccgata ngccttctnc g	751

&lt;210&gt; 728

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 728

tngnnntttnt	ttaacnttgt	ttgacgcctt	tctgcaggat	ccctcgattc	gcactggcta	60
cctgcagatt	gcagagcggc	gagagcccat	aggcagcatg	tcacccatgg	aagtgaacgt	120
ggacatgctg	gagcagatgg	acctgatgga	catatcggac	cangaggccc	tggacgtctt	180
cctgaactct	ggaggagaag	agaacactgt	gctgtccccc	gccttagggc	ctgaatccag	240
tacctgtcac	aatganatta	ccctccaggt	tccaaatncc	tcagaattaa	gagccaancc	300
nccttcttnt	tcctncacct	gcaccgactn	ggncacceng	nacatcanng	agggtgggga	360
gtncncnnt	gttcagtccg	atgaggagga	anttcangtg	gacactgncc	tgncacatn	420
acacactnac	agagangcca	ctcnnngatg	tgntnangac	agcaactntt	aaattgggac	480
atgggcgtn	tntggccaca	ctggaatcca	nntttggctg	tatgcggaat	ttcacctgcn	540
aagccaggtt	nnttnataga	cgttcttgat	tattacataa	ttgccaatca	tgtggtgagn	600
aacttgtgng	aacantttta	caattaantg	tgaagaccgt	acaangaatt	agttaaangc	660
natnagggc	taaacaagct	attacttntg	annnaantta	angnatntaa	nnttttctgn	720
ttctnaaaat	nttcaatntn	nngggaacan	ttgtaanttt	nnent		765

&lt;210&gt; 729

&lt;211&gt; 743

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 729

tannntttnc	tntannnttt	ctgangccct	tntgcaggat	cccatcgatt	cgaattcggc	60
acgaggagat	ctctgggatg	tcagtgaggc	tggttgaaga	ccagaggtta	actgcagagg	120
tcaccacccc	caccatgtcc	caggtgatgt	ccagcccact	gctggcagga	ggccatgctg	180
tcagcttggc	gccttgtgat	gagcccagga	ggaccctgca	cccagcacc	agccccagcc	240
tgccaccca	gtgttcttac	tacaccacgg	aaggctgggg	agcccaggcc	ctgatggccc	300
ccgtgccctg	catggggccc	cctggccgac	tccagcaagc	cccacaggtg	gaggccaaag	360
ccacctgctt	cctgccgtcc	cctggtgaga	aggccttggg	gaccccagag	gaccttgact	420
cctacattga	cttctcactg	gagagcctca	atcagatgat	cctggaactg	gaccccacct	480
tccaactgct	tccccangg	actgggggct	cccangctga	nctggcccag	agcaccatgt	540
caatgagaaa	gaaggaggaa	tctgaacctt	gggtaaggat	ttggggcaca	gtaccaggaa	600
gggggcttgg	tgccagacct	tatgaggaag	aaggattttc	ctatgtacag	agaangggac	660
cctgtntctg	tgggaagtgc	ttgtgcaaac	ctaaccaagt	tactaaccac	tctgntttct	720
gtgctacaca	aaggggataa	att				743

&lt;210&gt; 730

&lt;211&gt; 744

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 730

ttntttcctt	cctctaatec	ttttancgcc	tttctgcagg	atcccatoga	ttcgaattcg	60
gcacgagggg	tcctccaaga	gtttggggcg	cggacnnnag	taccttgctg	gcagttatgt	120
cggcgtntgt	agtgtntgtc	atttcgcggg	tcttacaaca	gtacttgagc	tccactccgc	180
agcgtctgaa	gttgctggac	gcgtacctgc	tgtatatact	gctgaccggg	gcgtgcagc	240
acggttactg	tctcctcgtg	gggaccttcc	ccttcaactn	ttttctctng	ggcttnatct	300
cttgtgtggn	tgagtttnat	cctagcgggt	tgcttgataa	tacngatcaa	cccacngaac	360
aaagcngatt	tccaaggcnt	ctgcccagag	cnagcctttg	ntgannttct	ctttgccagc	420
accatcctgc	accttgttgt	natnancnta	ggtgnctgaa	tcattctcan	ttncntaatt	480
gangagtang	anactaaaag	aatgttgact	ctttgaatct	gctggataag	agactngaga	540
tggcagctta	ttggacacat	ggattttctt	cngatntgca	cttactgcta	gctntgctan	600

ctatgcagga gaaaagccca tagttactgc gtgtnacaac aactntctaa cnaacattca	660
ttaatccann ngannccctt caangaatgg taancctatg ccnttcaana tactgaactt	720
nntgccactt ntggcaaaaa aaat	744

&lt;210&gt; 731

&lt;211&gt; 746

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 731

cttattccct ttgnaactna ctctttntca tccctttgtg caggatccca togattcgaa	60
ttcggcacga gtgtccttat ctgaaattca gcgatcttnt tgaataagca tttctctgat	120
tgtggtatat gcctttaatt ttatttctag agtgacaaat ttttggtttt gacagttttt	180
ttctagcttt atagtttctt cttggggaga gaatatgtca acctcactcc atcatgctga	240
agtaaatctt catctcttaa ttttatctct caaaaatata ctaaggattc cctctggagc	300
ctgataagta attgcagtat ctgggttcta tgggtggatg attcaggatt ccaggaataa	360
tagttacttt ttagacctct aaagaagaag taacaaccac gtaaatgaaa agatgcttct	420
taaatcatgg agaatcaggg cttagtatca ctgtattttc aaactgtttc agccttactt	480
tataactgat ttagtatatt tttcttttaa tttcagactt cagtgaagtt ccttatgact	540
tcccctgaaa ttgcttcctt atcatggggg caaatgaaag taaaaggctc taatacaacc	600
tataaggact gcaaagtatg gccagggggt agtcngactt gggattggag agaaacagga	660
actgagcatt ctctggtgt gcacctgcag atgtgaagga agttgttgag aanggtgtcc	720
agactcttgt gattggncna nggata	746

&lt;210&gt; 732

&lt;211&gt; 756

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 732

ttnnnnnnnn nnatcctttn gatttnatc ctntntcang tcctttgtgc aggatcccat	60
cgattcgaat tcggcacgag gtggcccata agttttacct tttaaacata cggctgcctg	120
tgaatgagaa gaagaaaatc aatgtgggaa ttggggagat aaaggatata cggttggtgg	180
ggatccacca aaatggaggc ttcaccaagg tgtggtttgc catgaagacc ttccttacgc	240
ccagcatctt catcattatg gtgtggtatt ggaggaggat caccatgatg tcccgaaccc	300
cagtgtctct ggaaaaagtc atctttgccc ttgggatttc catgaccttt atcaatatcc	360
cagtggaatg gttttccatc gggtttgact ggacctggat gctgctgttt ggtgacatcc	420
gacagggcat cttctatgcg atgcttctgt ccttctggat catcttctgt ggcgagcaca	480
tgatggatca ncacgagcgg aaccacatcg canggtattg gaagcaagtc ggaccattg	540
ccgntggctc cttctgcctc ttcataattg acatgtgtga gaaaggggta caactnacga	600
atcccttcta cagtatctgg actacagaca ttggaacana gctggccatg gncttcatca	660
tcgtggctgg aatctgcctc tgctctact tctgtttct atgttnatg gnatttcaag	720
tgtttcngac atcantggga agcaatccac ctgcn	756

&lt;210&gt; 733

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 733

cntatccttt nntttattcc ttnataagnc cttnngcagg atccatcgat tcgaattcgg	60
---	----

```

cacgagctca cacctgcttt ggatgcttca agcacctcag ccctctgaac tacaaaaacag 120
aagagcctgc aagtgaacaa ggaagtgagg cagaggccca catgccccca ccgttcacac 180
cctacgtgcc tcggattctg aacggcttgg cctcggagag gacagcactg tctccgcagc 240
agcagcagca gcagacctat ggtgccatcc acaacatcag cgggactatc cctggacagt 300
gcttggcgca gagcgccacg ggcagtgtgg ctgctgcccc ccaggaggcc tgaggctggg 360
tctcactgct ctgaaaagac acaaccagaa tggcctgggg ctcaggccct tggctgagt 420
ggaatgcgtt gggactgccc agctgagcta tcaggtgccc atcttttctg gtcccagcag 480
tggtagggag agcacaggca ggcctcgccc ctcccttgc caccagttt cccctncggc 540
acaagcttcc agctctgcag ctggggtgac atcccagtg gtttgcgcc aagacatgtg 600
gtggactttt cgccccccaa actgatgagt nccggagaat atatggagag agagatgtaa 660
aaaaaaaaa nnnnnnnnt nntnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 720
nnnnnnnnna annnnananc tc 742

```

&lt;210&gt; 734

&lt;211&gt; 749

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 734

```

nntanaatcc ntttnnctnt aatccctcta ncaaatecct tgggcaggat cccatcgatt 60
cgaaaattta tagtaatgac aaatgactta tcagtgttca tcatctgaaa gctaagtggg 120
tcgttcaatc actttttcaa agttgatagt agattgcatg gtttcatgtt tctcatatt 180
ggtttattaa ttctatttaa tcaaggaaaa taacttcaga ttccataaag ttccagttta 240
tttttagttt actactaggt gagatagcac attacatact tttactatca aatattattt 300
tagcagcttc ccatagtacc aaatgatttg attccctact ctcatTTTTT aaagcatata 360
aatatttatg ggcttaaaaa ggggggtttt aaaaactgag gatatcagta ataaattgca 420
gaatattttt caaagctttc ttttggaag caaacttttg tgccctgccta tatgcaaagt 480
attttatcag ggacttgaac aaagacctca ctctttttca cttgtcttat gtcgagagaa 540
aagggtattg gcagccacat tctaagact ggggaatggg gtgtcccttt aaatttgaag 600
ataactttan gtaattatng gaactcctca aagaggagaa agtaattttt tncagacatt 660
ttctcaatct gggnttttca cacactantt tncatagtcg agaatctggg tttaccatt 720
gggctnggaa tgtccaatat cagtcctgg 749

```

&lt;210&gt; 735

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 735

```

gngntnngnn gttnnntnt tttnaatnta atccttgnt naantcctt tgcaggatcc 60
catcgattcg aattcggcac gaggtgccc atcaccacac ccagctaaact tttgtatttt 120
tagtagagac ggggtttcac catgttgccc aggctggtct tgaactcctg acctcgat 180
ccgcccgcct tggccccgca aagtgtctggg attacaagca tgagcccagc gcctggctgt 240
atctttcatt ttaccgaagt cactttacc aagtaagtaa ttaggggaaa gcctgagtct 300
tgtaccacct gttcatttgg ggaactgtgg gaaacggagc caacggacct aagtgcctt 360
tgacagttag tttcatacca tttcagtagt gtatttctt cttaatctga ataaaccaga 420
atgatactct cagcacagaa gaataaaggg agcgagtcac taacgttntc tttttaaac 480
tttatgatga cttnttatg aattactgaa cgaacactgg aatgggactc acgtatcctg 540
aggacatctc tcaactctgg ccttantttc ccctctgtaa aattaggggtg ccaactaaat 600
gatctacaag gtccctttnc aagcggccgn cattctgtaa ttacatcatg tggaactgna 660
ttaaacatac accagtgaac tggcangcat tgggaatgta actttcccag taaaatgctt 720

```

tnggttttgggt tcaaaatata cnttgaactt cttttcaaag acnggttnng

770

<210> 736

<211> 746

<212> DNA

<213> Homo sapiens

<400> 736

tttnnctttt attcaaatnc ttgcnggatc ccttgattcg aattcggcac gagggatgnc	60
catcgatgct natcnggcac gaggtgatgn cagcttgcaa actggtctac atnncaaact	120
gatagtacat tgccatctnc aggaagactt gacggctttg ggattttgtt taaactttta	180
taataaggat cctaagactg ttgcctttaa atagcaaanc agcctacctg gaggctaagt	240
ctgggcagtg ggctggcccc tgggtgtgagc attagaccan ccacagtgcc tgattggtat	300
agccttatgt gctttccctac aaaatggaat tggaggccgg gcgcagtggc tcacgcctgt	360
aatcccagca ctttgggagg ccaaggtggg tggatcacct gaggtcagga nctcgagacc	420
agcctggcca acatggtgaa accccatctc tactaaaaat acaaaaatta gccangtgtg	480
atggtgcatg cctgtaatcc cagctcctca gtaggctgag acaggagcat cacttgaacg	540
tgggangcag angttgcagt gagcccgaga ttgcaccacc gtactnnaac ctgggtgaca	600
gagcgagact tatcttatan ataaatagat ngatcttcac ctgggtgaca naacgagact	660
tatagataga tagatagata gatggataga tngatngatn gatagataga ttgataaacg	720
gaattggggcc ttttgcttta atgaaa	746

<210> 737

<211> 751

<212> DNA

<213> Homo sapiens

<400> 737

ntnnnncttt ttgatcantc ctttnttggga tcccnttgct acttgttctt tttgcaggat	60
cccatcgatt cgaattcggc acgaggctga cctacagcag aagctgctgg atgcagaaag	120
tgaagacaga ccaaaacaac gctgggagaa tattgccacc attctggaag ccaagtgtgc	180
cctgaaatat ttgattggag agctgggtctc ctccaaaata caggtcagca aacttgaaag	240
cagcctgaaa cagagcaaga ccagctgtgc tgacatgcag aagatgctgt ttgaggaacg	300
aaatcatttt gccgagatag agacagagtt acaagctgag ctgggtcagaa tggagcaaca	360
gcaccaagag aaggtgctgt accttctcag ccagctgcag caaagccaaa tggcagagaa	420
gcagttagag gaatcagtca gtgaaaagga acagcagctg ctgagcacac tgaagtgtca	480
ggatgaagaa cttgagaaaa tgcgagaagt gtgtgagcaa aatcagcagc ttctccgaga	540
gaatgaaatc atcaagcaga aactgaccct tcttcaggta gccagcagac agaaacatct	600
tcctaaggat acccttctat ctncagactc ttcttttgaa tatgtccac ctaagccaaa	660
accttntcgt gttaaagaaa agttntctgga caaaacatgg acatngagga tctaaaattt	720
ggtcanagca tctgtgaatg agcatganga t	751

<210> 738

<211> 795

<212> DNA

<213> Homo sapiens

<400> 738

aatccctttg ctttaancct tgtttgaacc cctttggaac tncctctntn tgnaggatcc	60
catcgattcg aagagcncan gcaggaagag agagaccctn actgctgggg anttntctgc	120
acactcaagt cccaaccca ctggaatctc ccctactaca agtgccatgt anacccttg	180

aaaaggggag	gggcctaggg	agccgacctt	gtcatgtacc	atcaataaag	taccctgtgc	240
tcaacccaaa	aganaantan	aaaaaactcn	agcctctaga	actatagtga	gtcttattac	300
gtagatccag	acatgattng	anacattgat	gagtnngac	aaaccacanc	tcgaatgcng	360
tgaaaaaat	gcnttatntn	tgaaanntga	natgctatat	nnntcattnn	ttaccattnt	420
antctgcagt	aaacaaantt	tacagcancn	nttgnntnga	tttcatgtnt	caagttcaag	480
gnganntgtt	tggcgtnnat	ntaatteggc	ccnacncng	acccttttgc	attgggcccn	540
nnacccanct	ntagttccct	nttagngagg	ggnaattgcg	cncctttggc	taataatngg	600
gcanangctg	nttttcccn	tgttnaaatt	ggtttatcca	gtttannaat	ttcaacacga	660
tnaatatcaa	acccggttaag	cnattaaatg	gtnaaaaacn	ntgnggggng	cccttaanga	720
gttgaactta	accnganatt	aaattgcnnt	tncgcnttna	atntcccn	ttttaaatcc	780
nggaaaacct	tcccc					795

&lt;210&gt; 739

&lt;211&gt; 763

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 739

ttnnnnnccct	catnaatccc	ttctttgatc	cctcncncna	aaacccttgg	cnactcgctc	60
ttntngcagg	atcccacga	ttcgaattcg	gcacgaggca	nccttcgcct	cctgggttca	120
agtattcttc	ctccctcaca	tcccagtag	ctgggactac	aggcagtg	caccacacc	180
agctaattnt	tgcattttta	gtacaggcag	ggcttcatca	tgttgccag	gctggtctca	240
aactcctgat	ctcaagtnat	ctgcccactt	tggcctccca	aagtgctggc	attacaggaa	300
tggagccacc	gcgccagcc	tgatttcttt	anntangtct	tgtcangaaa	natattgant	360
ctnttgattc	ntnaacatgg	cnttnggtcg	tctttaatnn	gnctcatcan	tgccctccatg	420
tgttnttgat	gccttngaac	tggatttttt	aaaatnncaa	tttctaattg	nnnattatnn	480
aaacacaatt	gggntnnata	tattggcatt	gtattaatgc	aactttccta	aactcactag	540
taattctagt	agcnnantt	ggtanattct	taaggatttn	ctgngtnaat	agncattgtca	600
tctgtgaatn	aagccattct	ttganccttt	tcaaattttg	agccttgat	ttcttattct	660
taccatatca	cattggcaaa	gacctccagt	atganattga	ataaangtgg	tganagaaaa	720
cacctncta	aaantgctng	aattacaggc	atgaaccacc	ntn		763

&lt;210&gt; 740

&lt;211&gt; 765

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 740

tnnnnnnnnn	tttttnaacc	ntttnttgna	tnctctntc	aaatcgcttg	gctacttgtt	60
ctttttgcag	gateccatcg	attcgctagc	ctgggcaata	tagtacgacc	ctgtctttac	120
taaaaatgca	aaaattaacc	acgtatgggt	gtcacacct	gtagtcctgg	ctactgagga	180
ggctgatgca	ggagaatcat	ttgaaccag	gaggtcaagg	ctgcagttag	ctatgattgc	240
accactgcaa	tccagcctgg	acaacacagt	gagacctgc	ctcacaaaa	ttatattctg	300
atthttctgag	tccatgaaca	cattgtccaa	atggattttt	ctagctcctc	caagttacag	360
atagttccac	gcacacacag	aactcaccac	tctcaaata	tttccccact	agtattacta	420
ttaaattttt	caaacatgca	aaagatgaaa	gaattgctca	gtgaacacca	tgtaccacc	480
acctagattc	tacaattaac	atthttaccct	actttcttta	tcacatatat	gtacctatcc	540
atctatccat	tcttccatga	atccatcaat	tcatctaatt	ttttatatat	ttcaagttaa	600
gttgacagata	tgtagcttat	gtttcacctt	aaatgtttct	gcctggctat	tattaactgg	660
agtgaatat	gtttttggnt	cttctttatg	gtaaaatcta	tgttcagtga	aatgcacaag	720
acttangtat	gccattaata	gggtttgacg	aatagacaaa	ccttn		765



&lt;210&gt; 741

&lt;211&gt; 753

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 741

ttngancnt tnnntnttn nntnaatgaa gccatttgct acttgntctt tttgcaggat	60
cccacgatt cgaggaaggt ggaggggcag gnaacaggac ggacaggccc cgggctctgg	120
cacatcctgg ggaacaaggg accacaagga cgggggcagt ctccagactt cccctgggcg	180
cttgacccca ggccttgag gggagagagc cagggcctcc ctccaggtctt tggtcatgct	240
gttttccctg ccgtggacac cctttcccgc tctccgattc tctaaatcct gcccacatctc	300
ccagatcttg ttcattgtcca agcttttcca ggaagtctta gcagctccca caccgcagag	360
ctcgagatgt ctccctgact tggctccaga ccccaactat gtgcaagcat ccacttatgt	420
gcagagagcc cacctgtact ccctgcgctg tgcctgggag gagaagtgtc tggccagcac	480
agcctatgcc cctgaggcca ccgactacga tctgctgggtg ctactgcgct tccccanccg	540
gtgaagaacc agggcacagc agacttctnc ccaaccggca cggcacacct gggagtggca	600
caactgccac cagcattacc acagcatgga cgagttcanc cactacgacc tactggatgc	660
aaccacaggc aaanaangtg gccangggc acaaaggcca atttctgnct ggaggacanc	720
acctgtgact tnggcaacct naaacgctat gcn	753

&lt;210&gt; 742

&lt;211&gt; 767

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 742

tnganccttt cgnntctncn ctccaaagcc tttgctactt gctctttttg caggatccca	60
tcgattcgca ggacatggag cagtacctgt ccactggcta cctgcagatt gcagagcggc	120
gagagcccat aggcagcatg tcatccatgg aagtgaacgt ggacatgctg gagcagatgg	180
acctgatgga catatcggac caggaggccc tggacgtctt cctgaactct ggaggagaag	240
agaacactgt gctgtccccc gccttanggc ctgaatccag tacctgtcag aatgagatta	300
ccctccaggt tccaaatccc tcagaattaa gagccaagcc ancttcttct tctnccacct	360
gcaccgactc nggcaccggg gacatcagtn aggggtggga gtcccccggt gttcaanccg	420
atnaggagga agttcagggtg gacactgccc tggccacatc acacactgac aganaggcca	480
ctccggatgg tggtagggac agnactctt aaattgggac atgggcnttg nctggccaca	540
ctggaatcca ngtttggtg tatgcngaata tncacctgga aaagccaagg ttggtntata	600
ganggtcttg atttttacnt anttgncaat aatgggttga gnaaacttaa agaaccagtt	660
taacaataaa atngttaggg acccgtnan aaaatggang tctnccttcc atntnaacct	720
ggannccctn aaacntttnt gngtcncaat tttcgttnca tccannn	767

&lt;210&gt; 743

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 743

naancctttc nnncttcgcn attcnaannng ntnggaaagc tcantcgtctc natagnccnn	60
gggcttcgcg agnnntggga natnacanaag gctngttanc ataccngttt ttnactgcan	120
aggnnnccac angcagcatg gcccatgnaa tgnccatgcc antgatggcn ggnggccatg	180
ctgtcagcgg annccgactt gtgaggancc nntntggann engtannena canncacccc	240
cagtctggna cccnagtgtt cttactacac caantgaaac gctggnnagc caagagcccn	300

```

gatggcccac gtnccctgca tgganccccc tgancngact ccaccagcct atacangngg 360
aagccanaag cagctgtttt cngccntgcc ctgctgataa tgccttgaag accccatacg 420
acctnnacgg nctacattga cantnngact gtgncancct ngatcagatn atcctggaac 480
tgggnccnng attccaggan cttncntca atggacctgg gngcttgtaa tcngttntgg 540
accatacanc cnttgtanna gataaaaagan ngaggaaatc tgaaaccntn gnaataagat 600
ctgnggcatt agtnnntcaa ggggaggntn ggtnncaaaa cnctatgagg aagaacgatg 660
gnactatgtc catgnaaggg gaacatntan tgttgganna tgcnatgcaa ncntnnccnt 720
gatntaacnc tttganaaac tnanngcttna caaaggggga aaaanact 768

```

&lt;210&gt; 744

&lt;211&gt; 757

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 744

```

tnnnnnccnt tnnnttnat ncntctctca aatcgcttgg ctacttgttc tttttgcagg 60
gatcccatcg attcgcttga cctctgtact ttaaaggaaa tcactaacca aattttcaaa 120
gtttccctttt aaatgcgttt agctagaaat ctatgtattt atccctttcc tattttgcat 180
tcttctccca ctatttttaa aaactcattt acagtagaaa ccattcttct ttctcccaac 240
agtatccctt gccagacca tgagaacagt aaggagcatg ttgttgggtca gggtttcaga 300
atacgcgtag tgcactgag aatgtttgct cacagtcaat aattgtcttt gtggatgtga 360
taattttgga gatacacttc tggtcagaac tcaggtgaga taatcttgca atactccaaa 420
tgcagatact ccagccaccc gcaaggttcc aggaaaggac aatgtcctgc gagaaaatca 480
ggaggcctcc acttcctggg ccacttgaga agttcctggg catgtcacta catgttgggt 540
gactcagcca tttctcatgc tgnnttgttt cttgcgggtg ccacttaacc ccaaagaatg 600
aanggaggat ccacagtga agtgccctgag tttctctatg agaccagatg ctgtcgaaac 660
caaacatctt tccttttgc ctatnggaac attttaaggg ttgggttgca caactggttt 720
tcagactnng aagattacca agtttgggtc cccctn 757

```

&lt;210&gt; 745

&lt;211&gt; 751

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 745

```

cttnttnnnt ttnntttgat ncctctacnc aaacccttgg ctactnctc tttntgcagg 60
atcccatcga ttcgaattcg gcacgaggaa naacagacag gtttcaacat ggatggatct 120
gaaatgctgt tgaagcatat catttgcata aaaatcaggg acagtttcca aagaattata 180
tatttttttc agttggctct ctagttagtt tttttgggag taaggacaaa cctggaatag 240
atagcaaaac tgaaaatcan cagtgcctgat ggtggtacat atgtctttcc tttagcttct 300
cccctgataa tcccatctg cttttacttc gggtgagcag agggggatgt gtgtgtgcgt 360
gtgtgtcagt ctgtttgtga gtgtgttaaa ggctacagac cacagttagt ttaaaatgct 420
tggaacttcc caaactggct ttactttatg tttatacagt gctcaggggt aacgcagtac 480
atccatgcc a ttgctgtggg aggtatcccc ggatgcatgt gttttgagtc tataaatata 540
gaaaatatat attggtttct ttttccaact taatangttt attaaagcat gaaatgaaag 600
ggtgcataat atgcattcaa gntatntcct aatttttggg ctgacagtgc atgtctttgg 660
agcatgctga aacaanaatn acacaggaat tgantaaccn gaaagaaaca ttgttaaatg 720
tccaacattt gttatgcatt tntattgggg g 751

```

&lt;210&gt; 746

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 746

tnnnnnntntn	nnnnnttttn	nttentnnnn	ctttgaancc	ctttgctact	tgtctttttt	60
gcaggatccc	atcgattcgc	tgaacaaaa	gatgtatttc	aattaaaaga	cttgggagaag	120
attgctccca	aagagaaagg	ctttactggn	tntgtcangt	aaaagaagtc	cttcaangct	180
tagttgatga	tggatgggtt	gactgtgaga	ggatcggaac	ttctaattat	tattgggctt	240
ttccaagtaa	agctcttcat	gcaaggaaac	ataagttgga	ggttctggaa	tctnagttgt	300
ctgagggaag	tcaaaagcat	gcaagcctac	agaaaagcat	tgagaaagct	aaaattggcc	360
gatgtgaaac	ggaagagcga	accangctag	caaaagagct	ttcttcactt	cgagacaaaa	420
gggaacagct	aaaggcagaa	gtagaaaaat	acaaagactg	tgatccgcaa	gttgtgggaag	480
aaatacgcca	agcaaataaa	gtagccaaaag	aagctgctaa	cagatggact	gatnacatat	540
tccaataaaa	tcttggggcca	aaagaaaatt	tgggtttgaa	gaaaataaaa	ttgatagaac	600
ttttggaatt	ncagaagact	ttgactacct	ngactaaaaat	attccatggt	ggtgaaagat	660
tttcaagctt	gnngaattgt	aaattttnaa	ctattatcta	actaatgtnc	tgaattgcn	720
ttggctgtac	tgggttatca	ttttattaat	gttaataaaa			760

&lt;210&gt; 747

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 747

tnngncttta	nncnttttn	attgnnnnnn	nttgaaaccc	ttggcnactn	gctctttntg	60
caggatccca	togattcgaa	ttcggcacga	ggaggctgtg	tcaaagaatg	aatggaacgc	120
ctactatgag	gaggtgggtg	tacgtntctag	anggagatcg	agtacatgat	ccagaagctc	180
cctgagtggg	ccncggatga	gcccgtggag	aagacgccc	anactcanca	ggacgagctc	240
tacatccact	cggagccact	gggcgtggtc	ctcgtcattg	gcacctggaa	ctacccttc	300
aacctacca	tccagcccat	ggtgggcgcc	atcncctgcan	ggaactcagt	ggtcctcaag	360
ccctcggagc	tgagtgagaa	catggcgagc	ctgctggcta	ccatnatccc	ccagtacctg	420
gacaaggatc	tgtaccaggt	aatcaatggg	ggtgtccctg	agaccacgga	gctgctnaag	480
ganaggttcg	accatatact	gtncacgggc	agcacggggg	tggggaagat	catcatgacc	540
gctgntgcca	agcacctgac	cctgtnacgc	tggaaactggg	aaggaagagt	ccctgctacg	600
tgggacaaat	aactgtgaac	tggaccttgg	ncttntaact	attggncctg	gggggaaatt	660
catnaacaag	ttngccaana	cctgcgtggg	cccctgaaat	acattctttt	nggacccctt	720
tgnatccaga	accccaattg	nnngnngaaa	acttnaaana	aantnncttt	naaaannntt	780
tttntct						786

&lt;210&gt; 748

&lt;211&gt; 722

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 748

tggaaactngc	tctttntgca	ggatcccatc	gattcgaatt	cggcacgagg	aggaagaggc	60
ctgctccact	tgtctgggaa	cctgggcagg	aggcacagag	gaagccaagg	cctggagctg	120
caggtcccc	ggcatctctc	tctgtcccgg	cagcccagga	tggcctggtg	ccccacctg	180
ctgcagcagg	agccccaagg	agtgtctagct	gaggggtggt	gctgggggtg	tcctcatgga	240
cagtgggtg	tgcaagggtg	cactgagggg	ggtgggaggg	gatcacctgg	gttcaggcc	300
atccttgctg	agcatctttg	agcctgcctt	cgggtgggag	canaaaaggc	cagaccctgc	360

tgagttanag	gctgctggga	tccactgttt	ccacacancn	ggaaggtgc	tgggaaacagg	420
tgccanagaa	gtgccatggt	tgcgtnaac	cttgcantct	tncanctggg	gactggtntct	480
tgctgaaacc	cacgagctgn	acantnanga	gctgtccanc	ttgcttggct	cactgngacc	540
aggaaagcct	gtctttgggt	agctcgtgtc	ttctgcagga	aaaaaaaaag	gatgtgtcat	600
ttggccatga	tatttgaaaa	aggggaagga	tngccnaant	ttgtttacca	tttattccag	660
tanttgga	attttttgac	cccctnngct	taattctttt	gcaanaacta	ctgggggggt	720
tg						722

&lt;210&gt; 749

&lt;211&gt; 821

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 749

tttnaanncc	cttgctactn	gttctttttg	caggatccca	tcgattcgtn	gacatagaaa	60
acatacagta	agaatatggt	attataatct	tacggggacc	actgtcaaat	cgcggctctgt	120
ctttgaaaag	ttgtnatggc	ggcgcatgac	tataaatacc	ctagctggtt	agcattttaca	180
ttccttgcca	gggagtttga	aatttatnct	nggcgggctg	nctttaggnt	ttaggttagag	240
ttaaagaggt	aaagcacatg	tttgccacaa	cccaggaaag	tatttttaag	aaagatttgg	300
attttcctac	ctttagagat	ctaaaaaaa	tttaataata	aaaatcattt	tgagntgggtg	360
tttattacta	gttcagaatg	agtggctgct	gaagggggcc	cccttggnat	tttcattata	420
acccaatttt	ncactttatt	ttgaactctt	aagtcataaa	tgtataatga	ctttatgaat	480
tagcacaggn	taagttgaca	ctttgaaact	ggccatttct	gnattacact	atcaaatagg	540
aaacattgga	aagatnggga	aaaaaaatc	ttatttttaa	atggcttaga	aaagttttca	600
agattacttt	ggaaaattct	aaacnttnt	ttctnggttc	caaaactttg	gaaaatatgg	660
tagatnggac	ctcattgcca	tttaagactg	gttttcaaaa	gctttccctc	aacatttttt	720
aaaggtgtgg	anttttccct	ttttaaatat	tccataattt	aantttcctt	ttnaaaggcc	780
nctnnttttc	ccaaacccat	ngncttttgg	ggnaaatccc	c		821

&lt;210&gt; 750

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 750

gnntnnnnnn	nnctttnttn	nntgnctntt	tetaagagct	tngcnnatgc	tnggtcggca	60
cgaggcaaca	tttgtctaca	actctactgt	aaaattggaa	atgctttttc	acagaaaaac	120
ctctcaaaat	gctgaatgca	aaagtggga	tcacagaaac	attgtgccta	tttttggctc	180
gctggaaact	gtatttntac	aaggtaatcc	ctgttctcaa	tatagttcct	gtcttgccac	240
tggtgggtttt	cttgtagcat	ttttctagtt	ctgagattgc	tactacccaa	agtattcatt	300
tctttctttac	tgggtgtgtcc	tctgtcttca	cagcctgctt	ctggattgta	ggttttttcc	360
tttctttctg	ttgagatatt	tatggcattt	gatagagtca	aaccagatgt	attgcagccg	420
gacatactta	tgtggcttca	gatgtgtaaa	ataagtaact	tcctatcttt	gtctgtctag	480
ctcaagagtt	gactgtggac	gaggaatgcc	tgtattgatt	cattaatgta	ataactattt	540
actgactgcc	taccatgtac	aaccagaaac	acagttccta	acctcatgaa	cttaccatgt	600
aacatgggaa	gacaagccta	agttcttatt	tggntggnaa	ttgcgataac	gctcacagaa	660
caaattcccg	attcctacga	acccatgtat	aggggggaaa	tatttaaggt	cccatttaat	720
actgacattn	gcccnccttc	ctnntatttt	aagctgagaa	tctgaaggnn		770

&lt;210&gt; 751

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 751

cgttnnnttt	ccncccttga	agcccttttt	gcaggacttt	cnaatncttg	gtagacttta	60
tgtagacttt	gtgtagactt	tatgtcagtt	tttgtcatta	tttgaaaatc	tattctgaca	120
actttttaat	tcctttgac	ttataagtta	aagctgtaac	aactgaaatt	gcatggatca	180
agtaagcata	gttttatcca	gggagacngc	tcnnnggaag	ccatagaatt	gctctgggtca	240
aaaccaagca	caccatagcc	ttaactgaat	atthaggaat	tctgcctaatt	ctgcttatat	300
ttgggtgttg	ttttttgact	gttgggcttt	gggaagatgt	tatttatgac	caatatctgc	360
cagtaacgct	gtttatctca	cttgctttga	aagccaatgg	gggaaaaaaa	tccatgaaaa	420
aaaaaagatt	gataaagtag	atgattttgt	ttgtatccct	acccatctcc	tggcagccct	480
actgagtga	attgggatac	atttggtctgt	cagaaattat	accgagtcta	ctgggtataa	540
catgtctcac	ttggaaagct	agtcctttta	aatgggtgcc	aaaggtcaac	tgtnatgaga	600
taattatccc	tgctgntgt	ccatgtcaga	cttttgagct	gatcctgaat	aataaagcct	660
tttacccttat	ctggaaaaaa	aaaacattnt	anancaaaaa	aaaactnnga	gccttttana	720
actnttagng	agnccntttt	ccgtagaatc	ccngacntgg	ntaaggaanc	nnnc	774

&lt;210&gt; 752

&lt;211&gt; 778

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 752

gnnttgaann	centtgtttc	gnatectttt	tnnaggactc	tgaagncctt	tggtcggcnc	60
gagaagaaac	tctgcctcag	aaaatgttta	cagcttccag	tggaatcaaa	cataccatga	120
ccncaattta	tccaagttct	aacacattag	tagaaatgac	tcttggtatg	aagaaattaa	180
aggaagagat	ggaaggggtg	gttaaagacn	ttgctgaaaa	taaccacatt	ttagaaaggt	240
ttggctcttt	aaccatggat	ggtggccttc	gcaacgttga	ctgtcttttag	ctttctaata	300
gaagtttaag	aaaagtttcc	gtttgcacaa	gaaaataacg	cttgggcatt	aatgaatgc	360
ctttatagat	agtcacttgt	ttctacaatt	cagtatttga	tggtgctgtg	taaatatgta	420
caatattgta	aatacataaa	aaatatacaa	atttttggct	gctgtgaaga	tgtaatttta	480
tcttttaaca	tttataatta	tatgaggaaa	tttgacctca	gtgatcacga	gaagaaagcc	540
atgaccgacc	aatatgttga	catactgatc	ctctactctg	agtggggcta	aataagttat	600
tttctctgac	cgcctactgg	gaaatatttt	taagtggaaac	caaaataggc	atcccttacc	660
aatcaagga	agactgactt	ggacaccgtt	tggaaaatgg	gtaaaaacgg	tggnttactg	720
gtganttggtg	gagcnagaac	cggacccact	ggtatactgg	ggantaacaa	tttttttc	778

&lt;210&gt; 753

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 753

gcttttgaaa	cccttttggt	aacgcctttc	tgcattgatc	tctcgtcctt	gaaagggccc	60
taaaagagat	gaacaatacc	gtatcatgtg	gtttgaatta	gaaacccttg	tcagagccca	120
tatcaacaac	tcagagaaac	atcaaagagt	cttggaatgt	ctgatggcat	gcaggagcaa	180
acccccagaa	gaggaagaac	gaaaganacg	cggctgaaag	aggggaagaca	aagaggacaa	240
gtcagagaaa	gcagtgaaag	attatgaaca	ggaaaagtct	tggcaagact	cagagagatt	300
aaaaggaatc	ttagaacgtg	gaaaagaaga	attggctgaa	gctgagatta	taaaagattc	360
gcctgattcc	ccagaacctn	caaacaaaaa	accccttggt	gaaatggatg	aaactccaca	420

agtggaaaaa	tcaaaaagggc	cagtgtcgtt	attatccttg	tggagtaata	gaatcaatac	480
tgccaatcc	agaaaacatc	aggaatttgc	tggaccgttt	gaactctgtt	aataacagag	540
ctgaactata	tcaacatctt	aaagaggaaa	atgggatgga	gacaacagaa	aatggaaaag	600
ccagccggca	gtgaagagtg	acttgangaa	ctaaatttta	gcatattgca	aaaatatttt	660
gtgcgggaat	tcgatatnag	tacttttacc	agcaagatgg	natngttatg	tttgcttgga	720
ctggnntttta	catttttnaa	attttttcag	tgnccttttt	tggtcctaaa	ttatc	775

&lt;210&gt; 754

&lt;211&gt; 1032

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 754

ggnntttttc	ccaaaaaaa	ggggccccct	nggggntttt	tncncaanng	gnccccctttt	60
tctttgncca	gggnaacntt	ttttgngaaa	agancctt	ttttggatnn	accggggccc	120
cccggaaagt	tccnaaat	tnagggttna	aacccaaatc	cttggggaaa	aaaaaaaaaac	180
ccagggccnt	ntntggggnc	cccctnnggg	gggtngggaa	aaaaaaaaaaa	gggggaatgg	240
cccccaaaaa	aaaatnnggg	gcccctnngg	ggaaaaaaa	gggaaagccc	aggtngggaa	300
nggaaagggg	gaagntccc	ccggggggaa	aggaaatggg	tggtnggna	atggcccaat	360
ggttggaaaa	ggcccaaac	aatttgggnt	ntaaaacaat	ttcaacctgg	gggggtcctg	420
gcccanaaaa	aatgcngggc	accncngng	ggtctggctt	aagaattggt	tacaagggca	480
aagggaaagg	gaagagttct	agagataaag	aactatatgc	ttggatgaag	tgtgtgaagg	540
gacagcctca	tgatcacaaa	catttaatgc	caacccaaat	tatacctggt	tctgttttga	600
cagatcttct	agatgccatg	cacactctta	gggaaaaata	tggtattaaa	tcccattgnc	660
attggactaa	caaacagaat	ttacaagttg	gaaattttcc	tacaatgaat	ggtgtatctc	720
aagttttaca	gaatgntctt	aatcacagna	ataaaatttc	tctgtgcatg	cctgagtctt	780
cagcagcaaa	aatactctc	cgaagtctga	gaaaaatggg	ggcagcagcc	caagaagagt	840
gatgtaggca	cagataacna	aggntaacct	cctccagaat	ccccagtcac	cactgcactg	900
gttaagcaga	acttngcagg	agcaaaaaag	cccngangan	ggaaaaaaa	aannaaaaaa	960
aactcggagc	cctcttagaa	ctatangggg	ggccgnnnta	ccgnangatc	cccagactga	1020
anaggaaccc	cc					1032

&lt;210&gt; 755

&lt;211&gt; 798

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 755

ngnnnnnttt	nnccnacna	aatccctttt	ttgaagcctt	ctantgnctt	catcgtncctg	60	
gtaaattggg	tgaattattg	tattgaagct	tgagctgtat	tttnaagtaa	tttnggttnc	120	
ccctaagatg	ttattatggt	agggacataa	cacttttggg	aggttgttgt	gggagatggg	180	
tgatttaggt	tttcaaaagc	tagaaataaa	atttacatnn	ccccgntnn	cataaaattc	240	
tgctctaatt	gggtggaagg	tgctgtatct	aacttgtgtt	cctnctaagg	ttatgtccta	300	
ataactattc	ttttaggagt	atacttctac	tttatagaag	gttgcttttt	ctttttaatt	360	
ttntctaaca	aagaaaagaa	tnaagtattt	attaataaag	aaccagaaag	cacttgaaac	420	
tgatgttttt	aaatgggctc	acttanggta	gatttattta	tctcatatc	ttaaaaacag	480	
ctatgtgnat	tgaataaagt	cacaacagaa	cttgaaaccc	agggtgggtg	tctgagcaat	540	
cccctttctt	atggggaaaa	acaaatgggt	cttgtttgaa	cangaaggta	tcattgcagt	600	
cngcattcac	ccgtgtataa	ttggnatata	agntgnataa	tatgctcgta	aaggctnaag	660	
gtnagctgga	tctggatgcc	cttnaccaaa	ttangatttt	aacttttaan	aataaaattt	720	
naaancta	at	tgncnaaata	aaaaaaatan	naaacttcgg	ncctctacaa	nttntagatg	780

ngtcgattnn cgnncanc

798

&lt;210&gt; 756

&lt;211&gt; 834

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 756

tttgaacccc	ntttnttnaa	gcctttttta	tgactttanc	gncctttatt	cggcacgagg	60
tccttcagct	ggtagcttnc	attcganttt	nnanatanta	tntgtgcatg	cncnnttgaa	120
tttttgggga	agaacagant	gcagaagaag	gcnaggaaag	ccgaagagan	tnntnccggca	180
ncagaagctt	aaagnaggcc	aaactggtgg	tgcnctttcc	tcggnacaga	agctggatga	240
ctatggccaa	tttggagaaa	nagctccagg	agatggaggg	acggttcgag	aaggagtttg	300
nagatggatc	ggatgaaaat	gaaantggaa	gaacatganc	tcaaagatga	ngatggatgg	360
taangacagt	gatgaggnc	gaagacnctg	agctctatga	tgacctttta	ctgnccanca	420
tgtgacaaat	cgtnaanaac	agtaaaggcc	atgaanaatc	acntagaagt	caaangaaag	480
cnnttgggga	aaatggnggn	nctttgntaa	aaccacnagc	tgganggang	gaagaannna	540
aaatttttta	agnacctcaa	attgattgaa	aaatncatta	tgatgacaat	tcctgnanga	600
ataaattggn	agatgcncta	naancaaaan	gcnttttttn	antnnaaana	nacaaannt	660
nnagcctntt	ngaacntata	gtnnannctn	cntttanctn	tntatccccg	actttntnt	720
ggataccntt	gactnagctt	ttggacaaaa	ncncnacttt	gtattncatt	ngnnaaaaaa	780
atgcntttat	tttccgnaaa	tttggatgaat	ncntaattng	ntnntattnn	nnnc	834

&lt;210&gt; 757

&lt;211&gt; 1062

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 757

tttttccaaa	aaaatcnc	ccnttttttg	gccttnaana	nanngggccc	cctttttttt	60
gggccagggg	aatnccccca	atnccggaat	tttccggggg	ntttgggggg	nttggaaagg	120
gccccttggg	gaaagggn	tttccnaagn	aaaggggtng	gaaaattttt	taaatggcct	180
tttngggggg	aaaaagcccc	ctnggaatnc	ccccaaaaaa	cccttgggga	aaagggggga	240
aaaagggggg	aaccttttng	gnaatccttn	ccnttnaat	aatttggggg	aattaaancc	300
ctggttttgg	aaagggaaaa	gggttgggtc	tggtcttggg	ggaanggaat	tgggggccaa	360
nttaaaatgg	aaggttttgg	canaatnggc	cncctcgggg	gcttnttcaa	aagccaagcc	420
tttgggancc	ctgcttcatt	tttngggccc	tttntctgcca	aggaanccca	acccttaact	480
tancaggaaa	anggagatga	aaggccttct	tccaaggaag	gtaaggctct	ttggctgccc	540
cnacttaaat	gctttttgaa	antctcttag	atgtggnaaa	tattttttcc	gaaccttgaa	600
atcaactngg	tagaatttca	attggaagca	taatccattg	taaaatatat	tttagttgat	660
atttggtaaa	atgccttttt	tgggtggtgt	gttngaattc	tgggtttccc	aagaatcttg	720
natttcaaat	ggtttaacaa	angggaagga	aaggganctt	ttcccttaac	cttccctttt	780
tgaccaggaa	agatttttna	aagtaccttt	ctttttaagg	aaaaaaaaaa	attaaatttt	840
gaagaaaaat	tgggatttgg	attttanana	aaangggaaa	aaaaatatna	ntattnatan	900
ntcnnannat	nttnatnnt	ctanntant	nctntnnnta	ntnctnntnt	ntnnannnna	960
nannnannaa	ataaatantc	nnncatnctt	anctacanat	nccntcttn	ntntannnac	1020
tttnannnta	nttatctaan	tctntcccta	ttntaccctn	nc		1062

&lt;210&gt; 758

&lt;211&gt; 845

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 758

aaancccttn	tttnaaatcc	tttttanang	attcatcgat	tcgaattcgg	nacgaggcgc	60
tagcgtcggg	tccgcntggg	cccttgcggt	gcgctgnngg	caggcgggtga	ggcttacgcn	120
tntgtttacg	ggcaaaaacc	tgcacacgca	ccanttccc	tnnccgttgt	ccaacaacca	180
gaaggtgatt	gcctttgggg	aanctttctan	gncaacnacn	tgaacntatg	gacagtgcgc	240
tgntttggac	agaantggga	acnttnaggn	tgntgtgcgc	ttcnagcatn	tgggcacctt	300
tgtgttcctg	tcantcacgg	gtgagcanta	tgggaagcccc	atccgtgggg	cagcatgaag	360
gtccacggca	tgccaattg	caacacgcac	aaatacttgg	aangccatgg	aangcatntt	420
natcaagcct	aatgtgggag	cccttttgca	agtcacgaat	taactctnaa	nngtntggat	480
ggattgggtg	ggantggang	gttgcaagtt	ngggccnttt	tgaagggcca	ctttttggna	540
aaaaactttt	gggtttttta	ngggttcntc	aaaaagccct	ttgnaaattn	aaagaaatgt	600
tgggcctatt	naaaaaaan	atnatacttt	atntaatctn	nataataata	nttantaata	660
aaantcttnn	agccttttta	aaanttttta	atgaancctc	ttattttanc	gttanantnc	720
ntaacnttta	attaaaggaa	taacaatttg	ttgaantttt	ggtataaana	nccccantt	780
tttaaaattc	ntntngaaaa	aaaatncntt	tattttggta	aaaatttgng	gaatcnnttt	840
tgctn						845

&lt;210&gt; 759

&lt;211&gt; 947

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 759

tnnggggggg	ccccnnttt	ggggccccc	acccttnggg	gaaaccccc	ttnnnnnttt	60
ttnccttttt	gggggggaaa	ngccccccc	caaangnaaa	aaccnttttt	nnnnaatttn	120
ngggngangg	ntntggggnc	ccnttaaccc	caangggggg	gggttttnan	cctggggggn	180
naaaatnggg	ggaanaantn	nnnaatgggn	antcccttna	angggaaaaa	naatttnncc	240
ttaagggnat	gggncattaa	tnttnatccc	tantggattn	caatttcatt	cgnattaaag	300
gctttttactg	gnataatcct	tnnccggccc	cncgtgtagt	ttaaagtgcc	canaanttga	360
atgggaaatn	acgggttttg	aaaatcgcac	aaagcagtc	cnggcacnga	ggngtcacgc	420
cngtaatncc	agcatttttg	gaggcctgag	gcangcggat	cacganggca	anagagtcca	480
gaccattnct	ggctaacacn	gggaaacccc	gggnctaata	aaaaatcaaa	aattaggntg	540
gacatggtgg	cacgtgccng	taatcncagc	tacttangga	agctggatgc	aggaagaatt	600
gcgtggnanc	cngggcccng	tgggaangntg	cattgatacg	aagaaccgtg	ccaaatgaan	660
ttanannctg	ggcngaannn	gagcggaaaa	agccctnttt	aaaaaaaaan	gggantggaa	720
aaantggtgc	canagncatn	nggggaaaaa	attttnnnt	tnnttnancg	gttttnanct	780
tgnggaaggc	cntctttaat	nttggggaaa	aggcactttt	gggntnggtt	ttggaaaacg	840
nntggctttt	ccctttnaaa	agggaaaaan	ggntttaanc	ccctgaaaaa	ngngcngnnt	900
tttaangggg	gnnnnaaaca	nggggncttt	ggaancccca	nnaaacc		947

&lt;210&gt; 760

&lt;211&gt; 759

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 760

gnntttctaa	tgcttgtnnn	nngcntttnt	gcaggatccc	atcgattcga	attcggcacg	60
agaagatatg	cagagatatt	ccaggatcct	ttagcttttg	tgcggtctcc	tggagacagt	120
gttatcgcgc	aacagtgtgt	tgaatatgtc	acatccattt	tgcagtctct	ctgtgatcan	180



gacattgcac	ttatcttacc	ggctcttctg	aagggctctat	ttctgaactg	gagcagctct	240
ccaattctct	accaaataaa	gaattgatga	cctcaatctg	tgactgtctg	ttggctacgc	300
tagctaactc	tgagagcagt	tacaactggt	tactgacatg	tgtcagaaca	atgatgtttc	360
ttgcanagca	tgattatgga	ttatttcatt	taaaaagttc	tttaaagaaa	aacagtagtg	420
ctctgcatag	tttactgaaa	cgagtgggtca	gcacatttag	taaggacaca	ggagagcttg	480
catcttcatt	tttagaattt	atgagacaaa	ttcttaactc	tgacacaatt	ggatgctgtg	540
gagatgataa	tggtctcatg	gaagtanaag	gagctcatac	atcacggacg	atgagtatta	600
atgctgcaga	gttaaaacag	cttctacaaa	gccaaagaag	aaagtnacga	aaaatttgn	660
ccttgaacta	gagaaacttg	ntntggaaca	tttcaaaaga	tgaatgacaa	tctggattcn	720
ttggtngaca	gtgtaatttg	gactttaacc	ngatgctcg			759

&lt;210&gt; 761

&lt;211&gt; 752

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 761

cctnactaaa	cctttgcnaa	ngccttntnt	gctgatecca	tcgattcgca	ggcctggact	60
tcgccccag	gcctaggacc	gcggtgggtg	ttaccctgc	tnctgcccc	acagggactc	120
caatcaatcg	gagttctccc	cttgccggag	ctgcccttca	cctttggggc	ccgagacagt	180
cataagggat	ggacttacnt	ttcttgcagg	gaaaaaggtg	gacagccgtg	tttcttaagg	240
atgctgaggg	catggggcca	ggaccagggg	agaggcacag	ctccttcctg	agcagcctct	300
caccactgcc	acaaggctcc	ctaattgctg	tctctgctcc	actccccggc	ttcccgtgag	360
gcangaggca	gagccacagc	caaggccctg	accacttctg	tgccagttgt	ctaagcagag	420
cgcctcaggg	acgctggaaa	tgccttaagg	atagaggctg	ggcatcacat	caaattgggac	480
tgtggtggtt	ggtgaaaacc	ttcctgagga	tctggattca	ggaccctcca	tgactggcct	540
atttactggt	tacagctggc	cagtgcana	ctgctgctct	tttacctttt	taggcccctg	600
taacttncca	cctttaaact	gcccanaag	catgcctntt	ccacaggaag	aaggagcag	660
acagggaaat	ctgcctacca	anaagggtgt	tgtgtgtctt	tgtgcccaca	cgtgggtggc	720
ggggaatgcc	tggtatggtg	cgtggntgat	ct			752

&lt;210&gt; 762

&lt;211&gt; 1032

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 762

ttctaagtct	tggaacgc	ttgatgnang	atnccatcga	ttcgaattcg	gcacgagggc	60
aagtggtagt	ggcgcttntc	gggtgntgtg	cttcacgttt	tggtctaaag	gncgagactg	120
ttgtggcnac	ngngnaantn	tacnggaang	gnttaaantn	tnnntgnagt	nggaanaatt	180
cnatcnga	gaanttgagg	gggntagnnn	nggttanatn	attgatgaat	ggnttcaana	240
tngnaaantt	tatnancgan	atgnnatant	tnnaaangan	gaccaactgg	gntnanatgg	300
agnannnatn	aannggntaa	ncnatana	tantncattt	ggtanganaa	tngangaagg	360
attntcaa	agncatgtng	gangatgaac	ntnnaggnnn	nagaatattt	ggataaaatt	420
ggtantatga	agatntggnn	taataatacc	nanaaatnnn	nnantttnat	nanngangaa	480
ntagganttn	atgntctatg	ggatanntn	nanntatnat	agngataaan	tatgatactg	540
tttannttat	ntnganttag	tnattnaatg	ntcttgnan	aanttatatt	ncgntagtta	600
gntagnnnta	tnnacttttg	naancanana	tgtaattctc	tctanacggg	aatntttnta	660
tnntnnntat	caagaggtnt	ntnnattgna	aatantatac	nnntgnanaa	antatatcna	720
tanaanaaan	ggnnattatt	ntatatganc	aaanaaaaaa	ntattngnga	mntanattat	780
ctctcatnat	ngattatn	gtantgtata	atggnnnata	antatgtnnn	ntaanataa	840

atggatataa gtnttatant atgcncntna aggnnggtcng anaantatgt aattatattn	900
angctanata cnatnnanar gtntnactaa atatngntgt gaaangtntg cngngnaaaa	960
tntgttanta ntnaaacang gtataganat atanatngn ngaatatcta ctatntgtan	1020
atacttatan ca	1032

&lt;210&gt; 763

&lt;211&gt; 817

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 763

aanncccttn tttctaantc ttggctactc gtncctttctg caggatccca tcgattcgaa	60
tttcggcacg aggggagggg cccttggggg caggttgttg gtagccagtt gcagtctgtg	120
gcctccctca gaggtttgga gtcgggcgtg gcatgctgct gttggcctct ttccgagggg	180
gtgccatcca ctccctgtcc caccgctnnc cctngtgagg acagtgaggg cagtgtctacg	240
tgggtggggg gtgtgtgtga agccacggaa gggcttcaca gggcaaatgc caaggccagt	300
ggggcccgga cagagtnagg ctccctgggc ggncttgtgt cttgggtggc ctgatcatcc	360
tgccaatgca naaagccagc aggcagaga cccctactcc ctttaaggac cattagcata	420
aacaaaccat tngttgaat gcaatgatec aggtgcactt tnagggtaca agctggactn	480
gttggaacag gattacatgg aaaannggaa angggggcan gctgtctctt gggacatnag	540
taatgtcttt ttaccantt gncactctng aanttcaaan ttggncatgt tttctggggc	600
ctnctngnaa aagcagtttt ttcaccncat natgaagaaa aaacttggtg gcttgganng	660
tanngggatt nttgntnana cttnccttaa anggntncct ttnggggcat ttntgaagg	720
taaataatgg gggatacctt tttaannttc cttgcagatt taaaaatgtt ccttaaanga	780
nncctcaatg nttnggtctt nttccaaaaa acnattc	817

&lt;210&gt; 764

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 764

taatgcttgg ntctcgnntt tntgcaggat cccatcgatt cgaattcggc acgaggtcca	60
cgggtgctgaa catcatcatc tttgaagact gtaggaacca gtggtctatg tcccgaccac	120
tacttggtct gatattgctt aatgaaaagt atttttctga cctaagaaac agtattgtga	180
acagccagcc acccgcgagc cancnggcca tgcacctgtg ttttgagaac ctgatggaag	240
gcatcgagcg aaatcttctt acgaaaaaca gagacaggtt caccagaaac ctgtcagcat	300
tccgtcgaga agtcaacgac tcaatgaaga attccactta tggcgtgaat agcaatgaca	360
tgatgagctg acacctnctt ggactctacc tgtacagagc agcgtccctt tggtttggcc	420
cagaggggag aacaattgca agggagaggg cctggctgat cctggctctt ttctccaggg	480
gtgtggggaa aaatggcaaa ggtcaactag ctgcttcccc aagggaatag ggggtgtgag	540
acactcacta nggggcaagg cgctgcttgg ttcttggggg gactgggtgg gaaaggggtg	600
tnganggag ataaagagat tcaaactgag actccagtct ttcttcttgg gggccaccca	660
aagttgggga gnaacccct antggtncct gccacaacc ttgccttggg attaaacatt	720
ntncattttt ttcantaana tttttgaaca aagggttant attgncnaa gtttann	777

&lt;210&gt; 765

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 765

nttttcta	atg	cttggctctc	gntttgatgc	angatcccat	cgattcgga	aatgcaagtc	60
aaaacagctt	tgtaggtctc	agagtttgct	tttaagaagt	agtacaagaa	ggaatagtta		120
tatcaataca	ccagtggctg	aaattatcat	gaaaccaa	gttggacaag	gcagcacaag		180
tgtgcaaa	gctatggann	gtgaactcgg	agagtctagt	gccacaatca	ataaaagact		240
ctgcaaaagt	acaatagaac	tttcagaaaa	ttctttactt	ccagcttctt	ctatgttgac		300
tggcacacaa	agcttgctgc	aacctcattt	agagaggggt	gccatcgatg	ctctacagtt		360
atgtgtttg	ttacttcccc	caccaaactc	tagaaagctt	caacttttaa	tgcgtatgat		420
ttcccgaa	atg	agcaaaatg	ttgatatgcc	caaacttcat	gatgcaatgg	gtacgaggtc	480
actgatgata	catacctttt	ctcgatgtgt	gttatgctgt	gctgaagaag	tggatcttga		540
tgagcttctt	gctggaagat	tagtttcttt	cttaatggat	catcatcagg	aaattcttca		600
agtaccctct	tacttacaga	ctgcagtggg	aaaacatctt	gactacttaa	aaaaanggga		660
catatttgaa	aaatcctggg	agaanggact	atttggtcnc	ttttgccaac	ttacttcata		720
ctggnaagcc	agattantng	ctcaaggaag	ttttgatgag	ccaaaaaagt	tttn		774

&lt;210&gt; 766

&lt;211&gt; 779

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 766

ttnnncgctn	ntgaanaccc	cttctcctna	aatccttttt	aantnccttg	ctgnntgatc	60
ccatcgattc	gcgaaattcg	gtggcgccac	gtccgcccgt	cttngccttc	tgcattngcgg	120
cttcggcggc	ttccacctag	acacctaa	gtcggcgagc	cggccgcgtc	gtgaggggggt	180
cggcacgggg	agtcggggcg	tcttgtgcat	cttggtacc	tgcgggtcga	agatgtcggg	240
catcgagac	tggttcagga	gcatcccggc	gatcacgcgc	tattgggttcg	ccgccaccgt	300
cgcggtgccc	ttggtcggca	aactcggcct	catcagcccg	gcctacctct	tcctctggcc	360
cgaagccttc	ctttatcgct	ttcagatttg	gaggccaatc	actgccacct	tttatttccc	420
tgtgggtcca	ggaactggat	ttctttat	ggtcaattta	tatttcttat	atcagtattc	480
tacgcgactt	gaaacaggag	cttttgatgg	gaggccagca	gactatttat	tcattgctct	540
ctttaactgg	atttgcacgc	tgattactgg	cttagcaa	ggatattgca	gttgctgatg	600
attcctctga	tcattgtcag	actttatgtc	tgggcccanc	tgaacagaga	catgattgna	660
tcatttttgg	tttggaaac	gaatttaagg	cctgctat	accctgggggt	atccttggat	720
tcaactatat	catcggangc	tcngtaatca	atgagcta	tggnaaattn	ggtggacac	779

&lt;210&gt; 767

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 767

gnnnnnnntn	cccgctttt	gaaanccct	tctttcta	gcttggtcaa	cgcctttgct	60
gcaggatccc	atcgattcgt	ggatactgac	aatgggtggc	ggcatttcaa	gccttttaaa	120
ttagtacttt	ttgtcgnctt	gcttattaaa	attttgtaa	ttttagcaa	gaccaattgt	180
tgtgataaac	tgggtgtttt	nngatgcttc	aagcacagc	taaccaatcn	gccaatnccc	240
ctttnggttc	ctcccattgn	tctaaaatag	gactttcata	ttattaaaac	ctcaaaagat	300
gatccaccca	ggatgaacaa	agatcaccaa	ggggaaagaa	aacatttttt	atctttacag	360
aaaacatggt	aagattatat	atagatgtat	tctttacatt	ggatattgta	ttagagtcc	420
ccttacaaga	aatgaaatag	gttttttagca	ctcttagcat	tagagtcc	agattggtgt	480
tgatagctac	agttttaaaa	tgtataacct	gaaaatgaag	gttaattttg	cattgtaaag	540
agcacatttg	atctatgtaa	aaagtgtcca	tttggtgtat	tttttttaaa	aaagagaaa	600

```

cactttcata ttaagtagca tgtgtatgaa ttttaagattt tcatatttgn tngtctctgg 660
attcagtga gtaaaattga gcatttttaa agtttggtgg atggcaacca ttaactatta 720
aattaaaagc caccttatac tctgctgctt aacttgcttg naaattgcac ctttgggnacc 780
ctgcacattt tcatattnc 799

```

```

<210> 768
<211> 826
<212> DNA
<213> Homo sapiens

```

```

<400> 768
gnnnntnnn ccctttctaa tggtctgttt ctaaagtctt tttcnaatcc ttggtacatg 60
atcccatcgn ttgcgcgtgt gcttgagacc aacctgacgg gtaccttcta catgtgcaaa 120
gcagtttaca gtcctggat gaaagagcat ggaggatcta tcgtcaatat cattgtccct 180
actaaagctg gatttccatt agctgtgcat tctggagctg caagacnggg tgtttacaac 240
ctcaccaaat ctttagcttt ggaatgggccc tgcagtggaa tacggatcaa ttgtgttgcc 300
cctggagtta tttattccca gactgctgtg gagaactatg gttcctgggg acaaagcttc 360
tttgaagggt cttttcagaa aatccccgct aaacgaattg gtgttcctga ggaggtctcc 420
tctgtggtct gcttctact gtctctgca gcttcttca tcaactggaca agtnggtgga 480
tgtngatggg ggccnggagt ctctatactc actcgtatga ngtcagatc atgacaactg 540
gcccaaggga gcangggacc tttctggtgt caaaaaagat gaaaggagac ctttaaggag 600
aaagctaagc tcttgagctt gangaaaaca aggggtcctt ccatncccca aatgccttta 660
catttttggg ggatatgect nnnngnacnt ttttaaaaaa gcttatnagt tngntatggg 720
naaaacaatt ttttcttan tttttaaagt ggntaataaa tnaaantcct aatggnaaaa 780
aaactantcc ttggnaanta ttttccaggc cttnantgtt cccnncn 826

```

```

<210> 769
<211> 802
<212> DNA
<213> Homo sapiens

```

```

<400> 769
gnnnttctaa tgctgttcta atgcttgtca atncttgana cgttcatcga ttcgggaagc 60
caagcctgga gctgcaggtc ccccggcac tctctctgtc ccggcagccc aggatggcct 120
ggtgccccca cctgctgcag caggagcccc aaggagtgtc agctgagggg ggttgcctgg 180
gtggtcctca tggacagtga ggtgtgccc ggtgactga ggggtggtgg aggggatcac 240
ctgggttcca ggccatcctt gctgagcatc tttgagcctg ccttccggtg ggagcagaaa 300
aggccagacc ctgctgagtt agaggctgtc gggatccact gtttncacac agcgggaagg 360
ctgctgggaa caggtggcag agaagtgcc tegtngcntt gagccttgca gctcttcagc 420
tggggactgg tgcttgctga aacccaagag ctgaacagtg aggaggctgt ccacctgtct 480
tggctcactg ggaccaggaa agcctgtctt tggttaggct cgtgtacttc tgcaggaaaa 540
aaaaaaagga tgtgtcattg gtcattgat tggaaaagg ggaaggangc cnaaanttgt 600
tcccatttta ttcaagtatt ggaaaatatt tggccccctt ttggctgaaa ttctttttgc 660
aanaactaac tngtggctt gttcncttac cctttttcan gnttaattgg tttnaatttt 720
ttgcattgaa attaaagacg tttttaaatt tcntttncan naacaaaggg cttanatncc 780
ngantcnana nattggnant tc 802

```

```

<210> 770
<211> 1157
<212> DNA
<213> Homo sapiens

```

&lt;400&gt; 770

cccttttttt	ttttcccn	aaaaaaan	at	tgggggccn	tttttttggg	nttttttttc	60
ccnaaaaaa	aattgggncc	ctttttggg	ggnntnaaaa	aaannnnnnn	ccccccntt		120
tttttggggn	nnnnnaaann	tnnnnnncnn	nttnnnnnnn	nnnnnnnnnn	ggnnntnnng		180
gggnnnann	cncccccca	ttcccggn	attnttccg	gcccaatttt	tgggaccccc		240
cagggnnnag	aataaggccc	gggnttttt	tttncnagg	ncccaaaagg	gcccttgggc		300
caaaggnaaa	tcnttggga	aattttggg	atttggccct	tggnanntcc	caataccggn		360
aaaaatgggg	aaangnaaaa	aaggnttn	cn	ccaaattggt	tggggggggg	ttccaaagat	420
tttcattggg	ggtncntggg	ctttcaacc	naaggnaang	ggtttnttt	caaaaaatta		480
cctttaattg	ccattaagca	attcccaang	gttannaag	ggtgtttntt	ctcanctatg		540
cttcganagn	gaaaatcaac	naatggaaaa	tgtgttgtaa	ttggtctgca	ntctacanga		600
gaagctagaa	cattagaagc	tttggaanag	ggcgngggag	aattgaatga	tnnttgnttc		660
aactgccaaa	gagtgtgtt	gcagtcactc	atttgaaaaa	ctattttcct	gtccagaca		720
ngaaaaaaac	tttatangtt	tactaggaat	cgatttgaca	agcnttcang	taacaaacag		780
ttctnccaag	agatatacct	gttnaagaan	nattanaata	ncnngaaagc	ggaaanngtg		840
aataaatnnc	ttcnagaagc	ccaaaaannc	antctngatt	ncctctgatt	antgaatgaa		900
agcacgttct	tgacnacaga	tggaaattga	antctngatt	ncctctgatt	antgaatgaa		960
aagggtgacta	ttnaanagct	cttnanatac	catgagtntt	tggancattg	attgaccaat		1020
ttcaanncca	tttttangat	ngaattntta	tnaatgattn	attnanaant	gannnccttn		1080
gtttaaatta	nnaaanaanc	cntcnaaana	cnaaggggga	tttataaaat	ctaataanan		1140
ttttnnncnt	ntnaann						1157

&lt;210&gt; 771

&lt;211&gt; 760

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 771

ngncctttna	tncttntga	ancntttgn	aattnctcnn	nnngttgatc	ccatcgattc	60
gaattcggca	cgaggtggaa	gaaaattttt	tgctgcttct	ggttnccaga	aaaggagacc	120
attttaacag	acacatctgt	caaaagaaat	gacttgctga	ttatttctgg	ctaatttttc	180
tttatagcag	agtttctcac	acctggcgag	ctgtggcatg	cttttaaaaca	gagttcattt	240
ccagtaccc	ccatcagtg	accctgcttt	aagaaaatga	acttatgcaa	atagacatcc	300
acagcgtcgg	taaattaagg	ggtgatcacc	aagtttcata	atattttccc	tttataaaaag	360
gatttgttgg	ccaggtgcag	tggttcatgc	ctgtaatccc	agcagtttgg	gaggctgagg	420
tgggtggatc	acctgaggtc	aggagttcga	gaccaacctg	accaacatgg	tgagaccccc	480
gtctctacta	aaaataaaaa	aaaaatttagc	tgggagtggg	ggtgggcacc	tgtaatccta	540
gctacttggg	aggctgaacc	aggagaatct	cttgaacctg	ggaggcanag	ggtgcaagtg	600
agcccgagat	cgtgccattg	cactccaacc	agggcaacaa	gagtgaaact	ccatcttaaa	660
aaanaaaaaan	gaaaactcga	gcctctagaa	ctatagttag	tcgtattacg	tagatccaga	720
catgataaga	tacattgatg	aattttggac	aaacccann			760

&lt;210&gt; 772

&lt;211&gt; 777

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 772

gaaancccat	ttnnnnnttc	cncttcnaat	cccttggnta	ctcgnctttt	ntgcaggatc	60
ccatcgattc	gaattcggca	cgagctctac	taaaaataca	aaaattagct	gggctggtg	120
gcacacacct	gtaatcccag	ttacttggga	ggctgaggca	caagaatcgc	ttgaacccgg	180

gaggcggagg	ttgcagttag	ccaagatcgc	cctgctgcnc	tccagcctgg	gcaacagagg	240
gagactctgt	ctccaaaaac	aaaaacaaaa	actgttagtg	aagggtccct	gggacttttg	300
atattttaaa	aattgttctt	atgactagta	gataaattca	ttgccataat	gaggctagct	360
cccagataaa	cagtgtattt	tcttcttttt	tttttttgg	gagtgggtcca	gagctttaag	420
ctacttttcc	agtagtttgc	cactttctcc	gaggtanttt	ggctgctctt	tcagtaatgc	480
taattgtgtg	tcaaattttg	tctacaacag	taggcaacag	atgaagataa	gttggttgaa	540
tgtctccagc	actatgcac	cctattttct	atattttggg	gtacactcac	tttcagtaat	600
gngtttcaaa	ctggtatttt	ttaaaaaaca	aatcaatgta	aggactgaag	ttgaaatanc	660
caatgtaata	aagttaatta	gggttatttt	taaaaaaaan	aaaaataana	actcnagccc	720
tctagaaaact	atangtgagt	cgnnttacct	tgaatcccag	accttgataa	gatacnc	777

&lt;210&gt; 773

&lt;211&gt; 782

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 773

gnntnnatcc	ccctttcnaa	tncttggcaa	acgctctctn	tgttggatcc	catcgattcg	60
aattcggcac	gagacagtct	cgggtttcat	atatttgcgt	ttttgatgga	catggaggaa	120
ttcagacctc	aaaatttgct	gcacagaatt	tgcatcaaaa	cttaatcaga	aaatttccta	180
aaggagatgt	aatcagtgtg	ncncccgccg	tgaagagatg	ccttttggac	actttcaagc	240
atactgatga	agagttcctt	aaacaagctt	ccagccagaa	gcctgcctgg	aaagatgggt	300
ccactgccac	gtgtgttctg	gctgtagaca	acattcttta	tattgccaac	ctcggagata	360
gtcgggcaat	cttgtgtcgt	tataatgagg	agagtnaaaa	acatgcagcc	ttaagcctna	420
gcaaagagca	taatccaact	cagtatgaag	agcggatgaa	gatacagaaa	gctggaggaa	480
acgttaaggg	atgggcgtgt	tttgggcgtg	ctagangtgt	cacgctacat	tggggacngn	540
cantacaagc	gctgcngtgt	nacctttgtg	ccccgacatc	agacgctgcc	agctnacccc	600
caatgacagg	ttcattttgn	tggccttggt	atnggctctt	naaaggnctt	tnccccatna	660
aggaagccng	tggaaactttc	atcttgnctt	gnantcgang	atnaaaaaagn	atncagaacc	720
cggggaaggg	gaaaatcctn	aannctgact	tcccggtttc	caaaccagtn	ttgnaacaaa	780
nc						782

&lt;210&gt; 774

&lt;211&gt; 793

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 774

gnannngccn	cgnttttgat	tccccttntt	caaatecttt	gnnaatcgcc	ctenctgttt	60
tgatcccatc	cgattcgaat	tcggcacgag	atggcagttg	cttttgaagt	atatgatggn	120
ttcctccact	acaaaaaggg	gatctaccac	cacactggtc	taagagacct	tttcaacccc	180
tttgagctga	ctaatcatgc	tgttctgctt	gtgggctatc	ngcactgact	cagcctctgg	240
gatggattac	tggattgtta	aaaacagctg	gggcaccggc	tggggtgaga	atggctactt	300
ccggatccgc	agaggaactg	atgagtgtgc	aattgagagc	atagcagtgg	cagccacacc	360
aattcctaaa	ttgtagggtg	tgccttccag	tatttcataa	tgatctgcat	cagttgtaaa	420
ggggaattgg	tatattcaca	gactgtagac	tttcagcagc	aatctcagaa	gcttacaaat	480
agatttccat	gaagatattt	gtcttcagaa	ttaaaactgc	ccttaatttt	aatatacctt	540
tcaatcggcc	actggccatt	tttttctaag	tattcaatta	agtgggaatt	ttctggaaga	600
tggtcagcta	tgaaagtaat	agagtnttgc	ttaatcattn	ggaattcaaa	catgctatat	660
tttttttaaa	aatcaatgtg	aaaacataga	cttattttta	aattgntacc	aattacaata	720
aaaataatgg	gcaattaatt	tttnaaaact	ttttaaaata	gnatgctcat	attttttaaaa	780

ataaaanttt tnc

793

&lt;210&gt; 775

&lt;211&gt; 1009

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 775

```

agcntttttt ngaantttcc ctttnnttna aaaatcccct tttttggcaa aaaattnccc      60
ccntntntna nngtttttnn gatncccaca tncngnaatn tncgggcncg ggnnactgnc      120
nannggcnc cttcgggggn ccngtgntaa gncnatnctt gtntntanaa agntggnnnt      180
nttttncgat ngngactatt gncnacnctc ttcctntttg gcagngngtc tgganggttg      240
nggtngctca tntggntaan ccnatcctgg ngaccaanng gccgnggtgn gcntgcaagc      300
tttgncacn tgggaaancc gnnagtggtn gtctcanttg cntgntgggn ncntgncccc      360
atcttgncgt ctgnancctt ggggagcagg nctnggtng tggtnctgcc tgcttgctgc      420
tngttccccg ggcctgcgtg nncannaagg gncatgcntn gggcaanaag gtgcgtggnc      480
ancgttngna tnnnnaggac caccntgggt cgngaacnn tgggttncct gataggaacc      540
ntnaannnct gcngntttta ttaaattggga nnanangggg ncanttcaaa gccagttnaa      600
tgcccttatg gaangngtg natnacatan cnnntatgt gtcttanann angaaatcgt      660
tnnncaaatt tnnacaanaa tntttntaan aaagggtatt tnantntngg tgaaanaaca      720
angntttaaa gtnaaatgnt tntancanaa ttaantaaac nggtnttnat gattncttac      780
naaantaacn atncnnaagc atttacngct tanangtcen cnggatactn ncanaatatg      840
gnnnnaattn tannanatng cgataatctn gnananactn tcatnnnnna tngtgaatc      900
antanntacn tgatttnnnt naaatgaaaa catntgatnc aagattaatn cattanntat      960
acnaaaatnt tcanatanta natntacata taatgggttc naataaacn      1009

```

&lt;210&gt; 776

&lt;211&gt; 785

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 776

```

gnnnnnnnntt cccctttcta atcncttgga nntcgctctn tntgnangat cccatngatt      60
cgaattcggc acgagagaaa cacaggtgtc gtgaaaacta cccctaaaag ccaanatggg      120
aaaggaaaag actcatatca acattgtcgt cattggacac gtanattcng gcaagtccac      180
cactactggc catctgatct ataaatnngg tggnttcgac aaaagaacca ttgaaaaatt      240
tganaaggag gctgctgaga tgggaaaggg ctccttcaag tntgcctggg tcttgataa      300
actgaaagct gagcgtgaac gtggtatcac cattgatatc tccttggtga aatttgagac      360
cagcaagtac tatgtgacta tcattgatgc cccaggacac agagacttta tcaaaaacat      420
gattacaggy acatctcagg ctgactgtgc tgnccgtatt gttgctgctg gtgtnggtga      480
atttgaagct ggtatctnca agaattgggca naccnnaaag catgcncctn tggcntacac      540
actgggtgtg aaacaactaa ttgtcggngt taacaaaatg gattcacttg accaccctan      600
aggccngaag agatattgan gaaattgtta aaggaagtca gcacttncat taagaaaatt      660
ggcctacaaa tccnnganac aataancatt tgtgccatt tnnnggttgg gaatgggtga      720
ccaacattgc ttggagccca agtgnttaac aatgccttng gttnaaaggg antggaaaag      780
ttacc      785

```

&lt;210&gt; 777

&lt;211&gt; 1366

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 777

ananaann	annnnnnnaa	ggnaanaana	nnnnnnnnnn	naanangnaa	ananaannnn	60
tnnanaann	aagnngnttc	nanncttttc	aaagcttgga	aaacgcannc	aannnnnggg	120
aaagcaagaa	agaacagcta	aagnnngncn	cagaganagc	ttttangang	tntangaaga	180
aggaatan	gnngncaata	nnnnnnnnnc	ngaaantatc	atganacnca	aatganggan	240
aaggcagcac	aagctgngca	aacagctatn	gngacggggg	ggccgggaga	gnctaaangn	300
cananatnca	atatataagg	actgcatgcn	aagggatacn	aaacaagnan	actnntctag	360
gaagaaataa	ntnttgacnt	ancnnacntt	cataacgaat	agcaccgtac	atcgagncaa	420
ccaactaana	ggcnctaagg	aatggcaaan	nacnttaatn	nntgagcnaa	ggaagggngt	480
atngnccnan	anngaaatgc	ntcntaacca	anttttaatn	gtaacggnat	nangatnaan	540
ncntnanccc	acgcaactca	aaaanattac	attanntaaa	aaaganctat	ancaaaacta	600
gtnttcaaaa	tngnacgagn	aaatgggnaa	nantttntnn	ccgggaaaat	tggngagat	660
ccanaaacac	tggntnaggg	naatanatgn	ccgcccnaaa	aaacctnna	cataggnatn	720
ggctancata	gangagatat	ancnatnagg	ggatcaanan	cntaggnatt	ngaaaantaa	780
ncgagttaaa	acancnagat	nnggnantac	gaganatagc	ttggacngt	atcaaactcg	840
accctnggat	gggcntang	aaaaanaaaa	aggntngagn	gaanttcctc	anaggaanng	900
tganagagcn	aaanaaanatn	aagggccttg	gngaaaang	aaaaacagat	agngtcatnc	960
nataatnncn	natgananan	tggggnaatn	taatctacnn	tanatnnggg	ggaaaaaaat	1020
cnnncatgac	nnnaaaanga	gntaatgnna	nnatgagaga	ttaaaccnnat	aaaacnagag	1080
aantttgngn	aaanctgnga	gataaaaaat	aaataaatc	tntntggaac	atntanaccn	1140
tctatnnaaa	aaaaagaggg	gaaaccatct	ngattatgca	cananaaatn	tnacntngng	1200
gaaataaatn	gggnacaata	acatatatgn	ggatgtacan	tnntggncng	aaaaactata	1260
caacntgaga	nnnnacnang	atataaagcn	nnaggngatn	tatangggca	tcatcaangg	1320
gaagntataa	agcaactgna	nnctcatata	naaaactggn	cnncaa		1366

&lt;210&gt; 778

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 778

gntttnnatn	cctctttcta	atnncttggc	tactcgntct	ntctgnanga	tcccatcgat	60
tcgaattcgg	cacgagagat	tatgagcatg	tagaagatga	aacttttcct	cctttcccac	120
ctccagcctc	tccagagaga	caagatgggtg	aaggaaactga	gcctgatgaa	gagtcaggaa	180
atggagcacc	tgttcctgta	cctcccgcgg	ccgaacagtt	aaaagaaata	taccaagct	240
ggatgctcag	agattaattt	cagagagagg	acttccagcc	ttaaggcatg	tatttgataa	300
ggcaaaattc	aaaggtaaag	gtcatgaggc	tgaagacttg	aagatgctaa	tcagacacat	360
ggagcactgg	gcacataggc	tattccctaa	actgcagttt	gaggatttta	ttgacagagt	420
tgaataacctg	ggaagtaaaa	aggaagttca	nacctgttta	aaacgaattc	gacttgatct	480
ccctatttta	catgaagatt	tttgtttagca	ataatgatga	agttgcggag	aataatgaac	540
atgatgtcnc	ttctactgaa	ttagatccct	ttctgacaaa	cttatctgaa	agtgagatgt	600
ttgcttcttg	agttaagtag	aagcctaaca	gaaggagcca	accacaaaga	attgagagaa	660
atnaacaact	gggccttngg	aaagaaangc	nggccaagct	gcttgagtaa	tagtcaganc	720
ctanggaat	gatntgggta	atgaattcac	cccaggncac	accngttga	agagc	775

&lt;210&gt; 779

&lt;211&gt; 781

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 779



```

gcttttnann nccctncttt cnaancctct tcaaatccct ggntatcggt ctntctgnng      60
gatcccatcg attcgaattc ggacagagag acaaagaaaa aggtggcaat catagaagag      120
ttagtagtag gttatgaaac ctctctaaaa agctgccggt tatttaaccc caatgatgat      180
ggaaaggagg aaccaccaac cacattactt tgggtccnnt nctacttggc acaacattat      240
gacaaaattg gtcagccatc tattgctttg gagtacataa atactgctat tgaaagtaca      300
cctacattaa tagaactctt tctcgtgaaa gctaaaatct ataagcatgc tggaaatatt      360
aaagaagctg caaggtggat ggatgaggcc caggccttgg acacagcaga cagattttatc      420
aactccaaat gtgcaaaata catgctaaaa gccaacctga ttaaagaagc tgaagaaatg      480
tgctcaaagt ttacaaggga aggaacatca gcggtagaga atttgaatga aatgcagtgc      540
atgtgggtcc aaacagaatg tgcccaggct tataaagcaa tgaataaatt tggatgaagca      600
cttaagaaat gtcattgagat tgagagacat tttataggaa atcactgatg accagtttga      660
ctttcataca tactggatga aggaagatta cccttagatc atatgtggac ttattnaaac      720
tatgaagatg tacttttnaca gcatncattt tacttcaagg cagcaagaat tgcttttaga      780
c                                                                                   781

```

&lt;210&gt; 780

&lt;211&gt; 783

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 780

```

gnnttttnan nncnngnttt ctaatnctnt tcnatnctt tgnnancgtt ctntatgcan      60
gacccatcga ttcgggaatc tcctagaaaa gttgtgattt tcgagccata tccttctgtg      120
gtagatccta atgatcctca natgttggtc ttcaacccca ggaaaaagaa ctatgatcga      180
gtaatgaaag cactggatag cataacttct atcagcnaaa tgacacaagc accatatctg      240
gaaatcaaga agcaaatgga taaacaggac ccccttgctc atcccttact gcaatgggtt      300
atatcaagta atagatcaca tattgtgaaa ctgccagtta acaggcaatt gaagtttatg      360
catactccac atcagttcct tcttctcagc agtccaccag ccaaagaatc caattttaga      420
gctgctaaaa aactcttttg aagcaccttt gcatttcatt gctcacacat tgaaaactgg      480
cactccatcc tgaggaatgg tctggttggt gcttctaata cagattgca gctccatggt      540
gcaatgtatg gaagtggaat ctatcttagt ccaatgtcaa gcatatcatt tggatctcag      600
ggatgaacaa gaaacagaag gtgtcagcca aggacgagcc agcttcaagc agtaaaagca      660
gcaaatacat cacagtcacn ggaaaaaagg acagcaatcc caattcctgc caaagccgta      720
acttaaaatg catagncctt atgtgaaagg gatcaccttc atctggacct gcacaaacat      780
ggc                                                                                   783

```

&lt;210&gt; 781

&lt;211&gt; 796

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 781

```

gnnntnccgc ttcaatnctn ttcantctnt tcaatctttg aatcntcttt gttgtccatc      60
gttcaattcg gacgagaccc ttatggcaga tccccacagt ctggggcaga agagggcgtc      120
aggngccaga agtgnccgga gcagcagccg cagcagccca aagagaggca agagaaagag      180
aaagcggccg gtggaggggt nncggaaga gctgggtccc gtggttgagc tgggtccccg      240
tggttggaatt ggaagaggcc atagccccag gctcagaggc ccagggcgct tgggtctggt      300
ggggacgcgg ggggtgcccc caatggtgca gctgcagcag tcaccactag ggggtgatgg      360
agaggaaggg ggccacccca gggccattaa caaccagtag tccttcgtgt gagccaaccc      420
cacccgctcc acccttttta aacccccag cccttgctcg tgagattggg ctggggtagg      480
gacagaagag gcccgaaatc cctcccccat gcttntctgac ccttggttgg ccaaagggca      540

```

tctttgatgg	tacaaagcag	angcttcggg	anaagcttcc	gtcacaacac	tncaaggctcc	600
cttcccaagg	gcaaggggat	ttnggcttca	tgagctnctt	tgaggggctt	ttttttggtc	660
annccccacc	ttnggggccca	tttttcccaa	tttaacttacc	cccaacccca	agnccanggtt	720
nagggggnaa	agggtcttcn	anttccatta	aaggggggtt	gtttgttgnt	gttttaaac	780
aaaatgggga	aancnn					796

&lt;210&gt; 782

&lt;211&gt; 886

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 782

cggnnnnnnn	gnagccntt	tggnaaangc	ctctaaggga	aangcctttt	tgaaaaacnan	60
angaaaaact	ntgggaaaag	nccncannna	ttttngngaa	annggcnnga	gcnnanantn	120
ggacacngtt	ntaannnnan	nagngnngt	tttnnganan	agggnnnnna	gnngnannna	180
ngngnnggag	ggaannaagg	nanagnannn	ggnagnnaag	gnnnnaaaga	agnagnnang	240
gaganggnnn	gnngnggggc	atgangnggg	nncagaggca	cgaggagccc	aagaccatca	300
cngangagna	ngagcagggn	accnacatnn	acnnggacna	cgagaagngg	ggccagcgga	360
agaaggaagg	nagnacctng	agnaccgnta	ccaggaggan	cgggaccnac	agnagacanag	420
gnccnnnnnc	anacggannn	nanaaacgng	aagcaggann	nnnanggacc	aagggaaggg	480
nnngnncnn	ggaaaganng	ggaggagggn	ncgaaggcaa	aggggggann	cgnnannncc	540
aggaagnang	gaaggggggn	cgggagggna	annganaaga	ngaaccnngg	gggnncaggg	600
gggcgagggn	agcanaannn	nnccnnagnc	aanngaaggg	gananaagag	ngggaaaann	660
aannagaaag	agggaaaana	agnnaaggaa	anaaaagang	ngnnaannng	gganaaaaana	720
ngngganann	gnngganana	ngngnannan	aaaanngagg	aggncannng	gnaaanaana	780
nggggagggg	nganananag	ngaannagac	aaggaanagn	gaannagngn	anagnanngn	840
gnannaaagg	nannggggna	anaagnanna	nannnnnagn	gaagan		886

&lt;210&gt; 783

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 783

cnaatncttg	ctcttgnctt	ntttcnaatn	cttggcnact	cgctttctnt	gcggtatccct	60
cnnganncna	tcgttcgaat	tcggcacgag	cacaaggaga	agaaagttaa	ttaacattga	120
aagatgagaa	gacatcttgg	aagacttgaa	ttgggccttg	gaagaagaac	agccattcaa	180
atagatagaa	ttgtggtagc	aaaggcatac	ngntcggaaa	gtatagatct	ccaggggacag	240
tagtcatggg	gttggggcac	tggttgaatt	taaggttgga	aggatatatt	ggagcccctt	300
gaatacggta	acaaggcaca	ccttgggcag	tgagaggtta	tcagagtgtt	tgaaaaggag	360
ggttattgag	tataataata	gactggtact	ttaggaattt	taaaatgtgg	atcattgtac	420
tactaataac	tatntatttt	atatttacta	tctactaagt	aattttacatg	tattttcttg	480
tactgactgt	aaaccttctg	ggtgtgggtg	ttttaagtgc	cattttactg	ataaagaaac	540
tgangcttaa	atagntgaaa	tanntcacc	tgtagtgag	tggcacaatg	acaagtcann	600
atcttanggt	tgccnanntc	caaaanncat	ttaaanttnn	agnatnattg	annnttttnc	660
cttatggcnt	nnnaaatttg	gggagccatt	attgaaatcc	nttacnacnt	angaattgnc	720
caaaaaaat	actttttggg	gaaaactgga	tttattaatt	atccaaaata	atttnantgg	780
cttgnttggc	ttntttccac	tntnc				805

&lt;210&gt; 784

&lt;211&gt; 776

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 784

taatgctggt tactgccctt caaatccttg caatcccttg gnaancggnc cngcngaccc	60
atcgattcga attcggcacg aggttatatt aaattattct ttgntnttct ttgtctttta	120
ataaagcctg caagttacta aattgnagtt ncataaatc ttagttnaag tatcatcttg	180
gcagngtgcc aaaggtgaaa angntgcttn ctctaacaga gaaattctta gngactccag	240
tcgtanaaaa acgtctttac aacctgaata agatnganga attngaaaca taccatggcc	300
tattggatga atcatttgcc ggnggctana ncagactgta gggtttgatga tggatntatg	360
gagtatgtgg gtatagaaat catgaatntn ccatttgnnn ncagagattc aagcntanac	420
ttaatgggta gatcataaat gacagaatga attcaaaacc tagcacgtgc attgtaaattg	480
tgtgcccaga tatgtnttgg aaatggcagn tccttggggg catgtntcta ctggcaaaat	540
ttgctatagn gnnactattg nantgtaatt ataaaattna tcannattat ncaccgattn	600
gccaagtaaa ctgtactgtg cataggaatt ttgggaattg tgcanaaatt ggatcaattg	660
aanttnagaa cngatgtctg ggcttaaaaa ttatcnggg accacnnatt angaaactna	720
catntttcgg ngctgaggtt cattgnccaa ggccangaag gtntttncgg aaaanc	776

&lt;210&gt; 785

&lt;211&gt; 778

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 785

ttngaaaaacn ccttngcttn gttncacctt cngaaaccct tttgaaaacc ntttgcnnann	60
tcctctttnt gnaggatccc atcgattcgt gaaagaggag atcggtgacc tgggctcctt	120
atgtgcctga atgagtttga gtttcctgtt aactccaaat caacagtatt ttcaacaaga	180
aatgtgcaat tgaaatcaag tgctgtttta gtgcagctag gantccacag gaagacactt	240
gcagtgaaca gagttatgga gcagcaaaaa cacagatcta tttggaaaaa gagaaaacat	300
atgcgttgta ttttgcttca attataaaat accatcctct caaagggtgt tctaaattac	360
aaaggacttt gatttctagg tagattctgg gtagagactt cctttcatat tgaggcatta	420
atgacacctt ttaacctggg aagcaatatg actggagttg tactttgaga agattaatca	480
ggtttggttg cagaatgaaa gagaagatga agtcaagaga ttggtttaga ggctctagca	540
gaagcttagt catatttcaa aatgatcaaa tatcaagaaa aattctgagc tgcataactt	600
gtataaagta attttctagtg atttttttca tggttatgat aaaagaactg gattagcaga	660
aacttttacc ctgaatcaag atttaatttt tctttgagct catcttaagg atatcggaac	720
atagggagca aacgatggtg tggctgcctc antgcttgaa ttttaacngt tttgaaan	778

&lt;210&gt; 786

&lt;211&gt; 805

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 786

ngccccccct tccccccctn ttgaaanccc ctttgggnana nncnntttc aaatcncttg	60
naaatccttg gcnactcgtn ctntctgcag gatcccatcg attcgaattc ggacgaggag	120
aggatcactt gagcttagga gttcaaatcc agcctgagcc aacataacaa gactttgtct	180
ctaaacaaaa cagttattgt ttaaagaatc tgaaatcttc atctttaatt caggtagccg	240
tgaatcgagc ccaagtttgt ttgatatcca gttccaagtc tggagagagg catctttatc	300
ttattaaagt atcgagagac aaaatatcag acagcaatga ccaagagtca gcaaattgtg	360
atgcaaaagg gctatcaaag ggaggctttt tacagagaac taaggaagag aaggaggttg	420

ttaaagagac	ttgagatcag	aaaaagatca	agaacaactt	gaatctcaaa	gtatgaattt	480
gaagtatttt	gctgagcaaa	catttgaatg	cctgtatgta	ccgtaatcct	ctatcactgg	540
ggcccccaac	cccgtacca	gcccgtaggc	tgctagggac	tgggccgcac	agcaggaggt	600
gagcagtggg	tgggcaagcg	accattccca	cctgagcttc	ccctcctgtc	agatcagcag	660
cagcgtaga	ttctcatagg	agtgcataac	cctattgtaa	actgcccattg	ccaagggatc	720
tangttgcaa	cgcttcctta	tgagaanttg	aatgcctgan	ngaactgtca	ctgncttcca	780
tnaaccacca	gatgggtact	ngttc				805

&lt;210&gt; 787

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 787

ccttggnnag	nngccccctt	naaanccttt	gaaaaccctt	ggcaaangcc	ctnnnngnnn	60
gatcccatcg	attcgaattc	ggacgaggag	aggatcactt	gagcttagga	gttcaaatcc	120
agcctgagcc	aacataacaa	gactttgtct	ctaaacaaaa	cagttattgt	ttaaagaatc	180
tgaaatcttc	atctttaatt	caggtagcac	cgactcgagc	ccaagtttgt	ttgatatcca	240
gttccaagtc	tgagagagg	catctntatc	ttattaaagt	atcgagagac	aaaatatcag	300
acagcaatga	ccaagagtca	gcaaattgtg	atgcaaaagg	gctatcaaag	ggaggctttt	360
tacagagaac	taaggaagag	aaggagggtg	ttaaagagac	ttgagatcag	aaaaagatca	420
agaacaactt	gaatctcaaa	gtatgaattt	gaagtatttt	gctgagcaaa	catttgaatg	480
cctgtatgta	ccgtaatcct	ctatcactgg	ggcccccaac	cccgtacca	gcccgtggcc	540
tgctagggac	tgggcccgca	cagcaggagg	tgagcagngg	gtgggcaagc	cgaccattcc	600
cacctgagct	tnccccctct	gtcagatcag	cancagcggt	agattctcat	aggagtgcga	660
ccctattgta	aactgccatg	cnagggatct	aggttgacag	ctccttatga	ggaattgaat	720
gcctgatga	acttgnact	gncttccatc	acccccagaa	ngganctggc	taacc	775

&lt;210&gt; 788

&lt;211&gt; 774

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 788

gaaacccttt	tgtnaanagc	cncttcaacc	cnttctaattg	cttggcaatc	gctctntctg	60
cangacccat	cgattcgaat	tcggcacnag	attatttcca	aagcagccta	cagtagaaaa	120
tagtcattat	ggcagcagct	tctgatgttt	ttgtttggta	ggttttctga	tttcaatata	180
tagaatcata	ttcatagagt	atcttctntn	ccgcctngca	caaagtacc	atttaaaatt	240
tacatgcaca	gttcattgcc	acctttctta	ggcctatgca	tagttaataa	ggttataatc	300
tactcaacat	ggaaaatgga	gcctatttgc	aaacacacaa	gtaattaaag	taccaattct	360
ctcttagttt	ctttttttat	agtttggtta	ttttgcaatt	ataaatgtta	aacatcccta	420
gagatgaaag	ttaaaatggg	tgatcacaga	tcagtagcaa	aatacaaat	gacaattcaa	480
aattataaat	aaaactctgt	tgaggatgtt	taactttgag	tctccaaatt	taagagctaa	540
gcttggaaga	aacaaattta	taggttatat	ttccctctta	aattaaanaa	acaaacttcc	600
tctggcagta	gtttgggtgaa	ttcctttcat	tgnaatgata	ccatgattac	aggatcaaaa	660
atgcttaact	tacttgccat	tctgctcaca	tcacacagag	ttgtnttttt	tttaaagcac	720
tcnatgtagg	cattttaaac	cttcnggata	accagagtat	cttttgagaa	annc	774

&lt;210&gt; 789

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 789

ngcccctttg	aancnncng	aaatcctttg	gnantcncn	ctntctgtng	gatcccatcg	60
attcgaattc	ggcacgagag	cagatttgng	ataaacntnn	tnaggttna	accnaagggg	120
aactnntggt	gcaactatgn	ngnttggaag	atgctgcnta	tgtttattga	ggattgcann	180
anananattc	tgaatnctcg	ccntttncna	aggttggtat	aaagcactca	agccagctac	240
atatgtatag	aacggnttaa	aatcnatgag	gaagcctgga	ctaaatatnc	catnggactg	300
gngccnanaa	ngctgncgat	gaactttgna	tctggnnaga	agtntaaaga	atggcaggat	360
nantnnctaa	ngatgaattt	cannacnggn	nnccaccan	tcttnaatnc	tttaagatca	420
ttatacgaag	ncnangaaaa	ggtggcaatc	atngaanaat	gngnatnatg	ttangaaacc	480
tctctaaaaa	gntgacggca	ctttaacccc	natgatgatg	ggaaggagg	accaccaacc	540
acattanttt	ngggtccagt	actacttggc	acanccttat	nacgaaactg	gncngtncnt	600
ctattgcttt	gggagtaccn	taaaatacng	ccntngngag	tncacctnca	atgaatnnaa	660
ntctttntc	anganagctn	nngatccata	ngacntgctg	ganatnttta	aggaancttc	720
nangnggan	tggattaggc	ncaggccntt	ggacacanc	ntncttnatt	tnc	773

&lt;210&gt; 790

&lt;211&gt; 953

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 790

aanannnngg	gnnnnnnnnn	nnnnnnnnnn	nnnnnnnnan	ngngnnnttn	aaanccttnt	60
aanngncnnt	ncngcttnaa	accttggnaa	ncnccgccc	nttgcanana	angngaannn	120
atgcttngtg	aagcctgann	ccaaanctna	agganaggac	ctggatcccc	ttatatngaa	180
naancgggtnt	ggaggaanga	gnntgtcngg	gaggatgggg	cagaaaatga	ngnnggcaga	240
ntggncctgg	gggtctgca	naccagcctt	ggagcctgct	cattctgggc	ccttgctgcc	300
aagganccca	gcctnaccta	gcangaaang	anatgaaagc	ccttctccca	ngaggtaggg	360
tctaggctgc	ccnaacttaa	atgcattnag	aaanctcnta	gatgtggaaa	natttttncg	420
aacctgaaaa	tgcagctggt	anaatntcaa	tgggaagcat	aaatnecatg	aaaatataat	480
tnagntngaa	tatnanngta	aaaatgcact	tttnngcggt	gtgacngatc	ctgggncccc	540
annatctggn	attnaagngn	tttacnaang	gaanggaaag	gacctttnc	taaactacct	600
ttttgaacag	ancattaaga	angnncnttc	ttttaagnaa	aaaaaaatca	aattttgang	660
aaaantggna	ttngaattgn	nagaaaaang	gatananaan	aaaanccaat	nntaannacc	720
nannctctct	gganttcnac	tatctccact	acntacntnt	acntatngcg	ntaanatnna	780
ctnttacntc	nnntantcn	cacanaacntc	ntcnaacnta	atnangcncn	canaatcctc	840
tatannatnt	antgtnnttc	acannncnna	cnggntaant	ntnnncaacg	ccatatacacc	900
nctnnnatcg	ncnagntana	taacacntat	atcgncactc	ncacananac	tcc	953

&lt;210&gt; 791

&lt;211&gt; 798

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 791

tggnanngcn	ctntntgttt	gatcccatcg	attcgaattc	ggcacgagga	tcattgttaa	60
ttagtgacat	agtaacatct	gtagcagctg	gttagtaaac	ctcatgtggg	ggtgggggtg	120
gggtgtattc	cttgggggat	ggtttgggcc	gaatggggag	tggaatattt	gncttcncc	180
tgttttaaat	tctaggatag	attttaacat	cctttgcggt	cccagtcaca	ggtangctgg	240
tgctcatagtc	ttctcactcc	taatccatga	ccactgtttt	tttctatttt	atatcaccag	300

gtagcctact	gagttaatat	ttaagttgtc	aatagataag	tgtccctggt	ttgtggcata	360
atataactga	atttcatgag	aagatttatt	ccaccanggg	tatttcannc	tttgaaacca	420
aatctgtgta	tctaatacta	acccaatctg	tttggatgtg	gattttaaaa	aaatgtttgc	480
taaacctacc	caaagtnaga	tttacctgna	tttaaattggc	ctttnggggtc	ttgaaaaagc	540
tttntnaacc	tcttggcttt	aaaaatgcgtt	ttattctnga	taagatactt	cnaaatance	600
tnncaaaagg	tgttngatnc	naattacttt	aaaaataaac	ctgtaattgn	ataatgncat	660
aatgntgntc	catgcctnan	tccccttcta	gnntnanaaa	cntnantaan	aantatatca	720
atnntcgatn	aaatnntann	actataaaaa	ctnccggcct	cttananaact	tnatncttga	780
agttctcant	ataaccnc					798

&lt;210&gt; 792

&lt;211&gt; 788

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 792

ctnttgttct	ttttgcagga	tccatcgatt	cgaattcggc	acgaggcaga	gctcacatcc	60
tgtgcgcagc	atcttctgtc	ccctcatgtc	cttccgccag	ggggcctgcy	tggtagcggg	120
cagtgaggac	atgtgcgtgc	acttctttga	tgtggagcgg	gcggccaagg	ctgctgtcaa	180
caagctgcag	ggccacagtg	cacctgtgct	tgatgtcagc	ttcaactgcg	acgagagcct	240
actggcctcc	agtgacgcca	gcggcatggt	catcgtctgg	aggcgggagc	agaagtaggg	300
tcctgtcngc	cctgctgctg	tcctccatcc	cacctctctt	actccacctc	gtgttgtaaa	360
taaagtttcg	gtggtcatgc	tganggccgg	ctcccagctc	tgccggggac	ggacagggca	420
gaaggcancg	ggcaacttca	ggaacacggg	gaaaaaaaaa	aaaaaaaaaac	tcgagcctct	480
agaactatag	tgagtcgtat	tacgtagatc	cagacatgat	aagatacatt	gatgagtttg	540
gacaaaccac	aactagaatg	cantgaaaaa	aatgctttat	tttggggaaa	atttgggatg	600
ctattgctta	atttgnnaac	cattntaaac	ctgcaaatta	aaccaagttt	aacaaccaan	660
caattggcan	ttcattttta	atggttttta	aggttcaagg	ggggaaggtt	tttgggaagg	720
tttttttaaa	attnncgggn	ccnnngngnc	ccaatgcatt	tggggccccc	ggncccaaaa	780
nttttttt						788

&lt;210&gt; 793

&lt;211&gt; 806

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 793

gaatcccttt	gcttctgtcc	tttaagnnat	cgttggaaac	accatgnctt	ttttaggtg	60
aagtgttctc	tctgcatgca	acagtaaaaa	ttaatatata	attttttncca	caaaagaaac	120
acttaacaga	ggcnagtgcc	aatttataaa	atttatgata	taaaggggga	aatcatggat	180
tataaagtcc	ttcagccctt	tgggactcta	aattggnggg	ggattaaaaa	gaatttataa	240
taattttnga	accgaattta	ttttcccttc	agtttttgag	ggcattaaaa	aggcattaaa	300
tcaagacaaa	tcatgtgctt	gagaaaaata	aaattaatga	aaacncagca	ctttatgttg	360
gtttaacntg	cancctnctt	tggaggtaga	atttatttat	ttaaaattac	tgggtgcatc	420
angaacccat	agggtgtaca	aaangttcta	ttaaaatctg	cnttatagag	acaaagaggc	480
aggcaaatcc	atgtnacaaa	gggtaaagct	tacagtttac	aaactngaa	cgccanggtg	540
taggatataa	aaacgcactc	ttgagaaaac	anatggtcat	cagggtgctg	aaaacttgca	600
tgggtctttt	caacattagc	ctttgggtcca	caaatttctt	gtatttgaca	ggatccatag	660
tgtgccatgg	ggcaaganac	nattttgccc	tctatggtnt	tctttaaaaa	ttttcanttt	720
aaaaatacct	cttttnncag	gaatcctaata	tttggcnccg	aagcntattn	ntggtnccac	780
atttaccgtt	gcccttgccn	ttggan				806

<210> 794  
 <211> 815  
 <212> DNA  
 <213> Homo sapiens

<400> 794

tttcaaattnc	cttggcttta	nccctttgtt	tganntcctt	gttcgaattc	ggcacgaggc	60
cttctctggc	ctcaccaatt	aggtcaaagt	ttccttattt	tgtgttggtg	ggcatggctc	120
tnctgtgag	gacctgtccc	agcttggacc	tcgccttccc	tgcgactgta	ttggtgtctn	180
tcctctcaa	gcctatgagc	tcttgcaagg	gcagggaccc	tgtatgattt	tgcctatcgt	240
atgtcctcca	gccccagca	cangcgctg	gtgtccagt	agagctcagc	aaatactttg	300
tgagttaaan	gacangcggg	cttggggtag	atggatccgt	ctgcctanac	agggcangtt	360
attcccgtt	gtgagcaact	cttaanagaa	acttcatttt	ttttcggcgc	ctgcncgaac	420
tttcaaagat	gtttcccgcc	cangaacnct	ggctcacacc	tgtaatccca	gcactttggg	480
aggcttgaag	tgggtngatc	accttgaggt	cangannttn	tagaccagnc	tggccaacac	540
cgggtgaaacc	ccgtcctctn	ctaaaaatac	aaaanttaac	tgggtgtngt	tggtnngggc	600
ctttgnantc	tcactacttn	ggaangctga	ngcnatgaan	aatttgcttn	aacccnngga	660
nggcngaagt	ttcaattgan	gtcnanactt	nanccatttt	gcgccttcan	accctggggc	720
aacangtatc	annaacttna	acnattaaaa	aatnaanana	nctcttatcc	ctttannaac	780
nattattgan	gntacntatt	ntcntagaaa	tcctt			815

<210> 795  
 <211> 1050  
 <212> DNA  
 <213> Homo sapiens

<400> 795

tttctaattgc	ttggctttga	gnctctnttt	taaaatcctt	tggcnactac	tctgcacgat	60
gcccgcgtga	cccggncggg	cccacaccgc	ctcttttctc	ttctttgccc	cggactccct	120
ttcctgcttc	caagacctgg	gtgtctacaa	ctgtgagccc	agcttggncc	aaaggcagtc	180
cccatgggac	ctagactcac	cttncctttg	cctctatgaa	accttctgct	tgggcccanc	240
ccctgttcca	gtccccgacc	tgcacttcc	tgtctgggact	cangcctcca	agctccctgc	300
ccagcnagcg	gncttcagcc	accgtcttcc	cctttctttc	gggcccgtgt	tgtnagcanc	360
tttgagaaaa	cccananggg	acctngtgcc	ccttgcnagg	nctgtcgcct	tggtgcaaga	420
ctgnccgtgn	ctgcatcatt	ttncatgggt	gncgggggtg	tggggntnnn	cnnngcgnnn	480
cntgntcaca	atcaancatn	tatncctnan	ntnggggatn	acnaatggcc	tnaagantgc	540
tacntcttan	nnnganttn	tcangnnntn	ttactaacnt	ncnatngnnc	ntnganatag	600
ncatgnantn	ttagtntntg	atntancnc	nattgcagcc	ncataattat	cctacaccac	660
anannaancc	ntccttnnag	aanntgnent	ctatgnaana	gnctnnnaat	gtggcnnna	720
atataanntn	ntntnctnnc	atcntannnn	nntcctacgt	nannnnnncat	nnncnctntn	780
ggnnactatc	ncatantaca	tcnntnannn	cacccatnct	ntntntnanat	ntctcntggg	840
nantnnntc	tcctnnanac	ncnctaatna	ngatctctca	ntacatgan	ntanatnacn	900
natanngnnn	anactnannn	ngtctctct	atnnnttatn	nanngntcan	nttacnnnan	960
nanannaang	tatnntngtt	cnaaanntat	ntataaancn	ncgtnnnttt	nnannagatg	1020
tacnccnntn	anntaannat	ctangctccg				1050

<210> 796  
 <211> 884  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 796

ggnnnntttng	agctcgga	aa	tcncttnggt	nnagcctttc	nttgacccca	ttgttcgaat	60
tcggcacgag	acggcctggt	ggagcagctg	tncgaccttt	ncctggagtt	cctgcacagc		120
caggcacact	gcatcggtt	cccgacctg	gggctgcctg	tggtcctgca	gntgaagtcg		180
ttcctccggg	agtgcagggt	ggccaactac	tgcggcgagg	tgcagcagct	gcttgggaag		240
gttcaggaga	actcggcata	catntgcaag	ccgccgccag	agggttncct	tnggcgtttc		300
tgagcagcag	gcagtgggaag	cctggganaa	gctgacctcg	gaagagggga	cacccttgac		360
cttgctctac	agccacttgg	cgcaagcttg	cgttgacctg	ggaagatcca	acttgggaga		420
tcaannnggc	aaaagaaccg	gcttggaaag	acctggaact	ttcccttgag	atcaaaaccg		480
aaanggaaga	atgggcttga	canggaangg	atgaaggaca	gggaagccaa	ttttaaaaga		540
ccctctttga	cctgnacaag	ctcttgaaaa	aggacgacac	ccgaggggat	tcttcggaga		600
nnagggatac	tgangccccc	tgagcacctc	ggcatggggg	tngggaagac	cattgnaaac		660
aaggaccaag	gaaggaagg	ccnaaggaag	ggacaagcan	ncaaactcgg	aangntgna		720
atgggncctt	ngggantngg	aggaaccca	naacccaaa	aaggccgggg	ggcttgggcc		780
cccttggggg	gaancttnc	aacaaaatnt	gggccccag	ggggccccgg	aaaggaacga		840
aaccttgga	gggaatcttg	ncaagcttct	tanaaaagg	ancg			884

&lt;210&gt; 797

&lt;211&gt; 773

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 797

taatgcttgg	ctctgtctnt	tgttgaccen	tngttcgttt	gtgcctgagc	accacaaatt	60
tcaggattta	gactgtgtgg	gcacctcagc	tttcctcttg	ntgtaaccac	tccttgggtga	120
nagagggaac	tcctaaccan	tccatttgn	caaaggctag	gcaatcttca	ttctgcttgg	180
ctttagtcat	tcttgtcatt	gggctgcaga	agaaaaacaa	ctttgctggg	tgatccact	240
gccttgattt	cacctcggan	cgaggctggg	ccatgtccaa	gtcttatgag	gtcaccctga	300
ctagaaaaaa	ttgaactcac	ctacaaatag	tctgaaagag	tggtgtatat	caaatacgtg	360
ggtagtggtg	catttcaaat	gangctcttc	tgggttgaaa	tgatatattt	ataaaaccag	420
aatatcaaaa	atgggtgatg	tataatgtct	ctttagtttt	tttgggtattt	ggcctctttt	480
aaagcctgtc	ngatgtatgg	gagaaaaaca	atgaaccgtg	ctttgatttc	ctatcaagtc	540
actcttaaga	acatacatat	tggttaaagt	aactcgtctc	ttttttatct	gattctttga	600
ggcactatgg	gtagcaaaat	aaccacttac	aaattttaat	gtaatataca	cttcttttct	660
gngtgtcaag	tccttatttt	tangtgctta	attggacatt	ttaaaagggt	aaattattng	720
gttggcata	taatntcaaa	aatctatta	attnatttta	atgcctggta	ccg	773

&lt;210&gt; 798

&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 798

gtcaatnctn	ttcatgacct	tatcgattcg	aattcggcac	gaggctggag	cacgctggag	60
aggccatecc	tgccctggca	gccgcggct	gggggagact	cctttgcccc	attctttgccc	120
ggtttcctgc	cattattggt	gtgcaagaca	aaacagggct	gcacagtggc	agagaagtcc	180
tttgacgtgg	ggaccttggc	agagactatt	cagggcctgg	gtgctgcctc	agcccagttt	240
gtgtctcggc	tgtccctgt	gctgttgagc	accgccccag	aggcagacct	cgaggtgcca	300
agcaatgcc	tcttcgggat	gggcgtgctg	gcagagcatg	ggggccacct	tgcccaggaa	360
cactttccca	agctgctggg	gtcccttttt	cccctctggc	gcgggagcca	catgatcgtg	420
tccgtgacaa	catctgtggg	gcacttgccc	gctgttgatg	gccantccca	ccaggaaacc	480



agacccaag	tgctggctgc	ctactgcatg	ccctgncact	gaaaggagga	acttgnaaga	540
atgggtcacc	atttgggcgc	ctttttaact	ttctgtacca	gancaacccc	ttgacaaggt	600
tataaaatgt	nggctccccg	aaccttnttg	cgtattcttg	cagncctcaa	ttcttggett	660
gaccaaccaa	aggattoccca	cccangaaaa	ccnaanggg	ccnaaactt	gttnncttgn	720
ttnccttgga	ccgtttcctt	ggggccaaaa	acagggnanaa	cccggacang	gttttttnaa	780
accagntttt	tggggcttta	aattggcctt	gg			812

&lt;210&gt; 799

&lt;211&gt; 758

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 799

ctaatagctt	ttcattcnaa	tgcttgatg	ccctcgattc	gaattccggt	gctgtcggac	60
agattgccct	agtacccacc	cacctatcag	ggttatgcaa	tggaaacatcc	tcgcccgaagc	120
tcttgagaga	ggcaaagaca	actttgtaca	gtgccctggt	gaagcactca	aatgggaaga	180
aaggaaatgt	ctcatcctgg	aagaaatcct	ggcctaccag	cctgatata	tgtgcctcca	240
agaggtggac	cactatcttg	acaccttcca	gccactcctc	agtagactag	gctatcaagg	300
cacgtttttc	cccaaaccct	ggtcaccttg	tctagatgta	gaacacaaca	atggaccaga	360
tggttgtgcc	ttatcttttc	ttcaaaaccg	attcaagcta	gtcaacagt	ccaatattag	420
gctgacagcc	atgacattga	aaaccaacca	gggtggccatt	gcacagaccc	tggagtgcaa	480
ggagtcaggc	cgacagttct	gcatcgctgt	tacccatcta	aaagcacgca	ctggctggga	540
agcggtttcg	atcagcttaa	ggcttggtga	ctcttcagaa	cctgcaaaac	atnacccaag	600
gagcccaaga	ttnccttat	tgtgtgtggg	gacttcaatg	canaccaaca	gaanaagggtc	660
tncaaacact	ttgcttcttn	cagnctnaac	cttganagnc	ggcctacaag	ntgctgaatg	720
cttgatgggc	aatttagaac	ccccatacac	ctacctgg			758

&lt;210&gt; 800

&lt;211&gt; 770

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 800

ttnaaancng	cnttggactc	cttgcaggat	cccatcgatt	cgtttaaact	gagctccaaa	60
tgacgttcaa	acacccctct	cgggtagagt	tttcatgggtg	gaacggttgc	gcccaccaa	120
cagaagctta	tgtttttggc	acagaagcct	gggccatttt	catggacacc	tggctggacc	180
tcggtggaag	tgaactccgt	aggttgttgc	gttcaactgca	gcacctcaca	tgataccgtc	240
ccctctcatg	gaacggagcc	tccccatgc	agccccact	caaattggagt	tttaaaggct	300
gggttcagg	tacggggg	tttctcacg	tctgaatgcg	gaggacagag	acnagctcca	360
gggagcgtgg	gcgggtgacg	gcgctgagat	gcgtgatgtc	tcggaaacgt	cctcgcatcc	420
ctcanccggg	gcgctgactg	ccgcggccct	tgctgtctct	caggagcgct	ccagcttcgc	480
ccacacaccc	cgggtgatg	tccctcgtc	ccggcggcct	gcagacccca	nagtgcctgt	540
ctcgggaggg	ctccccattc	acacgaccct	gagtttgggt	ccaagttagc	ttctgtccca	600
aagtaccngt	attcccaaag	cgcacccggt	aaagganccg	ggccggncct	tntttgcggg	660
gccggggg	ggggccggga	actcgtnggg	ggttgccngg	aanggggtta	accgtncggg	720
ttnttcgnc	cttncgtgca	aggcttnccc	cgttaagnng	cccaaaccnt		770

&lt;210&gt; 801

&lt;211&gt; 573

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 801

ggagccctag	agctccacaa	caggactcag	agcctctaac	cagttccagc	actccagact	60
ccagccacac	tccaacacag	caccatgatc	ccagccaccc	gctcgcttct	ctgtgcagcg	120
ctgctgctgc	tggccaccag	ccgcctggcc	acaggtaggt	ctcgccactg	ccactggggg	180
aggagggacc	tctggtgagc	gcagcctccc	acagtcccg	tgaccaagag	tcttctcca	240
tagggcgctt	atcgccaatg	agctgcgctg	tcagtgcctg	cagaccatgg	ctgggattca	300
cctcaagaac	atccagagct	tgaagggtgt	gccctcaggg	ccccactgca	cccaaaccga	360
agtcattgtg	gtatcttccc	ggttagcttc	tgccacttcc	agactcgccc	aaaccctccc	420
gcgccccac	acttctccta	gtgggaatgc	ctaacatgtg	ggtctatcct	tctctctgca	480
gagccacact	caagaatggt	cgcgaggctt	gccttgaccc	tgaagctccc	ttgggttcaga	540
aaattgtcca	aaagatgcta	aagtgagttg	tga			573

&lt;210&gt; 802

&lt;211&gt; 1390

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 802

tttttttttt	cacaaggaat	atcattttat	tactgtaatc	acaaaatcgt	aatttctgta	60
caggaatgta	taagtgaaca	ttattcaaag	cattggtaat	tcacttcata	aagagggtaa	120
acatactaca	gaacatattg	taaagaaaaa	atattgtaaa	attttctggg	cttgacgtgc	180
actatttagt	gcaagtattt	aagacacaat	agtggtcaat	tcagcaaagt	attgcagaat	240
gtcatgccac	agtcacttta	attcaaagag	ggtcaggaca	tgacgcttgt	aataaaatgt	300
cagagtgtgt	gtgtgtgtgt	gtgtgtgtat	ataaaaccac	atgtaattca	taaaatatat	360
agtggtttat	ttagatgggt	ttaaagatt	tcactgtgga	atccagcata	actggaacaa	420
catccaaggt	cttcttaacg	gcaacaatct	tattgctagg	caatggcytt	ggcttcagggt	480
argaatgcyt	cccagtattt	tatcagctgt	tgtgtgtttt	gaactagtga	ttctaagtac	540
ttgatgataa	cggtttttaa	atccttcact	cgttctttct	caaactcttc	cacttctttt	600
cgaatcggtt	tagatatctg	ttcaaaatct	ctttccctt	gttgcaactt	cgctccac	660
tctcttattt	catttttagc	ttgtgtgtat	ttatctgggt	tgtagcaac	catcattttt	720
gcttcagctt	cacgtttttt	gagcaaagta	atttgagcat	cttcccattt	ctgccagcac	780
ttcattcgat	ggtcaaacac	acctttcact	gcagcaataa	gacgaatgta	gtcactaagt	840
agttctgaaa	acataataaa	gtcagmaaaa	gcttggttct	gatgtaactg	gtctatcttc	900
tcctcaacct	ctgcaagctg	agacaaagct	ctagataaag	cagtatgatc	ctcagaatta	960
cctaacatgg	cagcactttt	agcaaaggca	gctgtgttgg	ctgaaagttc	ttttctatga	1020
cagamcaagg	cttcaacact	gacatgaagt	ttcctaagtt	gctgatccag	attctcaaat	1080
tgctgctgct	tttcttcaaa	ccatgcatcc	gattcattca	tcttgattgt	cattttgttg	1140
acagcgtcgg	cagccttggt	caccatcttc	aatattcctg	ctccactcag	agcctgtgta	1200
ttaactgctc	taggcagctc	tgaactttcc	aagaactgcc	ttaaactcagg	atcctgtagt	1260
aaagttggat	gttttactgt	tctttgaaga	tacctttcaa	gagctgctct	cogtttttct	1320
acaaactcag	tggatgatga	gtcttcttta	cccactttga	ccttggtcat	ccctactata	1380
ctcttttctg						1390

&lt;210&gt; 803

&lt;211&gt; 947

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 803

ggaacttctg	agtaattggt	atcatttcct	agtgactcgg	ctcttgact	ccaatccac	60
agtaaaacc	attgatctgc	actactatgc	ccagtcacgc	ctggacmky	kkcwsgsagg	120

ngagagcagc	ccagaacccc	tggacaacat	cttggttgga	gcctttgagt	ttgacatcca	180
tcaagtaatc	aaagagtga	gcacgcgcc	gagcaactgg	tggtttgtgg	cccacctgac	240
agacctgctg	gaccactgca	agctcctcca	gtcacacaac	ctctatttcg	gttccaacat	300
gagagagttc	ctcctgctgg	agtacgcctc	gggactggtt	gctcatocca	gcctgtggca	360
gctgggggtc	gattactttg	attactgccc	cgagctgggc	cgagtctccc	tggagctgca	420
cattgagcgg	atacctctga	acaccgagca	gaaagccctg	aagggtgctg	ggatctgtga	480
gcagcggcag	atgactgaac	aagttcgcag	catttgtaag	atcttagcca	tgaaagccgt	540
ccgcaacaat	cgcttgggtt	ctgccctctc	ttggagcatc	cgtgctaagg	atgccgcctt	600
tgccacgctc	gtgtcagaca	ggttcctcag	ggattactgt	gagcgaggct	gcttttctga	660
tttggtatctc	attgacaacc	tggggccagc	catgatgctc	agtgaccgac	tgacattcct	720
gggaaagtat	cgcgagttcc	accgtatgta	cggggagaag	cgttttgccc	acgcagcttc	780
tctccttctg	tccttgatga	cgtctcggat	tgcccctcgg	tctttctgga	tgactctgct	840
gacagacgcc	ttgccccttt	tggaacagaa	acaggtgatt	ttctcagcag	aacagactta	900
tgagttgatg	cggtgtctgg	aggacttgac	gtcaagaaga	cctgtgc		947

&lt;210&gt; 804

&lt;211&gt; 532

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 804

cctctgcct	cccaggttca	agccattttc	ctgcctcagc	ctcccagant	agactgggac	60
tgcaggtgcg	catcaccacg	cctggntaat	ttttgtat	tgagtagaga	tggtgtttca	120
ccatgttggc	caggctggtn	tcgaactcct	ggccctcaag	tgatccaccc	acctcagcct	180
cccaaagtac	agggnttata	ggcgtgcgcc	antntgcccg	gccgagaaca	attnttcaca	240
agnttacttt	tctagttttg	ccaatgcatg	gtgaaagtga	acccaagcct	gggaactgca	300
ggcctagaca	atgcaggrmm	ykksttsamm	cwsrsmrsmr	smsstysmar	ywmrsssagm	360
cttggaagg	agaagtgtga	ggcaggtgtg	ggtaggacct	ctttttagta	cctagaaaaa	420
ggctaagaaa	gtggcctgga	gatgtttaga	aggttaaaac	caacgaagaa	aaaaatcaat	480
gacaacctat	caggaacgtg	attgactctc	agaatggaga	actggcgaat	cg	532

&lt;210&gt; 805

&lt;211&gt; 552

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 805

aatgcattnt	tgatttttta	ttgcagatga	tgaaaaagtt	ttagatatag	acagtgccga	60
tggttacaca	atgttgtaaa	tgtatttaat	cccacttacg	aatgattaaa	atgataaatc	120
ttatgtttat	ttcatcacta	ccaaaaggct	gtgggtgcag	gggtgctggg	ttctggctct	180
agcctaagag	actggcagtt	tccaccttct	atctcttggg	acagttagctc	tgggagccct	240
gagctgtcat	gcaggaagtc	cagctaccct	gagaccacca	tgctggaaag	gccacaggga	300
ggagctctgt	ggacagtccc	agctgaacct	tgcttccag	ctgtccctgt	caagatgccca	360
ggsatgtgag	taaagccatc	atggacccty	tagaccagac	tgcccaccag	cagggtaccw	420
tctggcagcc	acatggagca	gaagaaccgc	ccagctgagc	cacttccaaa	ctcttgaccc	480
actaagtc	gatccacaat	gaacccatca	tagggatggg	tggctttgca	gtgtggataa	540
tgaggatgtc	at					552

&lt;210&gt; 806

&lt;211&gt; 1646

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 806

aactagtata	tttacaacat	cagaaacttc	aatatggaga	tttgttggtc	ctatatcatg	60
atcttttagca	gcaactacac	cataggcact	gcacaacctg	ggtcctagat	caggacgtac	120
aaaaaatcct	ggcaaatgag	aggccaaatt	gaattttcct	tctggattac	aatattctgg	180
caatggcaga	ctttttaaaa	gatcttcgta	tcttgctggc	atcatagtct	tgaagtcttc	240
tcctgaaggc	caatctttca	attttaaaac	aactgtttct	ccactcttgt	ttttctgccg	300
ttttgaaact	tcttcaaaac	catcccagaa	ttccttaaca	ttggcatttg	aaatgatgct	360
atctttgcag	ttcaggagat	cagcttggtg	gtctccaaaa	tcaagactaa	ttgattccgc	420
cttccatagg	ctaagtgtca	ttttcttatg	cacaccagaa	accactgcag	gctgtccttg	480
ttccaacat	tctttgaaaa	gcttccaatt	actgctatto	ttataatcct	taagccataa	540
aatatgcttc	tcacagatcc	aagaatgtgg	tatatcactg	tataatttat	tattttcatc	600
cactgcagat	attatgcttt	cttcaggctc	ttctttaagc	tctggtttta	catttatctt	660
ggaggtttta	cttgggtggaa	ttttgttttc	aacaactgaa	gcaattatgt	catcaagaat	720
gttaggcata	gtccgtccac	ttttgctact	tggggctccc	attgaatata	ctggggcaaa	780
ggcaatgccca	gcatctgtas	acccacacag	tagctttcca	gctgttgtag	tcagcaaata	840
ccgtaagggt	gagccttggt	cattattctg	ggacacaaga	ggtgatgttc	tgccatttgg	900
agattcagag	ttgtcttggt	ctctttcttc	tttaatttgg	ttttcaaggg	taagttcttt	960
gttttctttt	ttttctcttc	tggctttttg	ctctgcaaga	tctgctaacc	agtgcagtgg	1020
tgactgggat	tctggaggag	ttaacttggt	atctgtgcct	acatcactct	ctgggctgct	1080
gccaccattt	ttctcagact	tccggaggag	attttgctgc	tgagactcag	gcatgcacag	1140
agaaatttta	ttactgtgat	taagaacatt	ctgtaaaact	tgagatacac	cattcattgt	1200
aggaaaattt	ccaacttgta	aattctgttt	gttagtacia	tgacaatggg	atttaatacc	1260
atatttttcc	ctaagagtgt	gcatggcatc	tagaagatct	gtcaaaacag	aaccagggtat	1320
aatttgggtt	ggcattaaat	gtttgtgatc	atgaggctgt	ccyttcacac	acttcatcca	1380
agcatattag	ttctttatcc	ctagrammyc	tycctttctc	ttngccttgt	aacaatctaa	1440
gcaganccac	aawkcacat	tttkggcaga	cccagtnraw	kktaancawk	gntgcttcac	1500
atgcatcaca	catctcccg	actcctctca	ctgctctttt	ccaggcaatt	ttggcatcct	1560
ttttcaccca	ggacaaagct	gttttttcag	atgttactaa	ttgacagaac	ttatcaccta	1620
ttatatccaa	gatatattta	gaagtc				1646

&lt;210&gt; 807

&lt;211&gt; 1029

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 807

tggggctgtg	actgtattta	cttcattctt	gaatcccgcg	tccccgtggc	tgggggctga	60
cacatccctg	ggcaccactg	tgacttctctg	tgggtccctt	cccttctgtc	cctgactctg	120
tagaccccc	acaggaagg	tcctaggtag	ggggagggtc	ctcctccctt	gaaaccctgg	180
gccactctgt	caaggcaaag	ctctgggccc	agcaccttgt	aaaggctttg	atgagaggag	240
ctctggcttt	tgctcagggc	ctttggaccc	caccctccag	ccccaggaa	tgaggcgct	300
caaagcctgt	ggtnaggctg	cccgaagcac	gtgccgcagt	tcttctggag	tgggagcagg	360
gggacagagc	tttgggtaga	ggagggtcac	ctgcaaagct	ggaatgccag	gggagtgggc	420
ggtgcctcca	gctcctgggg	gccagggtgt	ctccatacct	catgggcctg	agcctgggca	480
ggggtctgga	gtgcacatag	ccccaggca	gggagagggc	agtgcagga	cagagccact	540
catctgtccc	aaagctgcac	caaggggtgt	cagcaacccc	aacctactga	cctacttttg	600
gaccacaggc	ccatctagt	caaagtaggc	ccagaaagga	gaaatgcttt	gctcaacagc	660
cacagtaggc	tgacgtaacc	tatgtaatgt	agggctcagg	tgggcctgag	ggatgancca	720
ggtggtgggc	aggtganaca	ccaggtcccc	tctggcctc	tgccccacc	agccctctcc	780

tgcacggcta	ccagaagatg	tccgggaaga	acanactagc	cctgagtagg	gagtgtggtc	840
agggtgcagag	gagggcaggg	gcccggatcc	tggcccagaa	acactctaaa	acagaatccg	900
atcctgagat	gatccaaatc	aaacagaata	cttgacggaa	atagtagagt	ctgaaaatga	960
tgcactctgc	gcacacatat	acaagacaca	cacacacaca	cgaatccacg	cacacgaggc	1020
acacccac						1029

&lt;210&gt; 808

&lt;211&gt; 836

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 808

aaaaccgggt	ataacacttt	aatatagatt	tgtggaactc	tggcccttgc	agccagaata	60
cacatttata	agccataaat	aaagcacgca	gaaaccataa	attaatcgga	cccagacct	120
ggattttcacc	gtgtcaagat	tgggaatgct	ttttttttct	ttttcttggg	catttacaac	180
agacccttac	attatttttt	ttcctgtttt	taaacaatag	tacaaccctc	tggttctggt	240
aaaactacat	ggtttttacac	cgagtcactc	acaaaatttt	tttttttttt	taagtaagac	300
ttccctgcaa	caacagcaat	ggaggagaac	aacaacaaca	aaaaaatcag	aatctgcagg	360
tgcttgaaga	agcaggagtc	tacacagtag	tggaaaccgg	aggctttttt	ttaactttat	420
attctttccc	gttttctctc	ttatatagaa	cgtggggtat	ctgtgtggcc	ctctgtttgg	480
gacggaacrg	ctgcagcggg	tgaaggaaga	ctgctgtctt	gggggtgttg	gggtgggggt	540
gttatggatt	tcttctccct	tgcttctctg	caacaccgtc	tccccaagt	ctcgaccccc	600
acttgctctc	tcacttrtcc	tcgatccggg	gtgccagagt	tagccnggcc	tgaagccgtc	660
gtcttcttaa	gaggagttca	taatgggccg	ggagtacacc	ccctggtagt	aggaggtatc	720
tgcgccagg	ggcgaggcgt	ccaggcccgt	tttgttcgtg	accggggcca	tggccaagct	780
gccaggcatg	ggggaaccgt	agccggggta	gtgcatcacc	tgttcgtagg	ccttga	836

&lt;210&gt; 809

&lt;211&gt; 1844

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 809

atcagggtgtt	cctcccatgg	caggagggaa	gaaaccacgc	aaacggccag	cctgggactt	60
aaagggtcag	ttatgtgacc	taaatgcaga	actaaaacgg	tgccgtgaga	ggactcaaac	120
gttggacca	gagaaccagc	agcttcagga	ccagctcaga	gatgccacgc	agcaggtaa	180
ggccctgggg	acagagcgca	caacactgga	ggggcattta	gccaaggtag	aggcccaggc	240
tgagcagggc	caacaggagc	tgaagaactt	gcgtgcttgt	gtcctggagc	tggaaagagc	300
gctgagcacg	ccaggagggc	ttggtgcaag	agcttcagaa	aaaacagggtg	gaattgcagg	360
aagaacggag	gggactgatg	tcccaactag	aggagaagga	gaggaggctg	caacatcaga	420
agcagccctg	tcaagcagcc	aagcagaagt	ggcatctctg	cggcaggaga	ctgtggccca	480
ggcagcctta	ctgactgagc	gggaagaacg	tcttcatggg	ctagaaatgg	agcgccggcg	540
actgcacaac	cagctgcagg	aactcaaggg	caacatccgt	gtattctgcc	gggtccgccc	600
tgtcctgccg	ggggagccca	ctccaccccc	tggcctctct	ctgtttccct	ctggccctgg	660
tgggcccctc	gatcctccaa	cccgccttag	cctctcccgg	tctgacgagc	ggcgtgggac	720
cctgagtggg	gcaccagctc	ccccaaactc	ccatgatttt	tcctttgacc	gggtattccc	780
accaggaagt	ggacaggatg	aagtgtttga	agagattgcc	atgcttgtcc	agtcagccct	840
ggatggctat	ccagtatgca	tctttgccta	tggccagaca	ggcagtggca	agaccttcac	900
aatggagggg	gggcctgggg	gagaccccca	gttgaggggg	ctgatccctc	gggcccctgc	960
gcacctcttc	tctgtggctc	aggagctgag	tggtcagggc	tggacctaca	gctttgtagc	1020
aagctacgta	gagatctaca	atgagactgt	ccgggacctg	ctggccactg	gaacccggaa	1080

```

gggtcaaggg ggcgagtgtg agattcgccg tgcagggcca gggagtgagg agctcactgt 1140
caccaatgct cgatatgtcc ctgtctcctg tgagaaagaa gtggacgccc tgcttcactct 1200
ggcccgccag aatcgggctg tggcccgcac agcccagaat gaacgggtcat cagcgagcca 1260
cagtgatttc cagctacaga tttctgggga gcactccagc cgaggcctgc agtgtggggc 1320
ccccctcagt cttgtggacc tggccgggag tgagcgactt gaccccggt tagccctcgg 1380
ccccggggag cgggaacgct tcgggaaaca caggccatta acagcagcct gtccacgctg 1440
gggctgggta tcatggccct gagcaacaag gagtcccacg tgccttaccg gaacagcaaa 1500
ctgacctacc tgctgcagaa ctctctgggt ggtagtgyta agatgctcat 'gtttgtgaac 1560
atttytccay tggaaagaaa cgtytccgag tccctcaact ctctacgctt tgcctccaag 1620
gtgaaccagt gtgttattgg tactgtctcag gccaacagga agtgaagacg gatccagatc 1680
tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtcct atgtctatgt atcgggtgag 1740
gggtgggagg gttgtcggag ggtgctttat tgggtggagg gcaccatgtc ccagggctat 1800
caaataaaga atagtttggg ttttttttta aataaagggt ttat 1844

```

&lt;210&gt; 810

&lt;211&gt; 489

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 810

```

gccccgctcc atgagcagtg actccccagc tcctcctggc accagtcccc agggctctcc 60
tgttggtakw wmmwgctwyw ywtsyysswm mywmmycgkg raccteraga tctyyaccct 120
aaaatarttc tggtgaattt caccctggcr atgtaaaytg akagcttata ttcacagatg 180
ysrganaakr gmcmayycmy cwkcawcct swgncwmays tswrwcwrat ksmtkycykw 240
kccctattta tgtaaaaata cagggtccct gagccagcct aaggcataag tgacttatcc 300
ctcctccctg ctcacatata aattgtgtat ttagtgaaag gctgatcaaa grttcaaagr 360
atgttatttg ttatctacct gtggaccacg naggtcccca attccagtta tttccacctt 420
tccaggaccg ggaccaatgt atatatgtaa ctggattggc tgttctcgtg tgtttggtta 480
aatgtgtgg 489

```

&lt;210&gt; 811

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 811

```

gcctcagcc acccccatcc ctgccccttc tgagactcac agcaccctt tccttcctct 60
cctccacct cctccctcag cccctcattc tccttgggaa tctgcagagg gctctgggac 120
tcaactgccg atgtgaaatc caggcgctcag ctgtttccta ggcaagggca ggaaagtgg 180
ctccagccct tgetccactc atgcctgggg gnctgggsyy gagggtatc cctacctggc 240
ctccccctgg cctctggcct ccagcgctgg gtttgtcgag tgagagagag agaggagctt 300
gggttgcttc cctgtcccg cccctctgt ggcattgtcc ctccactct tatttttcta 360
ccaattgcta tttttccgaa caatccttgt agagtatgta ccatccaaag gcaggagggc 420
cctcggtggc cggctctggt tggagatggt acagttttat tgtacagggt c 471

```

&lt;210&gt; 812

&lt;211&gt; 579

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 812

cccaatgaat	caacatactt	tattagaccc	actaagtgcc	aggggagggg	cctgtgccta	60
ngagccaggt	tacagggctc	acccgtagat	tcagtctggg	ctctcccat	catgcctctc	120
acttccagtc	tgggcttcta	ataggagggc	cccgacttct	tccctcccag	tcattctctc	180
gaatggagaa	tctttcctca	ttccagggac	accaaggctc	aggaaggggc	ctatccatca	240
tcagtagagc	cagacaagct	ctcccatcgg	acgtcctgtg	gctgggcca	gaaatgggtg	300
ccgctgcctg	tgggactgcc	cttccgggaa	ggaccagggg	gtcttcagtg	ctcttggcct	360
gcacgtggna	ggagagtagg	cagatgtctg	gtgctcttta	agctcaaagg	catcatggcc	420
ctctckgnwg	sarcrrrsrs	akamragkym	sssatcncag	scagcscwnk	arskstsgca	480
nwmwcatts	casmtgcasc	mmcmgrrrs	mkcsksywc	kmagnsktnm	scmtsgrgy	540
cagcgcagcg	tagggtagga	tcctcattgc	agatgcage			579

&lt;210&gt; 813

&lt;211&gt; 562

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 813

tttttttttt	tccagatgta	actcttgtct	tttattccag	catctcccag	agctccaata	60
tgtacagact	ttatttatac	acataataa	tacaccatat	atacttattt	atagatatct	120
acacaccagc	ccacacactc	gcacacactc	acacgcacac	acccttccag	gaggggagtg	180
tggctgcctt	ggagtcccg	tagscctaaa	caagtgtatc	tgggcttgcc	aggcagttgt	240
gaggttttgt	gttttttgc	tttaaaaaga	aggccatttc	ctccagatgt	gtcctccctc	300
tcccaagcc	ctaaaactcc	tcccaaaaac	actctgaaaa	aaattttttt	aaaacaagrg	360
gnttttcctt	tgctytggsc	caagtagttt	ctngganagn	tccrggscca	tccacaagny	420
ccgtgcaggt	cctagagcac	gagagccggg	cgtggccttg	gtcaggcctg	cagctgtgcc	480
ctctgagggg	agaggggagg	cgctatagca	tcaagggcac	ctgccagatg	aggaggggtg	540
tgctcgtctc	cccacacggg	gc				562

&lt;210&gt; 814

&lt;211&gt; 594

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 814

agcctgcct	gggcccgcct	gtggctccca	ttttcctttc	agcgggacaa	aggggacttg	60
ttaccaggcc	attttctgga	tggcctgtga	gatctctgcc	cctccaagac	ckccaaryc	120
tsmsyckgwc	scmswgytsk	smsmmwgmmt	ycwgcmssygs	smrccttgss	rryktswrk	180
tggcaccagg	ctgnagnctc	cccaatccca	gcccactttg	ctgtgtctct	ggcgggctgt	240
cctccttggt	gggagctgtc	ctgcacactg	taggatgctt	aaaggatatc	ctkgcctcca	300
cccaccccta	gccagcagct	cccagtcaga	caacagccag	awatgtctcc	agactctgcc	360
cagcctcccc	aggtagccac	cctcgagaca	cgacctcaga	gtctctgtgt	ctcctagaag	420
cctgacagag	accccagggg	cagtgggtgg	gtngcgggct	agagaccctt	gcctgtntcc	480
gggaccctgg	cgccgctctc	ccctcctgtg	gacccctccg	gactaacagt	gttcttagtn	540
ggcagangct	ggggcacccc	ttnggccctg	ncaggcatng	ccattggcgc	angc	594

&lt;210&gt; 815

&lt;211&gt; 812

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 815

aaaaccgggt	ataacacttt	aatatagatt	tgtggaactc	tggcccttgc	agccagaata	60
cacatttata	agccataaat	aaagcacgca	gaaaccataa	attaatcgga	cccagagcct	120
ggatttcacc	gtgtcaagat	tgggaatgct	ttttttttct	ttttcttggg	cattttacaac	180
agacccttac	attatttttt	ttcctgtttt	taaacaatag	tacaaccctc	tggttctggt	240
aaaactacat	ggtttttacac	cgagtcactc	acaaaatttt	tttttttttt	taagtaagac	300
ttccctgcaa	caacagcaat	ggaggagaac	aacaacaaca	aaaaaatcag	aatctgcagg	360
tgcttgaaga	agcaggagtc	tacacagtag	tggaaaccgg	aggctttttt	ttacttttat	420
attctttccc	gttttccctc	ttatatagaa	cgtggggtat	ctgtgtggcc	ctctgtttgg	480
gacggaacrg	ctgcagcggg	tgaaggaaga	ctgctgtctt	gggggtgttg	gggtgggggt	540
gttatggatt	tcttctccct	tgctctctcg	caacaccgtc	tcccaaagt	ctcgaccccc	600
acttgccttc	tcacttrtcc	tcgatccggg	gtgccagagt	tagccnggcc	tgaagccgtc	660
gtcttcttaa	gaggagttca	taatgggccg	ggagtacacc	ccctggtagt	aggagggtatc	720
tgcggccagg	ggcgaggcgt	ccaggcccgt	ttgttctgtg	accgggcccc	tggccaagct	780
gccaggcatg	ggggaaccgt	agccggggta	gt			812

&lt;210&gt; 816

&lt;211&gt; 999

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 816

aagccgcctt	ctgagccttt	ngcctctggt	gttcctcctg	ctgcctgtga	gttttcatgt	60
gtgcatttcg	gcttttgatc	ttgaagaaga	ctttgcenca	ctccttgagc	gggaagatgg	120
tgggtggggc	tgtctcgccg	ctggtgggtg	tgtgagaggg	tgancncttt	accncnacag	180
taccactctc	gggtgcencc	aggcttctgc	ttcccagags	gkrtrrmmmc	kmgggccttg	240
ctttgcccc	tgnaaaagct	gccccctanc	catagtatct	cccaggcaaa	gatgccatgc	300
tcactgcaaa	ctatggaatg	aggtcagaac	agaatcaaag	taacgcttga	tgggaaaagt	360
tggccccaag	acccagtagc	taagaggggc	gctgtcgtct	cacacacaca	cactcacagc	420
aagctttggg	ataaaaggca	accgggatgg	ttgacatctg	aatgcaatgg	aacatgaagg	480
tcagcttcag	tccctactgg	gaatgatttc	atgagaaggt	agcccagatg	aaacacctct	540
taaagatagt	tgtgccaatt	atattttccc	ccaaccccc	acaaaaacaa	atttttttta	600
ataaaaggaa	aagaaatagg	attttttttt	ctaaacctga	ataaaatgac	cactttttaa	660
acagrtagtt	taaaagggtt	acaaaacaag	caggcagtc	aggtttcctg	attaatgaag	720
atggaggccg	tgggttttca	ctgtctctaa	gtgacacaca	gggctttata	gttctgcgtc	780
accctgaagc	aagactgaat	cttgatcatc	caagagaaga	tcggtgtcca	caacttcagc	840
ctcttccatg	acacctccca	actgctggac	gacgtcgtcg	tcgaggatgt	ccacatcctt	900
gtatgggttt	gatcagactc	agctgggtcca	ggggcagcag	cmcgrcagca	ccccacgggc	960
ccgtagtctc	ctcaatcgtg	gctgccatct	cagctgcaa			999

&lt;210&gt; 817

&lt;211&gt; 653

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 817

atttttaywt	ttaaaacatt	ttatgaggga	taaaatatag	tctttttcta	tcagtatgtt	60
cacacttcct	ggcctctcat	tgggaagctg	taagatgtcc	ttcaataaga	tcctgaacac	120
gcgacagaat	aatctcatta	gagctgctgc	aattttcttg	accatattgg	gggtctatag	180
tcaggacccc	agccacacag	agagtccttg	gagcgtctcc	ctgttcagtg	atggggatgt	240
ggttcttctc	aagccatttc	tttaggctgt	tctttctctc	ttccagatcc	tctgggctgt	300
atgcttttga	gtctccagac	gtgaacaaat	gcacagctt	ctccctcact	ctatggtccc	360



cttcattcat	agtttcaaca	gtckgcacag	catgtcccat	aattccggtc	acagacatgc	420
tgccatcttc	aaggaagttc	acaaggacaa	tattggcaga	gactgggtct	gkagttaaam	480
cccatccttt	atactattc	ttctcactgg	ctgtcactcg	gacctctttg	taaatgtaat	540
cttgccattc	taaggggcct	ttcttcattc	attcactcat	gattgccacc	tggtctaaatc	600
agttaaaaaa	ctcctcgcaa	ctctgggtac	tcagcaacca	tgctttgagg	aag	653

&lt;210&gt; 818

&lt;211&gt; 1225

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 818

ggattctttc	actgagcaca	aagagttggt	ggggcttttag	catctgactg	atthttgttac	60
ggggttgatt	ctgaccatag	gaagtatgca	atgtgaatca	ctattttacag	agaaacctac	120
aacagatgct	tgatgttgta	gaaactggga	catatagata	ccaagcaaaa	ttataagaaa	180
cctataaggt	gttcaatacg	cttggtgttc	caaaattcac	tgtacatgat	cagtttggtg	240
ttcttgtagc	acagttttta	actgaaggaa	ccagttgtaa	cagtctcaat	tttaactaaa	300
acttgaagaa	ctaaaacaac	aatgcaaacc	tttcagcatt	gtttggccaa	acttggttaa	360
actgtaatgc	aagaaccaa	tgcactgtga	tgtggcacca	actaattagc	aagcatgaat	420
ttttcaccca	agagtgaaaa	aaggaaaatc	taccatggct	tgaagttaa	gagcagaact	480
cctgactacc	attctatgac	tgatcaaaaag	actaatagtt	aaaaacctca	gcaggccttg	540
ttcacgatat	gcagaaaaaa	aagtgcgtga	gttttagatac	ctctggaatt	ttccacagt	600
gtcacagggt	tgtaatactt	gaagccctac	atthttctaa	atatatttct	tgctcagttg	660
tttcakgcaa	gcccaagact	ttgtaatttt	ttaaaggccc	aagatttttt	tttttttttt	720
tttttcaaat	aacagaccag	cttctttttc	ttgcagttac	agatgtaatt	tcctttttgt	780
tgtcaaaccat	aaggtacca	atatgatgca	ataaattggt	ttgaaaaaca	gttgtgtgaa	840
tattttcaact	aatctgtgtt	gggcttctgt	gaaatacaca	ggtggaaaaca	gaggtgcaag	900
ccagagcaat	ngtaatatgc	tgtaaggcta	gtgcagatgg	gagcttttta	gaaggggcta	960
agtgcgtgtg	tcagggaaat	tcataatga	agtagaatgc	tgctcctgca	ttaagatttc	1020
attgagggca	aggctggtgg	caggactat	gaatgtaatt	cataatttaa	aaggaaaact	1080
aaaaactatt	ttgatttggg	aaaatgagcc	ttaatttgtt	aaacctatac	actgaggaac	1140
tagcctcagg	ctttaatatt	ctcattggca	tttgccaagg	tcctgaggcc	aaataagggt	1200
taagttaaaa	caaattccaat	tgtnt				1225

&lt;210&gt; 819

&lt;211&gt; 1024

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 819

gacaccccag	atgcagccac	caccagcaga	agcgatcagc	tgaccccaca	agggcacgtg	60
gctgtggccg	tgggctcagg	tggcagctat	ggagccgagg	atgaggtgga	ggaggagagt	120
gacarggccg	cgctcctgca	ggagcagcag	cagcagcagc	agccgggatt	ctggaccttc	180
agctactatc	agagcttctt	tgacgtggac	acctcacagg	tcctggaccg	gatcaaaggc	240
tcactgctgc	cccggcctgg	ccacaacttt	gtgcggcacc	atctgcggaa	tcggccggat	300
ctgtatggcc	ccttctggat	ctgtgccacg	ttggcctttg	tcctggccgt	cactggcaac	360
ctgacgmtgg	tgctggccca	gaggaggagc	ccctccatcc	actacagccc	ccagttccac	420
aaggtgaccg	tggcaggcat	cagcatctac	tgctatrcgt	ggctggtgcc	cctggccctg	480
tggggcttcc	tgcggtggcg	caagggtgtc	caggagcgca	tggggcccta	caccttcctg	540
gagactgtgt	gcacttacgg	ctactccctc	tttgtcttca	tcccatgggt	ggtcctgtgg	600
ctcattccct	gtgcctntgg	ctacagtggc	tctttggggg	cgctggccct	gggcctgtnc	660

aaccacccggg	ctggtaatca	ccctctggcc	cgtgggtccgt	gaggacacca	ggctgggtggc	720
cacagtgtctg	ctgtccgtgg	tcgtgctgcn	ccacgccctc	ctggccatgg	gctgtaagtt	780
gtactttcttc	cagtcgctgc	ctcnggagna	cgtggctcct	ccaccccaaa	tcanatctct	840
gccctcaaac	atcgcgctgt	cccctacctt	gccgcagtc	ctggccccct	cctaggaagg	900
nccgggtccc	acaggcaaca	cctaagtgga	ccaacccctc	tgctgtctct	gccccccaga	960
cgatgactga	aggctccttt	gacaccttga	gatgantctg	ctactttcca	gactttttctt	1020
acaa						1024

<210> 820  
 <211> 631  
 <212> DNA  
 <213> Homo sapiens

<400> 820						
atTTTTaywt	ttaaaacatt	ttatgaggga	taaaatatag	tctttttcta	tcagtatggt	60
cacacttcct	ggcctctcat	tggaagctg	taagatgtcc	ttcaataaga	tctgaacac	120
gcgacagaat	aatctcatta	gagctgctgc	aattttctgg	accatatggt	gggtctatag	180
tcaggacccc	agccacacag	agagtccttg	gagcgtctcc	ctgttcagtg	atggggatgt	240
ggttcttctc	aagccatttc	tttaggctgt	tctttctctc	ttccagatcc	tctgggctgt	300
atgctttgca	gtctccagac	gtgaacaaat	gcacagctt	ctccctcact	ctatgggtccc	360
cttcattcat	agtttcaaca	gtckgcacag	catgtcccat	aattccggtc	acagacatgc	420
tgccatcttc	aaggaagttc	acaaggacaa	tattggcaga	gactgggtct	gkagttaaam	480
cccatccttt	atactcattc	ttctcactgg	ctgtcactcg	gacctctttg	taaatgtaat	540
cttgccattc	taaggggcct	ttcttcatcc	attcactcat	gattgccacc	tggttaaate	600
agttaaaaaa	ctcctcgcaa	ctctgggtac	t			631

<210> 821  
 <211> 635  
 <212> DNA  
 <213> Homo sapiens

<400> 821						
aggttgctca	cctgaaggag	cacaggaggg	ttttccaggc	catgtggctc	aggttcctca	60
agcacaagct	gccccctcagc	ctctacaaga	agggtgctgct	gattgtgcat	gacgccatcc	120
tgccgcagct	ggcgcagccc	acgctcatga	tcgacttcct	caccgcgcgc	tssgacctcg	180
ggggggccct	cagcctcttg	gccttgaacg	ggctgttcat	cttgattcac	aaacacaacc	240
tggagtacc	tgacttctac	cggaaagtct	acggcctctt	ggaacctctt	gtctttcacg	300
tcaagtaccg	cgcccgcttc	ttccacctgg	ctgacctctt	cctgtcctcc	tccacctcc	360
ccgcctacct	ggtggccgcc	ttcgccaagc	ggctggcccg	cctggccctg	acggctcccc	420
ctgaggccct	gctcatggtc	ctgcctttca	tctgtaacct	gctgcgcggg	cacctgctt	480
gccgggtcct	cgtgcaccgt	ccacacggcc	ctcgagttgg	aacgccgacc	cttacgaacc	540
ctgggagagg	aggaccagc	ccagagccgg	gctttgggag	agttccttgt	tggttttttc	600
agggccttnc	agcggcatta	ccaacttgag	gtttt			635

<210> 822  
 <211> 752  
 <212> DNA  
 <213> Homo sapiens

<400> 822						
tgcttttatc	ttgaatgtag	ccttcaactt	tgtgtaattc	cttaccaaaa	aggccacatg	60

```

gottaaaatt caacacacat ttgtccccag tttgttggtt tataatttcc acattgccat 120
actgttcgat ccacagttta cccacaatga tattatgcac acagcaggtg ggattttgtcc 180
atgtatatgc ctcatgtgtg tcaaggagct ccaaggatgat gggttccttg gggtctgctt 240
ctacactctt cccccagaat ttcagtttgg gatagataga gccatgaaag atgaagtcac 300
tgtttaatcc ttcagcatga aatgcactga ttggtgggtg atggctgacc tgttcggaga 360
tgagtctaaa tccaagggtc tctcgacta attcataagt ctctcccagc agtgggttga 420
aagggtttcc agtccgttcc cactgagaag caacagcaga tacagcaaac gcagctacac 480
actgcacctt tccacagga tcagagagtg aactggcctt gtggaygagg taagtatgct 540
ccatgtattc agttaggcgc tgtaggaagc tcagaggctc attaaatata actggcatcg 600
tgatcttgga tagttccatt ccaatacatt ttctgaggat gctccagata ctgaagtcac 660
ttctggaaaa cataggagaa ggcaaacttg ttctgtgttt cttgatgcca ttggagagag 720
catctccgcc accacagtct ttttcttcgg ac 752

```

&lt;210&gt; 823

&lt;211&gt; 899

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 823

```

tttggccacag ggtaaacttt tatttttagaa tccaatcttt tccccacaca tacacaataa 60
attaaacaga atccacagta aatgtacatt ttttaacata aaaagtcagt tactgttact 120
tcattgatcac atgaggatcg tcacagctcc gtgtccatta gcacattacc ctcttctgtcc 180
ttaactctta tccgaccgga tctgtacttc gtttcttgat gaccgtttgc atatacgggtt 240
ttaacagtgc catctgggta ttcccgcttc ttgaactggg cagtatgtag ttctctttgg 300
ccattattaa actctatgag ttgttgcca tcacgttgta ctctgacaat tgtaccatct 360
gggaaaatgc tttcttcttg tccatcagga aataagtttt taacagtctg gtcaggaaac 420
gtgatttctt ttcttccatc tgggtaatgt ttttctrttt aaaaagttgt tacagttaa 480
attttttgaa ggaagggaag aatttaatga gaggttgagg caagtttgta cctatttgtc 540
cacttgagaa atgtaagact tccagtcctc cgggtatgtc gtgtgagtgg tctgggcagc 600
tgcatagtag tagatctgta aagacacaca gtcagtctgc cttttctcca gagatgggta 660
aactatggag gagaacactt ctggaaacat accactcttt ggtctggcat gacctgtctc 720
acgtcaccat taaagaaagt gacagtgatg gtcttcccat ctgcactcac ttcttttoga 780
gttccattgg gaaacagtat aacacggcac ccattcttat aaaccttttc cacctttcca 840
tcaggatgac tgattttctc ctgtatgtct tggctctctc cctctctctt atattcagg 899

```

&lt;210&gt; 824

&lt;211&gt; 1980

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 824

```

accgctccgg ggccggccaa tttgcatatt tggaatgcgc cgctataaac ccggctgggg 60
ttttgcagcg atttcttaga tgtaaaaatg agatctcaat agcagcgggc tgggcacatc 120
ctcksmwytc ysskwskskm tstgcccrga gctgggtttcc gtctctcggc tcggggctgg 180
aactccggcc caacctaggg gcgcancgcg sacgagatgg cgcacttccg atcaatgtca 240
aagccgcggg ggagccggga accccagcat gattcttggc ctttgttcgc ttctgatact 300
aagagcagca cggtagatta tttcacttgt cccgtctccc ttcataacag aaaaagggga 360
ctcacctca agaagtgatt ggtatggtaa tttaaagcaa cgcgcattcg ctaggcctcg 420
cgagcgtcgc cgcgcggaga agccagctgt cccttggcag tgatttcgga aatgtgtcaa 480
ggcaattcca aaggtgaaaa cgcagccaac tggctcacgg caaagagtgg tcggaagaag 540
cgctgcccct acacgaagca ccagacactg gagctggaga aggagtttct gttcaatatg 600

```

taccttactc	gagagcggcg	cctagagatt	agccgcagcg	tccacctcac	ggacagacaa	660
gtgaaaatct	ggtttcagaa	cgcagatng	aaactgaaga	aaatgaatcg	agaaaaccgg	720
atccgggagc	tcacagccaa	ctttaatttt	tcctgatgaa	tctccaggcg	acgcgggtttt	780
ttcacttccc	gagcgtggt	ccccccctc	tgtcttcagg	ctctgccagg	aactcgcacc	840
tgtgctggag	ccctgttcct	ccctcccaca	ctcgccatct	cctgggccgt	tacatctgtg	900
cagggctggt	ttgttctgac	tttttgtttc	tttgtgtttg	cttggtgctg	gttwatttgt	960
tgttttctgg	gggaaaaagc	catatcatgc	taaaattcta	tagagataga	tattgtccta	1020
agtgtcaagt	cctgactggg	ctgggtttgc	tgtcttgggg	tccactgct	cgaatggcc	1080
cctgtcttcg	gccgagcntg	gtttcctgcc	cagcctgggg	caaacctagc	cgaaggccga	1140
ggtcccattg	ttggcgtga	ggtgtctggc	ctgaggtcaa	tggtgcaaag	gagccgccac	1200
cggcatgtct	gcctggagtg	ctgtgctgtg	tttaatcagg	ggatacaggc	ccctgggtttt	1260
cttttttctt	tcttcttttc	ttccttggcc	aagagaaggg	cttacaggca	tggacatgca	1320
ggttggcaaa	cgggcttgac	tttggctgat	ttaaaaagtg	agaaagaaa	taaaaaagg	1380
taatttttcc	ttcctctgta	agatatccca	gctttaaaaa	gaaaaaaaaa	aagaattacc	1440
aagagaaggg	gacttctctt	ccagtttctg	taaggtctta	cattgcctga	ctaaaatggt	1500
tcatttacct	ctaaatttcc	atatacttct	ggctgtagat	aaataatgta	gttttgttta	1560
tgcatttgga	attagtggat	ttttttgtca	ttaaaattgt	taccactggt	aacatgtgac	1620
aagcacacca	caattctccc	tatcttgtga	agttgttttt	ttaaactgcc	ttgaacaaaa	1680
agtttttttt	tttgtttgtt	tttgctttct	gaaattcaca	gaagcctagg	aggactgggg	1740
taagcggaat	aaactagaga	agggagacat	tgtttggatt	tccttcctat	aaatacaaat	1800
ctgtataaat	gtctattatt	atgaagaatt	gccaatcttg	ttttaagcaa	atgcattcta	1860
tcgttattat	aaatgttagt	tctagctcta	tttacttcta	atcttaaatc	agaataaatt	1920
aatattgtat	tgctgctgtg	cgtggaaaaa	gacgatgttt	atgttcttat	agaataaaag	1980

&lt;210&gt; 825

&lt;211&gt; 333

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 825

tctagatatt	gcccaatcgc	tgcccacagt	gcacatacct	ttccaccagt	cacatgtgag	60
agggcagatt	ttccaaatgc	tcataccac	ttggcactgt	gtggactata	attttggtcca	120
gttaggaaat	ggcatctcat	tgttttcac	ttaatttgcg	tcagcctgat	tactcattga	180
aacttgtgag	gttgagaaac	ttttcttaag	cttattggcc	attcaagttt	cctcctttat	240
gaaatggttg	ttcatgtcat	ttkctcattt	ttatattaga	ttgkwttmt	wttttccagc	300
tgacttgtag	gaactctaca	tcttatcaat	att			333

&lt;210&gt; 826

&lt;211&gt; 658

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 826

tttttttttt	tttttttttt	ttttgaaggc	ttcatgaata	atttattcca	tttgaagttt	60
tgttttttgt	ttttgttttt	ttttttttta	aaagtataaa	cctttttcatt	tcctcaatca	120
caatttgtac	aactcagtg	tatggcattc	ggcagcaata	gtgtttgttc	cttattctct	180
ttttgtcacg	ttaaaaaana	agcaattgga	ccatattaaa	tgtcactgct	aaacaacaac	240
tttaaaacgc	cccttcataa	agtgaacca	ctatttttag	agggttgatg	ctgacatgtc	300
cagtaatgac	gttacaattt	gtagcttaaa	ctcaataact	ttaagggtcca	catatccagt	360
ttactttgaa	aactaaagat	gttttaaaac	ttcatgaata	catcaacctg	aggagtattt	420
taggkcccaa	atccagtttt	taaattttata	ctccacnaaa	aangaaaata	catacataaa	480

```
awtttaaacc mcngttytgg gcccattwaa acaccmaaaa agaccccccn aaaagttaag      540
anttcagct tanttctgga ngggtgggnc aaaatarraw kktwtawwma wwwymytwwt      600
ccnkmattca gacaaactaa aatcttaaga ggaaaccag accaaaatat cactcatg      658
```

&lt;210&gt; 827

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 827

```
attatagaga ttaatctcct ttgctcgaag tctntttaaa tattagtac atctaaaaca      60
tacttttaca gcaacatcta gactggtggt tgaccaaaca actgggcatc atagctgaca      120
cataaaatta accatcacia ccatgttcta ggcaactgtc ctactgcct gagaagacac      180
cgttatgttt attagggttt ttgagtttta tccacagctt ttggttatct gcaaccatgt      240
ctcccaccat taacatagtt cacactgaga tgaggattcc ctatttaaca cttggtccca      300
acttcttcac agtccatctg gttttgtaga gggaacataa ctggacattc tggtcagggt      360
aggtgagggtc aggccttcag gacgctattt tctactgagtt gctttataag gcacattatg      420
caaaattcca tcagctcttc tgttcactac att                                453
```

&lt;210&gt; 828

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 828

```
aagagaagga cctagagatt gagaggctta agacgaagca aaaagaactg gaggccaaga      60
tggtggccca gaaggctgag gaaaaggaga accattgtcc cacaatgctc cggccccctt      120
cacatcgcac agtcacaggg gcaaagcccc tgaaaaaggc tgtggtgatg cccctacagc      180
taattcagga gcaggcagca tccccaaatg ccgagatcca catcctgaag aataaaggcc      240
ggaagagaaa gctggagtcc ctggatgccc tagagcctga ggagaaggct gaggactgct      300
gggagctaca gatcagcccc gagctactgg ctcatgggag ccaaaaaata ctggatctgc      360
tgaacgaagg ctacgcccga gatctccgca gtcttcagcg cattggcccc aagaaggccc      420
agctaactcg gggctggcgg gagctccacg gcccttccag ccagggtggag gacctggaac      480
gcggtggagg cataacgggg aaacagatgg agtcttccct gaaggcaaac atcctgggtc      540
tcgccgccgg ccagcgctgt ggcgcctcct gaccgtcgct tctcactcc gccttttcaa      600
atttttgtat aaccccggtg tgtgtaaata cagtttttgc tccggtaaaa aaaaaaa      657
```

&lt;210&gt; 829

&lt;211&gt; 775

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 829

```
ggtttgagaa aatcaattca aatctgnccc ttctgattgc anctctaacc aggttctgan      60
cgggtgcaga gacttcccaa tacatttccc ttctagnatg cctcataaat ccactcaaaa      120
gtaagacacc aaacacacac ctcatctcct gaactgtgac ttccaagctg acatttttct      180
gagaagcata attattggtt tcattgacaa ttaagttgaa tgtttcatca tcaaaaaata      240
attcaaaaag ctctactggg ttcaactttt cgctcttgag attcaaaagt ccagaatcca      300
gtgctgacca gcttgaaaaa ttgggtttta tgctcttttt ggtccaactc ttttctggga      360
aacatgatac cttaacttc ttttgagcag gctggatctc aggctcatta tctttttcca      420
catctgagtc accagagaat gagaggcctt ggagcagttc actcactoga gctttgtctt      480
```

tttttctccc	ttttcgggta	atgtctcctg	cagcatattc	cagggatgag	atgtgcatgc	540
gggcccacaa	atcacctggg	tgacggtcct	tcagagtgtt	caaagtgtgc	actgtccttt	600
cagtagcaat	aggagtacta	caaggaatct	ggggtgcaca	ctctctgttg	ggctttcctg	660
aggcttctcc	actttgttcc	atttcttcag	aagtttcttg	ctttgcttta	aacaatctat	720
ctttagttac	aatttcttca	gctgggtgta	gccccagctt	tttagaaggc	tgagg	775

&lt;210&gt; 830

&lt;211&gt; 413

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 830

agagcctgca	agtgacaaaag	gaagtgaggc	agaggcccac	atgccccac	cgttcacacc	60
ctacgtgcct	cggattctga	acggcttggc	ctcggagagg	acagcactgt	ctccgcagca	120
gcagcagcag	cagacctatg	gtgccatcca	caacatcagc	gggactatcc	ctggacagtg	180
cttggcgcak	agcsmcasgk	gcagtgtggc	ntgctgcccc	ccaggaggcc	tgaggctggg	240
tctcactgct	ctgaaaagac	acaaccagaa	tggcctgggg	ctcaggccct	tggtgagtgt	300
ggaatgcgtt	gggactgccc	agctgagcta	tcaggtgccc	atcttttctg	gtmccagcag	360
tggtgaggag	agcacaggca	ggcctcgccc	ctcccttgct	cancagttt	ccc	413

&lt;210&gt; 831

&lt;211&gt; 876

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 831

gctgacctac	agcagaagct	gctggatgca	gaaagtgaag	acagacaaa	acaacgctgg	60
gagaatattg	ccaccattct	ggaagccaag	tgtgccctga	aatatttgat	tggagagctg	120
gtctcctcca	aaatacaggt	cagcaaactt	gaaagcagcc	tgaaacagag	caagaccagc	180
tgtgnykaca	tgcakaagat	gctgtttgag	gaacgaaatc	attttgccga	gatagagaca	240
gagttacaag	ctgagctggg	cagaatggag	caacagcacc	aagagaagggt	gctgtacctt	300
ctcagccagc	tgcagcaaag	ccaaatggca	gagaagcagt	tagaggaatc	agtcagtga	360
aaggaacagc	agctgctgag	cacactgaag	tgtcaggatg	aagaacttga	gaaaatgcga	420
gaagtgtgtg	agcaaaatca	gcagcttctc	cgagagaatg	aatcatcaa	gcagaaaactg	480
accctcctcc	aggtagccag	cagacagaaa	catcttccta	aggataccct	tctatctcca	540
gactcttctt	ttgaatatgt	cccacctaag	ccaaaacctt	ctcgtgttaa	agaaaagtgc	600
ctggagcaaa	gcatggacat	cgaggatcta	aaatattgtt	cagagcattc	tgtgaatgag	660
catgaggatg	gtgatgggtg	tgatgatgag	ggggatgacg	aggaatggaa	gccaacaaaa	720
ttagttaagg	tgtccaggga	agaacatcca	aggggtgtcc	tgcaagggtc	gggtgtgggaa	780
ccangccagt	gtgggttcc	aggnaagcca	aaagtncaga	ctggtggtgt	tgactgtttg	840
ctgtgacccc	cacaaagttt	ncggaaccgc	ccacca			876

&lt;210&gt; 832

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 832

tagacataga	aaacatacag	taagaatatg	gtattataat	cttacggsam	mamygysrmm	60
trnsckkknw	rwmktkgwaa	agykgymyr	sgrcsyanra	mtanmmmtas	ctrgytrrky	120
mrywtwmma	tycctksccm	gggagtttga	aatttnatac	tatagaaata	acttttaggtt	180

ttaggtagag	ttaaagaggt	aaagcacatg	ttgnccacaa	nccaggaaa	gtatttttaa	240
gaaagattgg	attttcctac	cttttagagat	ctaaaaaaaa	tttaatatata	aaaatcattt	300
tgtgttggtg	tttattacta	gttcagatga	gtggctgctg	aaggggcccc	cttgtcattt	360
tcattataac	ccaatttcca	cttatttgaa	ctcttaagtc	ataaatgtat	aatgacttat	420
gaattagcac	agttaagttg	acactagaaa	ctgcccattt	ctgtattaca	ctatcaaata	480
ggaaacattg	gaaagatggg	gaaaaaaatc	ttatttttaa	atggccttaga	aagttttcag	540
attactttga	aaattctaaa	cttctttctg	tttccaaaac	ttgaaaatat	gtagatggac	600
tcatgcatta	agactgtttt	caaagctttc	ctcacatttt	taaagtgtga	ttttcctttt	660
aatatacata	tttattttcy	ttaaagcagc	tatatcccaa	cccatgactt	tgggrgatat	720
acccataaaa	ccmatataac	agcaggggta	ttggagcagc	tttctcaa		768

&lt;210&gt; 833

&lt;211&gt; 1604

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 833

aactagtata	tttacaacat	cagaaacttc	aatatggaga	tttgttggtc	ctatatcatg	60
atcttttagca	gcaactacac	cataggcact	gcacaacctg	ggtcctagat	caggacgtac	120
aaaaaatcct	ggcaaatgag	aggccaaatt	gaattttcct	tctggattac	aatattctgg	180
caatggcaga	ctttttaaaa	gatcttcgta	tcttgctggc	atcatagtct	tgaagtcctc	240
tcttgaaggc	caatctttca	attttaaaac	aactgtttct	ccactcttgt	ttttctgccg	300
ttttgaaact	tcttcaaaac	catcccagaa	ttccttaaca	ttggcatttg	aaatgatgct	360
atctttgcag	ttcaggagat	cagcttggtg	gtctccaaaa	tcaagactaa	ttgattccgc	420
cttccatagg	ctaattgttca	ttttcttatg	cacaccagaa	accactgcag	gctgtccttg	480
tttccaacat	tctttgaaaa	gcttccaatt	actgctatct	ttataatcct	taagccataa	540
aatatgcttc	tcacagatcc	aagaatgtgg	tatatcactg	tataatttat	tattttcatc	600
cactgcagat	attatgcttt	cttcaggctc	ttctttaagc	tctggtttta	catttatctt	660
ggagggttta	cttgggtgaa	ttttgttttc	aacaactgaa	gcaattatgt	catcaagaat	720
gttaggcata	gtccgtccac	ttttgctact	tggggctccc	attgaatata	ctggggcaaa	780
ggcaatgcc	gcatctgtas	acccacacag	tagctttcca	gctgtttag	tcagcaaata	840
ccgtaagggt	gagccttggt	cattattctg	ggacacaaga	ggtgatgttc	tgccatttgg	900
agattcagag	ttgtcttggt	ctctttcttc	tttaatttgg	ttttcaaggg	taagttcttt	960
gttttctttt	ttttctcttc	tggctttttg	ctctgcaaga	tctgctaacc	agtgcagtgg	1020
tgactgggat	tctggaggag	ttaacttggt	atctgtgcct	acatcactct	ctgggctgct	1080
gccaccattt	ttctcagact	tcggaggagt	attttgctgc	tgagactcag	gcatgcacag	1140
agaaatttta	ttactgtgat	taagaacatt	ctgtaaaact	tgagatacac	cattcattgt	1200
aggaaaattt	ccaacttgta	aattctggtt	gttagtataa	tgacaatggg	atttaatacc	1260
atatttttcc	ctaagagtgt	gcatggcatc	tagaagatct	gtcaaaacag	aaccagggtat	1320
aatttgggtt	ggcattaaat	gtttgtgata	atgaggctgt	ccyttcacac	acttcatcca	1380
agcatantag	ttctttatcy	ctagaactnc	tycctttcct	ttngccttgt	aacaatctaa	1440
gcaganccac	aawkccacat	tttkggcaga	cccagtnraw	kktaancawk	gntgcttcac	1500
atgcatcaca	catctcccgg	actcctctca	ctgctctttt	ccaggcaatt	ttggcatcct	1560
ttttcaccca	ggacaaagct	gttttttcag	atgttactaa	ttga		1604

&lt;210&gt; 834

&lt;211&gt; 617

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 834

```

gtccgtcagc tggtagcttt cattcgtaaa agagataaaa gagtgcaggc gcatcgaaaa    60
cttgtggaag aacagaatgc agagaaggcg aggaaagccg aagagatgag gcggcagcag    120
aagctaaagc aggccaaact ggtggagcag tacagagaac agagctggat gactatggcc    180
aatTTggaga aagagctcya ssangrtgrm srcrsgkkac gagaaggagt ttggagatgg    240
atcggatgaa aatgaaatgg aagaacatga actcaaagat gaggaggatg gtaaagacag    300
tgatgaggcc gaggacgctg agctctatga tgacctttac tgcccagcat gtgacaaatc    360
gttcaagaca gaaaaggcca tgaagaatca cgagaagtca aagaagcatc gggaaatggg    420
ggccttgcta aaacaacagc tggaggagga agaagaaaat ttttcaagac ctcaaattga    480
tgaaaatcca ttgatgaca attctgagga agaaatggaa gatgcaccaa aacaaaagct    540
ttctaaaaaa cagargaaaa agaacagaa accagcacag gatgtacctg gcaaatgttc    600
atatctgcct gcagctc                                     617

```

&lt;210&gt; 835

&lt;211&gt; 542

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 835

```

tttttttttt agaccaacat tctttaatca caaaggcact tgaggacccc tacaaaccca    60
aagtctctgc caagagtggc cctgcagacg cccacacctg caccctccat ccacccatcc    120
atccacacac tcagagttca tcgtgacctg cagagggctc cacactaggc ttgatgaaga    180
tgcccttccat ggccttccac gtattgtgcg tgttggcact gggcatgccg tggacctcat    240
gctgcccacg gatggggctt ccatactgct caccctgtac tgacaggaac acagaggtgc    300
ccacatgctn grarsgcaca gcagcctcac gctcccagnn gctgntccag agcagcgcac    360
tgtccatann gktccaggtc gtgcacctcg ccgtcttccc caaaggcact cacctcctgg    420
ttgttggaca gcggcgangg gaagtgggtg gtgtgcaggt tcnttgnccg taagcacatg    480
cgtgagcctc accgcctgcc cgcagcgcac cgcaaggggc caggcggagc cgacgctcgc    540
gc                                     542

```

&lt;210&gt; 836

&lt;211&gt; 542

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 836

```

tttttttttt agaccaacat tctttaatca caaaggcact tgaggacccc tacaaaccca    60
aagtctctgc caagagtggc cctgcagacg cccacacctg caccctccat ccacccatcc    120
atccacacac tcagagttca tcgtgacctg cagagggctc cacactaggc ttgatgaaga    180
tgcccttccat ggccttccac gtattgtgcg tgttggcact gggcatgccg tggacctcat    240
gctgcccacg gatggggctt ccatactgct caccctgtac tgacaggaac acagaggtgc    300
ccacatgctn grarsgcaca gcagcctcac gctcccagnn gctgntccag agcagcgcac    360
tgtccatann gktccaggtc gtgcacctcg ccgtcttccc caaaggcact cacctcctgg    420
ttgttggaca gcggcgangg gaagtgggtg gtgtgcaggt tcnttgnccg taagcacatg    480
cgtgagcctc accgcctgcc cgcagcgcac cgcaaggggc caggcggagc cgacgctcgc    540
gc                                     542

```

&lt;210&gt; 837

&lt;211&gt; 719

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens



&lt;400&gt; 837

aaaaggtccc	ccttctggga	aagaccgagt	gaagaaaggt	ggatcctaca	tgtgccatag	60
gtcttattgt	tacaggtatc	gctgtgctgc	tcggagccag	aacacacctg	atagctctgc	120
ttcgaatctg	grnttccgct	gtncagccga	ccgntgccc	actatngact	gacaaccaag	180
gaaagtcttc	cccantccaa	ggagcagtcg	tgtctgacct	acattgggct	tttctcagaa	240
ctttgaacga	tcccatgcaa	agaattccca	ccctgaggtg	tttnacatac	ctgcccattg	300
ncaaaaggac	cgccttgtga	gaccaaattg	ctgacctggg	tcagtgcattg	tgctttatgg	360
tgtggtgcat	ctttggagat	catcgccata	ttttactttt	gagagtcttt	aaagagggaag	420
gggagtgagg	ggaaccctga	gctaggcttc	aggaggcccg	cgtcctacgc	aggctctgca	480
caggggttag	accccaggctc	cgacgcttga	ccttcctggg	cctcaagtgc	cctcccttat	540
caaatgacag	ggatggacag	catgacctct	gggtgtctct	ccaactcacc	agttctaaaa	600
agggtatcag	attctattgt	gacttcataa	gtgagaattt	atgatagatt	attttttagc	660
tattttttcc	atgtgtgaac	cttgagtgat	actaatcatg	taaagtaaga	gttccctta	719

&lt;210&gt; 838

&lt;211&gt; 579

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 838

aagatatgca	gagatattec	aggatctttt	agctttgggtg	cggtctcctg	gagacagtgt	60
tattcgccaa	cagtgtgttg	aatatgtcac	atccattttg	cagtctctct	gtgatcagga	120
cattgcactt	atcttaccaa	gctcttctga	aggttctatt	tctganctgg	agcagctctc	180
caattctcta	ccaaataaag	aattgatgac	ctcaatctgt	gactgtctgt	tggtacgct	240
agctaactct	gagagcagtt	acaactgttt	actgacatgt	gtcagaacaa	tgatgtttct	300
tgcagagatg	attatggatt	atttcattta	aaaagttctt	taaggaaaaa	cagtagtgct	360
ctgcatagtt	tactgaaacg	agtggtcagc	acatttagta	aggacacagg	agagcttgca	420
tcttcatttt	tagaatttat	gagacaaatt	cttaactctg	acacaattgg	gatgctgtgg	480
gagatgataa	tgggtctcat	gggaagtagg	aggggagctc	atacatcacg	gacgatgagt	540
attaatgctg	cagagttaaa	ccagcttctt	ccaaggcaa			579

&lt;210&gt; 839

&lt;211&gt; 1172

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 839

aaccaaactt	cccaacttag	tgaaaacaag	gcattcaatg	acagaccagc	agcagaaact	60
gcntattacc	tcctaatacat	tttatgaaga	aatacctata	taaaaacaaa	cactaaagag	120
nacaaataga	tttaactaaa	gtgacaagca	taattataaa	taaataccag	attatcagat	180
tttaaacaat	aatctataac	agttttacta	tctaaggatt	ttcactccaa	gaagaaaaaa	240
tacatagtaa	cgccaagctt	gcaggacgat	gacttaacag	atacattttc	tcttaatgga	300
aacttatcta	gcttcagtaa	tattttctgga	tgtagcatca	agttgctggt	gcacattttt	360
aaaagactgg	tccagcagtg	tttcctcttc	atttaaagta	ttggcaatag	catcattaca	420
tggattgtcc	agaatgtctt	cgtttaatcc	atttgactcc	tccttttgat	cctcatcagt	480
attaacctct	tcaaccgtgt	gtgccctggg	tgtattcatt	aacatatcat	ttccyaggg	540
ctgactatta	ctcagcagct	tkgcctgcct	tctttccarg	gccagttgg	twattttcyc	600
caattctttg	ttgttgctct	tctgttaggc	ttctacttaa	ctcagaagca	aacatctcac	660
tttcagataa	gtttgtcaga	aagggatcta	attcagtaga	agtgacatca	tgttcattat	720
tctccgcaac	ttcatcatta	ttgctaacaa	aatcttcatg	taaaataggg	agatcaagtc	780
gaattecggtt	taaacaggtc	tgaacttcct	ttttacttcc	caggtattca	actctgtcaa	840

taaaatcctc	aaactgcagt	ttaggggaata	gcctatgtgc	ccagtgtctc	atgtgtctga	900
ttagcatcct	caagtcttca	gcctcatgac	ctttaccttt	gaatttttgc	ttatcaaata	960
catgccttaa	ggctggaagt	cctctctctg	aaattaatct	ctgagcatcc	agcttgggta	1020
tatttctttt	aactgttctc	tttggaggta	caggaacagg	tgctccattt	cctgactctt	1080
catcaggctc	agttccttca	ccatcttgtc	tctctggaga	ggctggaggt	gggaaaggag	1140
gaaaagtttc	atcttctaca	tgtctcataat	ct			1172

&lt;210&gt; 840

&lt;211&gt; 1145

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 840

cctcctactc	ccaaacaaat	ctttggggaa	aaaaaaacta	ccaactgtca	gccatgggcc	60
tgacggcgct	aagctctggg	gctccgtgca	ctgacgtggg	gccagccaca	gggaggcggg	120
gatsmrgymg	cgngassscm	ggakywkgrs	cwscwscsrs	gymrgkwgca	gnrgcrgygg	180
crhcrsganc	mrmagcagcn	tgmwgcagct	cawgcacctg	gagtcctttt	aygaaaaamc	240
yyctcctggg	cttatcaagg	aagatgagac	taagccagaa	gattgcatac	cagatgtacc	300
aggcaatgaa	cacgccaggg	aatttctggc	tcatgcacca	actaaaggac	tttggatgcc	360
actggggaaa	gaagtcaaag	ttatgcagtg	ttggcggtgc	aaacgctatg	gtcaccgaac	420
gggtgacaaa	gaatgccctt	tctttatcaa	aggcaaccac	aagtttagagc	agttcagagt	480
ggcacatgaa	gatcccatgt	atgacatcat	acgagacaa	aaacgacatg	aaaaggacgt	540
aaggatacag	cagttaaaac	agttactgga	ggatttctacc	tcagatgaag	ataggagcag	600
ctccmgttcc	tctgaaggta	aagagaaaac	caagaaaaag	aagaagaaag	aaaagcataa	660
gaaaaggaag	aaagaaaaga	aaaagaagaa	aaaacggaag	cacaaatctt	ccaagtcaaa	720
tgagggttct	gactcagagt	gacaaggatg	tgacttgttc	aacattctct	tctcaaacac	780
tgaccaagga	acagaggaag	atgcagtcag	agaaagcagc	aggatagaga	cgccgagaga	840
ggagtatatg	tgggttcacg	cagtgcagtc	ccacccgcct	tgagtggaag	atgtgacccc	900
aggagaggga	gtgtctcctt	ccagggtgcta	gctctggaca	gcagctgatt	ttaggcagga	960
aagtttcttc	atcgttgttc	tccttgctgg	tcacatgagt	ttacgattcc	tttgaagtgt	1020
ctcccacagg	gtggcaggac	tgggagaatc	tctgaggcgt	gtcttccagg	ccctcccaca	1080
gcttggtgcc	tccacagtgt	ggactcaggt	cccatagaca	tcaggctgga	gtcttctctg	1140
ttgtt						1145

&lt;210&gt; 841

&lt;211&gt; 642

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 841

ttttttataa	aaataaatat	ttattgccat	ttgaagcttt	atgtacacct	ttaaaagcac	60
atgtacaaat	gtgggaaatt	acaaaaatca	acctaaaacc	ctttttctca	aagtatacat	120
aaatgtacat	ccaagatcag	tggtgctacc	atcattagaa	taaaaaataa	gtctgtctgg	180
acataaacia	gcaatcattt	taagtgtcat	tcagatatcc	tcctttatat	ttaaaactcc	240
aaaaaatact	aagaggccca	atatatccag	aaaattgtgt	tttcaactta	ccctaaactta	300
tgaatagtgg	tatacaaata	tatttccatc	tttttgtcca	gccagcaa	gagagtctgt	360
acccgaccat	ttcacaaaag	accaatgttg	gtcagagaca	gskskgagrr	ksgymktasr	420
stkamysasa	akkarstsmm	amayrgsrmt	tnykcmasra	stcamkmtyk	ytgsyrcaasr	480
gwkrwctyws	rmswmwmmwk	msargmmcca	tttcagaata	ggctttgtga	cagactgaag	540
cttggttaaga	atcatcaatg	tgcatctttt	tcaggagttg	accagttttt	aaattccaaa	600
taacaatgtt	gttcataata	gtagtaccaa	gcagagcttc	tt		642

<210> 842  
 <211> 452  
 <212> DNA  
 <213> Homo sapiens

<400> 842  
 acggcctggt ggagcagctg tacgacctca ccctggagta cctgcacagc caggcacact 60  
 gcatcggctt cccggagctg gtgctgcctg tggtcctgca gctgaagtcg ttctccggg 120  
 agtgcaaggt ggccaactac tgccggcagg tgcagcagct gcttggaag gttcaggaga 180  
 actcggcata catctrcagc cgccgccaga gggtttcctt cggcgtctct gagcagcagg 240  
 cagtggaaac ctgggagaag ctgacccggg aagaggggac acccytgacc ttgtactaca 300  
 gccactggcg caantgcgtg accgggagat ccagctggag atcagtggca aagagcggct 360  
 ggaagacctg wacttccctg agatcaaacy aaggaagatg gctgacagga aggatgagga 420  
 caggwagcaa tttaaagacc tcttttgacc tg 452

<210> 843  
 <211> 805  
 <212> DNA  
 <213> Homo sapiens

<400> 843  
 ggcttataca acatagtggg gaacgcatgg gaatggactt cagactgggtg gactgttcat 60  
 cattctgttg aagaaacgct taacccaaaa ggtccccctt ctgggaaaga ccgagtgaag 120  
 aaaggtggat cctacatgtg ccataggtct tattgttaca ggtatcgtg tgctgtcgg 180  
 agccagaaca cacctgatag ctctgcttcg aatctggrnt tccgctgtnc agccgaccgn 240  
 ctgcccacta tngactgaca accaaggaaa gtcttcccca ntccaaggag cagtctgtc 300  
 tgacctacat tgggcttttc tcagaacttt gaacgatccc atgcaaagaa ttcccaccct 360  
 gaggtgtttt acatacctgc ccaatgncaa aggaaccgcc ttgtgagacc aaattgctga 420  
 cctgggtcag tgcatgtgct ttatgggtgtg gtgcatcttt ggagatcatc gccatatatt 480  
 acttttgaga gtctttaaag aggaagggga gtggagggaa ccctgagcta ggcttcagga 540  
 ggcccgctc ctacgcaggc tctgcacagg ggttagaccc cagggtccgac gcttgacctt 600  
 cctgggcctc aagtgcctc ccctatcaaa tgacagggat ggacagcatg acctctgggt 660  
 gtctctccaa ctaccagtt ctaaaaaggg tatcagattc tattgtgact tcataagtga 720  
 gaatttatga tagattattt tttagctatt ttttccatgt gtgaaccttg agtgatacta 780  
 atcatgtaaa gtaagagttc cctta 805

<210> 844  
 <211> 702  
 <212> DNA  
 <213> Homo sapiens

<400> 844  
 tttttttttt tttttttgca ggtgcatttg tttctttatt taaaaaatc atctgggggc 60  
 atggtctgag gaggacaccc ctcccatggc ttgggggagg acgcaggttc caggagtcac 120  
 agggcagaaa cacgcggggg ggggtggggg gtggccggag tggggagggg ctgtscagg 180  
 cacctggggg tggctcccac ggcaccaggt gggctagggc aacagtatgt acaggcgagc 240  
 agtgtcctcg gacccggctg gggccggctg gggccattt ctgcccagg ggagctctgg 300  
 ggcacagggt ctgagtccca tcttgggctk cagggaccgc gaggsctcc agggaggctg 360  
 gacagcgggg gcctttatct gggcccatca ggtggatgag aacggacact gcaaaccgct 420  
 caccacctgg gccagggcta ggctatccgg cagggcctcc cmmctgaat cctgctgctg 480  
 cagaactcaa gccggcatnc aggcagtkgg aacgnccgc angtgggct tggktgtsyck 540

crsgcacgtg	acaggtgggg	cccggtgcct	gataaacgga	caggaacaaa	aggaacgcaa	600
ggtctgggac	ccacggctct	gggagcagcg	ccaccaggc	tggctcctag	cagagaaatg	660
ggaatcgcaa	atgcattgca	atgtgcagtg	aagagacgcg	ag		702